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(54) Title: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR ANALYSIS OF GENE
EXPRESSION IN HUMAN BRAIN

(57) Abstract: A single exon nucleic acid microarray comprising a plurality of single exon nucleic acid probes for measuring gene
expression in a sample derived from human brain is described. Also described are single exon nucleic acid probes expressed in the
brain and their use in methods for detecting gene expression.

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HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL
FOR ANALYSIS OF GENE EXPRESSION IN HUMAN BRAIN

CROSS REFERENCE TO RELATED APPLICATIONS

5

The present application is a continuation-in-part of U.S.
patent application serial nos. 09/632,366, filed August 3,
2000 and 09/608,408, filed June 30, 2000; claims the
benefit under 35 U.S.C. s 119(e) of U.S. provisional patent
10 application serial nos. 60/236,359, filed September 27,
2000, 60/234,687, filed September 21, 2000, 60/207,456,
filed May 26, 2000, and 60/180,312, filed February 4, 2000;
and further claims the benefit under 35 U.S.C. s 119(a) of
UK patent application no. 0024263.6, filed October 4, 2000,
15 the disclosures of which are incorporated herein by
reference in their entireties.

REFERENCE TO SEQUENCE LISTING AND INCORPORATION BY
REFERENCE THEREOF

20

The present application includes a Sequence Listing in
electronic format, filed pursuant to PCT Administrative
Instructions 801 - 806 on a single CD-R disc, in
triplicate, containing a file named pto_BRAIN.txt, created
25 24 January 2001, having 25,840,972 bytes. The Sequence
Listing contained in said file on said disc is incorporated
herein by reference in its entirety.

Field of the Invention

30

The present invention relates to genome-derived
single exon microarrays useful for verifying the expression
of regions of genomic DNA predicted to encode protein. In
particular, the present invention relates to unique genome-
35 derived single exon nucleic acid probes expressed in human

brain and single exon nucleic acid microarrays that include such probes.

Background of the Invention

5 For almost two decades following the invention of general techniques for nucleic acid sequencing, Sanger et al., *Proc. Natl. Acad. Sci. USA* 70(4):1209-13 (1973); Gilbert et al., *Proc. Natl. Acad. Sci. USA* 70(12):3581-4 (1973), these techniques were used principally as tools to
10 further the understanding of proteins - known or suspected - about which a basic foundation of biological knowledge had already been built. In many cases, the cloning effort that preceded sequence identification had been both informed and directed by that antecedent
15 biological understanding.

For example, the cloning of the T cell receptor for antigen was predicated upon its known or suspected cell type-specific expression, by its suspected membrane association, and by the predicted assembly of its gene via
20 T cell-specific somatic recombination. Subsequent sequencing efforts at once confirmed and extended understanding of this family of proteins. Hedrick et al., *Nature* 308(5955):153-8 (1984).

More recently, however, the development of high
25 throughput sequencing methods and devices, in concert with large public and private undertakings to sequence the human and other genomes, has altered this investigational paradigm: today, sequence information often precedes understanding of the basic biology of the encoded protein
30 product.

One of the approaches to large-scale sequencing is predicated upon the proposition that expressed sequences - that is, those accessible through isolation of mRNA - are of greatest initial interest. This "expressed
35 sequence tag" ("EST") approach has already yielded vast

amounts of sequence data (see for example Adams et al.,
Science 252:1651 (1991); Williamson, *Drug Discov. Today*
4:115 (1999)). For nucleic acids sequenced by this
approach, often the only biological information that is
5 known *a priori* with any certainty is the likelihood of
biologic expression itself. By virtue of the species and
tissue from which the mRNA had originally been obtained,
most such sequences are also annotated with the identity of
the species and at least one tissue in which expression
10 appears likely.

More recently, the pace of genomic sequencing has
accelerated dramatically. When genomic DNA serves as the
initial substrate for sequencing efforts, expression cannot
be presumed; often the only *a priori* biological information
15 about the sequence includes the species and chromosome (and
perhaps chromosomal map location) of origin.

With the ever-accelerating pace of sequence
accumulation by directed, EST, and genomic sequencing
approaches – and in particular, with the accumulation of
20 sequence information from multiple genera, from multiple
species within genera, and from multiple individuals within
a species – there is an increasing need for methods that
rapidly and effectively permit the functions of nucleic
sequences to be elucidated. And as such functional
25 information accumulates, there is a further need for
methods of storing such functional information in
meaningful and useful relationship to the sequence itself;
that is, there is an increasing need for means and
apparatus for annotating raw sequence data with known or
30 predicted functional information.

Although the increase in the pace of genomic
sequencing is due in large part to technological changes in
sequencing strategies and instrumentation, Service, *Science*
280:995 (1998); Pennisi, *Science* 283: 1822-1823 (1999),
35 there is an important functional motivation as well.

While it was understood that the EST approach would rarely be able to yield sequence information about the noncoding portions of the genome, it now also appears the EST approach is capable of capturing only a fraction of
5 a genome's actual expression complexity.

For example, when the *C. elegans* genome was fully sequenced, gene prediction algorithms identified over 19,000 potential genes, of which only 7,000 had been found by EST sequencing. *C. elegans* Sequencing Consortium,
10 *Science* 282:2012 (1998). Analogously, the recently completed sequence of chromosome 2 of *Arabidopsis* predicts over 4000 genes, Lin et al., *Nature*, 402:761 (1999), of which only about 6% had previously been identified via EST sequencing efforts. Although the human genome has the
15 greatest depth of EST coverage, it is still woefully short of surrendering all of its genes. One recent estimate suggests that the human genome contains more than 146,000 genes, which would at this point leave greater than half of the genes undiscovered. It is now predicted that many
20 genes, perhaps 20 to 50%, will only be found by genomic sequencing.

There is, therefore, a need for methods that permit the functional regions of genomic sequence – and most importantly, but not exclusively, regions that
25 function to encode genes – to be identified.

Much of the coding sequence of the human genome is not homologous to known genes, making detection of open reading frames ("ORFs") and predictions of gene function difficult. Computational methods exist for predicting
30 coding regions in eukaryotic genomes. Gene prediction programs such as GRAIL and GRAIL II, Uberbacher et al., *Proc. Natl. Acad. Sci. USA* 88(24):11261-5 (1991); Xu et al., *Genet. Eng.* 16:241-53 (1994); Uberbacher et al., *Methods Enzymol.* 266:259-81 (1996); GENEFINDER, Solovyev et
35 al., *Nucl. Acids. Res.* 22:5156-63 (1994); Solovyev et al.,

Ismb 5:294-302 (1997); and GENESCAN, Burge et al., *J. Mol. Biol.* 268:78-94 (1997), predict many putative genes without known homology or function. Such programs are known, however, to give high false positive rates. Burset et al.,
5 *Genomics* 34:353-367 (1996). Using a consensus obtained by a plurality of such programs is known to increase the reliability of calling exons from genomic sequence. Ansari-Lari et al., *Genome Res.* 8(1):29-40 (1998)

Identification of functional genes from genomic
10 data remains, however, an imperfect art. For example, in reporting the full sequence of human chromosome 21, the Chromosome 21 Mapping and Sequencing Consortium reports that prior bioinformatic estimates of human gene number may need to be revised substantially downwards. *Nature*
15 405:311-199 (2000); Reeves, *Nature* 405:283-284 (2000).

Thus, there is a need for methods and apparatus that permit the functions of the regions identified bioinformatically - and specifically, that permit the expression of regions predicted to encode protein - readily
20 to be confirmed experimentally.

Recently, the development of nucleic acid microarrays has made possible the automated and highly parallel measurement of gene expression. Reviewed in Schena (ed.), DNA Microarrays : A Practical Approach
25 (Practical Approach Series), Oxford University Press (1999) (ISBN: 0199637768); *Nature Genet.* 21(1)(suppl):1 - 60 (1999); Schena (ed.), Microarray Biochip: Tools and Technology, Eaton Publishing Company/BioTechniques Books Division (2000) (ISBN: 1881299376).

30 It is common for microarrays to be derived from cDNA/EST libraries, either from those previously described in the literature, such as those from the I.M.A.G.E. consortium, Lennon et al., *Genomics* 33(1):151-2 (1996), or from the construction of "problem specific" libraries
35 targeted at a particular biological question, R.S. Thomas

et al., *Cancer Res.* (in press). Such microarrays by definition can measure expression only of those genes found in EST libraries, and thus have not been useful as probes for genes discovered solely by genomic sequencing.

5 The utility of using whole genome nucleic acid microarrays to answer certain biological questions has been demonstrated for the yeast *Saccharomyces cerevisiae*. De Risi et al., *Science* 278:680 (1997). The vast majority of yeast nuclear genes, approximately 95% however, are single
10 exon genes, i.e., lack introns, Lopez et al., *RNA* 5:1135-1137 (1999); Goffeau et al., *Science* 274:563-67 (1996), permitting coding regions more readily to be identified. Whole genome nucleic acid microarrays have not generally been used to probe gene expression from more complex
15 eukaryotic genomes, and in particular from those averaging more than one intron per gene.

 Diseases of the brain and nervous system are a significant cause of human morbidity and mortality. Increasingly, genetic factors are being found that
20 contribute to predisposition, onset, and/or aggressiveness of most, if not all, of these diseases. Although mutations in single genes have been identified as causative for some diseases of the brain and nervous system, for the most part these disorders are believed to have polygenic etiologies.
25 There is a need for methods and apparatus that permit prediction, diagnosis and prognosis of diseases of the brain and nervous system particularly those diseases with polygenic etiology.

30 Summary of the Invention

 The present invention solves these and other problems in the art by providing methods and apparatus for predicting, confirming, and displaying functional
35 information derived from genomic sequence. The present

invention also provides apparatus for verifying the expression of putative genes identified within genomic sequence.

In particular, the invention provides novel
5 genome-derived single exon nucleic acid microarrays useful for verifying the expression of putative genes identified within genomic sequence.

The present invention also provides compositions and kits for the ready production of nucleic acids
10 identical in sequence to, or substantially identical in sequence to, probes on the genome-derived single exon microarrays of the present invention.

Accordingly, in a first aspect of the invention, there is provided a spatially-addressable set of single
15 exon nucleic acid probes for measuring gene expression in a sample derived from human brain, comprising a plurality of single exon nucleic acid probes according to any one of the nucleotide sequences set out in SEQ ID NOs: 1 - 12,821 or a complementary sequence, or a portion of such a sequence.

20 By plurality is meant at least two, suitably at least 20, most suitably at least 100, preferably at least 1000 and, most preferably, upto 5000.

In one embodiment of the first aspect, each of said plurality of probes is separately and addressably
25 amplifiable.

In an alternative embodiment, each of said plurality of probes is separately and addressably isolatable from said plurality.

In a preferred embodiment, each of said plurality
30 of probes is amplifiable using at least one common primer. Preferably, each of said plurality of probes is amplifiable using a first and a second common primer.

In yet another embodiment, said set of single exon nucleic acid probes comprises between 50 - 20,000
35 probes, for example, 50 - 5000.

Suitably, said set of single exon nucleic acid probes comprises at least 50 - 1000 discrete single exon nucleic acid probes having a sequence as set out in any of SEQ ID NOS.: 1 - 25,434 or a complimentary sequence, or a
5 portion of such a sequence.

Preferably, the average length of the single exon nucleic acid probes is between 200 and 500 bp. It is preferred that the average length should be at least 200bp, suitably at least 250bp, most suitably at least 300bp,
10 preferably at least 400bp and, most preferably, 500 bp.

In another embodiment, the single exon nucleic acid probes lack prokaryotic and bacteriophage vector sequence. It is preferred that at least 50%, suitably at least 60%, most suitably at least 70%, preferably at least
15 75%, more preferably at least 80, 85, 90, 95 or 99% of said single exon nucleic acid probes lack prokaryotic and bacteriophage vector sequence.

In another preferred embodiment, said single exon nucleic acid lack homopolymeric stretches of A or T. It is
20 preferred that at least 50%, suitably at least 60%, most suitably at least 70%, preferably at least 75%, more preferably at least 80, 85, 90, 95 or 99% of said single exon nucleic acid probes lack homopolymeric stretches of A or T.

25 Preferably, a spatially-addressable set of single exon nucleic acid probes in accordance with the first aspect of the invention is addressably disposed upon a substrate.

Suitable substrates include a filter membrane
30 which may, preferably, be nitrocellulose or nylon. The nylon may preferably, be positively-charged. Other suitable substrates include glass, amorphous silicon, crystalline silicon, and plastic. Further suitable materials include polymethylacrylic, polyethylene, polypropylene,
35 polyacrylate, polymethylmethacrylate, polyvinylchloride,

polytetrafluoroethylene, polystyrene, polycarbonate, polyacetal, polysulfone, celluloseacetate, cellulosenitrate, nitrocellulose, and mixtures thereof.

In a second aspect of the invention, there is provided a microarray comprising a spatially addressable set of single exon nucleic acid probes in accordance with the first aspect of the invention.

In one embodiment, a genome-derived single-exon microarray is packaged together with such an ordered set of amplifiable probes corresponding to the probes, or one or more subsets of probes, thereon. In alternative embodiments, the ordered set of amplifiable probes is packaged separately from the genome-derived single exon microarray.

In another aspect, the invention provides genome-derived single exon nucleic acid probes useful for gene expression analysis, and particularly for gene expression analysis by microarray. In particular embodiments of this aspect, the present invention provides human single-exon probes that include specifically-hybridizable fragments of SEQ ID Nos. 12,822 - 25,434, wherein the fragment hybridizes at high stringency to an expressed human gene. In particular embodiments, the invention provides single exon probes comprising SEQ ID Nos. 1 - 12,821.

Accordingly, in a third aspect of the invention, there is provided a single exon nucleic acid probe for measuring human gene expression in a sample derived from human brain which is a nucleic acid molecule comprising a nucleotide sequence as set out in any of SEQ ID NOs.: 1 - 12,821 or a complementary sequence or a fragment thereof wherein said probe hybridizes at high stringency to a nucleic acid expressed in the human brain.

In one embodiment, a single exon nucleic acid probe in accordance with the third aspect comprises a nucleotide sequence as set out in any of SEQ ID NOs.:

12,822 - 25,434 or a complementary sequence or a fragment thereof.

In a fourth aspect of the invention, there is provided a single exon nucleic acid probe for measuring
5 human gene expression in a sample derived from human brain which is a nucleic acid molecule having a sequence encoding a peptide comprising a peptide sequence as set out in any of SEQ ID NOs.: 25,435 - 37,811 or a complementary sequence or a fragment thereof wherein said probe hybridizes at high
10 stringency to a nucleic acid expressed in the human brain.

Preferably, a single exon nucleic acid probe in accordance with the third or fourth aspects of the invention comprises between at least 15 and 50 contiguous nucleotides of said SEQ ID NO:. It is preferred that the
15 single exon nucleic acid probe comprises at least 15, suitably at least 20, more suitably at least 25 or preferably at least 50 contiguous nucleotides of said SEQ ID NO:.

In another preferred embodiment, a single exon
20 nucleic acid probe in accordance with the third or fourth aspects of the invention is between 3kb and 25kb in length. It is preferred that said probe is no more than 3kb, suitably no more than 5kb, more suitably no more than 10kb, preferably 15kb, more preferably 20kb or, most preferably,
25 no more than 20kb in length.

Preferably, a single exon nucleic acid probe in accordance with either the fifth or sixth aspect of the invention is DNA, preferably single-stranded DNA, RNA or PNA.

30 In another embodiment of either the third or fourth aspect of the invention, a single exon nucleic acid probe is detectably labeled. Suitable detectable labels include a radionuclide, a fluorescent label or a first member of a specific binding pair. Suitable fluorescent
35 labels include dyes such as cyanine dyes, preferably Cy3

and Cy5 although other suitable dyes will be known to those skilled in the art.

In a particularly preferred embodiment, a single exon nucleic acid probe in accordance with either the third or fourth aspect of the invention lacks prokaryotic and bacteriophage vector sequence. In yet another embodiment, a single exon nucleic acid probe in accordance with either the third or fourth aspect of the invention lacks homopolymeric stretches of A or T.

10 In a fifth aspect of the invention, there is provided an amplifiable nucleic acid composition, comprising:

the single exon nucleic acid probe in accordance with either of the third or fourth aspects of the invention; and at least one nucleic acid primer;

wherein said at least one primer is sufficient to prime enzymatic amplification of said probe.

In an sixth aspect of the invention, there is provided a method of measuring gene expression in a sample derived from human brain, comprising:

contacting the single exon microarray in accordance with the second aspect of the invention, with a first collection of detectably labeled nucleic acids, said first collection of nucleic acids derived from mRNA of human brain; and then

measuring the label detectably bound to each probe of said microarray.

In a seventh aspect of the invention, there is provided a method of identifying exons in a eukaryotic genome, comprising:

algorithmically predicting at least one exon from genomic sequence of said eukaryote; and then

detecting specific hybridization of detectably labeled nucleic acids to a single exon probe,

wherein said detectably labeled nucleic acids are

derived from mRNA from the brain of said eukaryote, said probe is a single exon probe having a fragment identical in sequence to, or complementary in sequence to, said predicted exon, said probe is included within a single exon
5 microarray in accordance with the first aspect of the invention, and said fragment is selectively hybridizable at high stringency.

In a eighth aspect of the invention, there is provided a method of assigning exons to a single gene,
10 comprising:

identifying a plurality of exons from genomic sequence in accordance with the seventh aspect of the invention; and then

measuring the expression of each of said exons in
15 a plurality of tissues and/or cell types using hybridization to single exon microarrays having a probe with said exon,

wherein a common pattern of expression of said exons in said plurality of tissues and/or cell types
20 indicates that the exons should be assigned to a single gene.

In an ninth aspect of the invention, there is provided a nucleic acid sequence as set out in any of SEQ ID NOS: 1 - 25,434 wherein said sequence encodes a peptide.

25 In a tenth aspect of the invention, there is provided a peptide encoded by a sequence comprising a sequence as set out in any of SEQ ID NOS: 12,822 - 25,434, or a complementary sequence or coding portion thereof.

In a preferred embodiment, a peptide may be
30 encoded by a sequence comprising a sequence set out in any of SEQ ID NOS.: 1 -12,821.

In a further aspect, the invention provides peptides comprising an amino acid sequence translated from the DNA fragments, said amino acid sequences comprising SEQ
35 ID NOS.: 25,435 - 37,811.

Accordingly in a eleventh aspect of the invention there is provided a peptide comprising a sequence as set out in any of SEQ ID NOs: 25,435 - 37,811, or fragment thereof.

5 In another aspect, the invention provides means for displaying annotated sequence, and in particular, for displaying sequence annotated according to the methods and apparatus of the present invention. Further, such display can be used as a preferred graphical user interface for
10 electronic search, query, and analysis of such annotated sequence.

Detailed Description of the Invention

Definitions

15 As used herein, the term "microarray" and phrase "nucleic acid microarray" refer to a substrate-bound collection of plural nucleic acids, hybridization to each
20 of the plurality of bound nucleic acids being separately detectable. The substrate can be solid or porous, planar or non-planar, unitary or distributed.

As so defined, the term "microarray" and phrase "nucleic acid microarray" include all the devices so called
25 in Schena (ed.), DNA Microarrays: A Practical Approach (Practical Approach Series), Oxford University Press (1999) (ISBN: 0199637768); *Nature Genet.* 21(1)(suppl):1 - 60 (1999); and Schena (ed.), Microarray Biochip: Tools and Technology, Eaton Publishing Company/BioTechniques Books
30 Division (2000) (ISBN: 1881299376). As so defined, the term "microarray" and phrase "nucleic acid microarray" further include substrate-bound collections of plural nucleic acids in which the nucleic acids are distributably disposed on a plurality of beads, rather than on a unitary
35 planar substrate, as is described, *inter alia*, in Brenner

et al., *Proc. Natl. Acad. Sci. USA* 97(4):166501670 (2000); in such case, the term "microarray" and phrase "nucleic acid microarray" refer to the plurality of beads in aggregate.

5 As used herein with respect to a nucleic acid microarray, the term "probe" refers to the nucleic acid that is, or is intended to be, bound to the substrate; in such context, the term "target" thus refers to nucleic acid intended to be bound thereto by Watson-Crick

10 complementarity. As used herein with respect to solution phase hybridization, the term "probe" refers to the nucleic acid of known sequence that is detectably labeled.

As used herein, the expression "probe comprising SEQ ID NO.", and variants thereof, intends a nucleic acid
15 probe, at least a portion of which probe has either (i) the sequence directly as given in the referenced SEQ ID NO., or (ii) a sequence complementary to the sequence as given in the referenced SEQ ID NO., the choice as between sequence directly as given and complement thereof dictated by the
20 requirement that the probe hybridize to mRNA.

As used herein, the term "open reading frame" and the equivalent acronym "ORF" refer to that portion of an exon that can be translated in its entirety into a sequence of contiguous amino acids i.e. a nucleic acid sequence
25 that, in at least one reading frame, does not possess stop codons; the term does not require that the ORF encode the entirety of a natural protein.

As used herein, the term "amplicon" refers to a PCR product amplified from human genomic DNA, containing
30 the predicted exon.

As used herein the term "exon" refers to the consensus prediction of the various exon and gene predicting algorithms i.e. a nucleic acid sequence bioinformatically predicted to encode a portion of a
35 natural protein.

As used herein, the term "peptide" refers to a sequence of amino acids. The sequences referred to as PEPTIDE SEQ ID NOS.: are the predicted peptide sequences that would be translated from one of the exons, or a portion thereof set out in exon SEQ ID NOS.:. The codons encoding the peptide are wholly contained within the exon.

As used herein, a "portions" of a defined nucleotide sequence or sequences can be and, preferably, are fragments unique to that sequence or to one or a combination of those sequences. A fragment unique to a nucleic acid molecule is one that is a signature for the larger nucleic acid molecule.

As used herein, the phrase "expression of a probe" and its linguistic variants means that the ORF present within the probe, or its complement, is present within a target mRNA.

As used herein, "stringent conditions" refers to parameters well known to those skilled in the art. When a nucleic acid molecule is said to be hybridisable to another of a given sequence under "stringent conditions" it is meant that it is homologous to the given sequence.

As used herein, the phrase "specific binding pair" intends a pair of molecules that bind to one another with high specificity. Binding pairs are said to exhibit specific binding when they exhibit avidity of at least 10^7 , preferably at least 10^8 , more preferably at least 10^9 liters/mole. Nonlimiting examples of specific binding pairs are: antibody and antigen; biotin and avidin; and biotin and streptavidin.

As used herein with respect to the visual display of annotated genomic sequence, the term "rectangle" means any geometric shape that has at least a first and a second border, wherein the first and second borders each are capable of mapping uniquely to a point of another visual object of the display.

As used herein, a "Mondrian" means a visual display in which a single genomic sequence is annotated with predicted and experimentally confirmed functional information.

5

Brief Description of the Drawings

The present invention is further illustrated with
10 reference to the following non-limiting figures and examples in which:

FIG. 1 illustrates a process for predicting functional regions from genomic sequence, confirming the functional activity of such regions experimentally, and
15 associating and displaying the data so obtained in meaningful and useful relationship to the original sequence data;

FIG. 2 further elaborates that portion of the process schematized in FIG. 1 for predicting functional
20 regions from genomic sequence;

FIG. 3 illustrates a Mondrian visual display;

FIG. 4 presents a Mondrian showing a hypothetical annotated genomic sequence;

FIG. 5 is a histogram showing the distribution of
25 ORF length and PCR products as obtained, with ORF length shown in black and PCR product length shown in dotted lines;

FIG. 6 is a histogram showing the distribution, among exons predicted according to the methods described,
30 of expression as measured using simultaneous two color hybridization to a genome-derived single exon microarray. The graph shows the number of sequence-verified products that were either not expressed ("0"), expressed in one or more but not all tested tissues ("1" - "9"), or expressed
35 in all tissues tested ("10");

FIG. 7 is a pictorial representation of the expression of verified sequences that showed expression with signal intensity greater than 3 in at least one tissue, with: FIG. 7A showing the expression as measured by microarray hybridization in each of the 10 measured tissues, and the expression as measured "bioinformatically" by query of EST, NR and SwissProt databases; with FIG. 7B showing the legend for display of physical expression (ratio) in FIG. 7A; and with FIG. 7C showing the legend for scoring EST hits as depicted in FIG. 7A;

FIG. 8 shows a comparison of normalized CY3 signal intensity for arrayed sequences that were identical to sequences in existing EST, NR and SwissProt databases or that were dissimilar (unknown), where black denotes the signal intensity for all sequence-verified products with a BLAST Expect ("E") value of greater than $1e^{-30}$ (1×10^{-30}) ("unknown") and a dotted line denotes sequence-verified spots with a BLAST expect ("E") value of less than $1e^{-30}$ (1×10^{-30}) ("known");

FIG. 9 presents a Mondrian of BAC AC008172 (bases 25,000 to 130,000), containing the carbamyl phosphate synthetase gene (AF154830.1); and

FIG. 10 is a Mondrian of BAC A049839.

25

Methods and Apparatus for Predicting, Confirming,
Annotating, and Displaying Functional Regions From Genomic
Sequence Data

FIG. 1 is a flow chart illustrating in broad outline a process for predicting functional regions from genomic sequence, confirming and characterizing the functional activity of such regions experimentally, and then associating and displaying the information so obtained in meaningful and useful relationship to the original

sequence data.

The initial input into process 10 of the present invention is drawn from one or more databases 100 containing genomic sequence data. Because genomic sequence
5 is usually obtained from subgenomic fragments, the sequence data typically will be stored in a series of records corresponding to these subgenomic sequenced fragments. Some fragments will have been catenated to form larger contiguous sequences ("contigs"); others will not. A
10 finite percentage of sequence data in the database will typically be erroneous, consisting *inter alia* of vector sequence, sequence created from aberrant cloning events, sequence of artificial polylinkers, and sequence that was erroneously read.

15 Each sequence record in database 100 will minimally contain as annotation a unique sequence identifier (accession number), and will typically be annotated further to identify the date of accession, species of origin, and depositor. Because database 100 can
20 contain nongenomic sequence, each sequence will typically be annotated further to permit query for genomic sequence. Chromosomal origin, optionally with map location, can also be present. Data can be, and over time increasingly will be, further annotated with additional information, in part
25 through use of the present invention, as described below. Annotation can be present within the data records, in information external to database 100 and linked to the records thereto, or through a combination of the two.

Databases useful as genomic sequence database 100
30 in the present invention include GenBank, and particularly include several divisions thereof, including the htgs(draft), NT (nucleotide, command line), and NR (nonredundant) divisions. GenBank is produced by the National Institutes of Health and is maintained by the
35 National Center for Biotechnology Information (NCBI).

Databases of genomic sequence from species other than human, such as mouse, rat, *Arabidopsis*, *C. elegans*, *C. briggsii*, *Drosophila*, zebra fish, and other higher eukaryotic organisms will also prove useful as genomic
5 sequence database 100.

Genomic sequence obtained by query of genomic sequence database 100 is then input into one or more processes 200 for identification of regions therein that are predicted to have a biological function as specified by
10 the user. Such functions include, but are not limited to, encoding protein, regulating transcription, regulating message transport after transcription into mRNA, regulating message splicing after transcription into mRNA, of regulating message degradation after transcription into
15 mRNA, and the like. Other functions include directing somatic recombination events, contributing to chromosomal stability or movement, contributing to allelic exclusion or X chromosome inactivation, and the like.

The particular genomic sequence to be input into
20 process 200 will depend upon the function for which relevant sequence is to be identified as well as upon the approach chosen for such identification. Process step 200 can be iterated to identify different functions within a given genomic region. In such case, the input often will
25 be different for the several iterations.

Sequences predicted to have the requisite function by process 200 are then input into process 300, where a subset of the input sequences suitable for experimental confirmation is identified. Experimental
30 confirmation can involve physical and/or bioinformatic assay. Where the subsequent experimental assay is bioinformatic, rather than physical, there are fewer constraints on the sequences that can be tested, and in this latter case therefore process 300 can output the
35 entirety of the input sequence.

The subset of sequences output from process 300 is then used in process 400 for experimental verification and characterization of the function predicted in process 200, which experimental verification can, and often will, include both physical and bioinformatic assay.

Process 500 annotates the sequence data with the functional information obtained in the physical and/or bioinformatic assays of process 400. Such annotation can be done using any technique that usefully relates the functional information to the sequence, as, for example, by incorporating the functional data into the sequence data record itself, by linking records in a hierarchical or relational database, by linking to external databases, by a combination thereof, or by other means well known within the database arts. The data can even be submitted for incorporation into databases maintained by others, such as GenBank, which is maintained by NCBI.

As further noted in FIG. 1, additional annotation can be input into process 500 from external sources 600.

The annotated data is then displayed in process 800, either before, concomitantly with, or after optional storage 700 on nontransient media, such as magnetic disk, optical disc, magnetooptical disk, flash memory, or the like.

FIG. 1 shows that the experimental data output from process 400 can be used in each preceding step of process 10: e.g., facilitating identification of functional sequences in process 200, facilitating identification of an experimentally suitable subset thereof in process 300, and facilitating creation of physical and/or informational substrates for, and performance of subsequent assay, of functional sequences in process 400.

Information from each step can be passed directly to the succeeding process, or stored in permanent or interim form prior to passage to the succeeding process.

Often, data will be stored after each, or at least a plurality, of such process steps. Any or all process steps can be automated.

FIG. 2 further elaborates the prediction of functional sequence within genomic sequence according to process 200.

Genomic sequence database 100 is first queried 20 for genomic sequence.

The sequence required to be returned by query 20 will depend, in the first instance, upon the function to be identified.

For example, genomic sequences that function to encode protein can be identified *inter alia* using gene prediction approaches, comparative sequence analysis approaches, or combinations of the two. In gene prediction analysis, sequence from one genome is input into process 200 where at least one, preferably a plurality, of algorithmic methods are applied to identify putative coding regions. In comparative sequence analysis, by contrast, corresponding, e.g., syntenic, sequence from a plurality of sources, typically a plurality of species, is input into process 200, where at least one, possibly a plurality, of algorithmic methods are applied to compare the sequences and identify regions of least variability.

The exact content of query 20 will also depend upon the database queried. For example, if the database contains both genomic and nongenomic sequence, perhaps derived from multiple species, and the function to be determined is protein coding regions in human genomic sequence, the query will accordingly require that the sequence returned be genomic and derived from humans.

Query 20 can also incorporate criteria that compel return of sequence that meets operative requirements of the subsequent analytical method. Alternatively, or in addition, such operative criteria can be enforced in

subsequent preprocess step 24.

For example, if the function sought to be identified is protein coding, query 20 can incorporate criteria that return from genomic sequence database 100 only those sequences present within contigs sufficiently long as to have obviated substantial fragmentation of any given exon among a plurality of separate sequence fragments.

Such criteria can, for example, consist of a required minimal individual genomic sequence fragment length, such as 10 kb, more typically 20 kb, 30 kb, 40kb, and preferably 50 kb or more, as well as an optional further or alternative requirement that sequence from any given clone, such as a bacterial artificial chromosome ("BAC"), be presented in no more than a finite maximal number of fragments, such as no more than 20 separate pieces, more typically no more than 15 fragments, even more typically no more than about 10 - 12 fragments.

Results using the present invention have shown that genomic sequence from bacterial artificial chromosomes (BACs) is sufficient for gene prediction analysis according to the present invention if the sequence is at least 50 kb in length, and if additionally the sequence from any given BAC is presented in fewer than 15, and preferably fewer than 10, fragments. Accordingly, query 20 can incorporate a requirement that data accessioned from BAC sequencing be in fewer than 15, preferably fewer than 10, fragments.

An additional criterion that can be incorporated into the query can be the date, or range of dates, of sequence accession. Although the process has been described above as if genomic sequence database 100 were static, it is of course understood that the genomic sequence databases need not be static, and indeed are typically updated on a frequent, even hourly, basis. Thus, as further described in Examples 1 and 2, *infra*, it is

possible to query the database for newly added sequence, either newly added after an absolute date, or newly added relative to a prior analysis performed using the methods and apparatus of the present invention. In this way, the
5 process herein described can incorporate a dynamic, temporal component.

One utility of such temporal limitation is to identify, from newly accessioned genomic sequence, the presence of novel genes, particularly those not previously
10 identified by EST sequencing (or other sequencing efforts that are similarly based upon gene expression). As further described in Example 1, such an approach has shown that newly accessioned human genomic sequence, when analyzed for sequences that function to encode protein, readily
15 identifies genes that are novel over those in existing EST and other expression databases. This makes the methods of the present invention extremely powerful gene discovery tools. And as would be appreciated, such gene discovery can be performed using genomic sequence from species other
20 than human.

If query 20 incorporates multiple criteria, such as above-described, the multiple criteria can be performed as a series of separate queries or as a single query, depending in part upon the query language, the complexity
25 of the query, and other considerations well known in the database arts.

If query 20 returns no genomic sequence meeting the query criteria, the negative result can be reported by process 22, and process 200 (and indeed, entire process 10)
30 ended 23, as shown. Alternatively, or in addition to report and termination of the initial inquiry, a new query 20 can be generated that takes into account the initial negative result.

When query 20 returns sequence meeting the query
35 criteria, the returned sequence is then passed to optional

preprocessing 24, suitable and specific for the desired analytical approach and the particular analytical methods thereof to be used in process 25.

Preprocessing 24 can include processes suitable
5 for many approaches and methods thereof, as well as processes specifically suited for the intended subsequent analysis.

Preprocessing 24 suitable for most approaches and methods will include elimination of sequence irrelevant to,
10 or that would interfere with, the subsequent analysis. Such sequence includes repetitive sequence, such as Alu repeats and LINE elements, vector sequence, artificial sequence, such as artificial polylinkers, and the like. Such removal can readily be performed by identification and
15 subsequent masking of the undesired sequence.

Identification can be effected by comparing the genomic sequence returned by query 20 with public or private databases containing known repetitive sequence, vector sequence, artificial sequence, and other artifactual
20 sequence. Such comparison can readily be done using programs well known in the art, such as CROSS_MATCH, or by proprietary sequence comparison programs the engineering of which is well within the skill in the art.

Alternatively, or in addition, undesirable,
25 including artifactual, sequence can be identified algorithmically without comparison to external databases and thereafter removed. For example, synthetic polylinker sequence can be identified by an algorithm that identifies a significantly higher than average density of known
30 restriction sites. As another example, vector sequence can be identified by algorithms that identify nucleotide or codon usage at variance with that of the bulk of the genomic sequence.

Once identified, undesired sequence can be
35 removed. Removal can usefully be done by masking the

undesired sequence as, for example, by converting the specific nucleotide references to one that is unrecognized by the subsequent bioinformatic algorithms, such as "X". Alternatively, but at present less preferred, the undesired
5 sequence can be excised from the returned genomic sequence, leaving gaps.

Preprocessing 24 can further include selection from among duplicative sequences of that one sequence of highest quality. Higher quality can be measured as a lower
10 percentage of, fewest number of, or least densely clustered occurrence of ambiguous nucleotides, defined as those nucleotides that are identified in the genomic sequence using symbols indicating ambiguity. Higher quality can also or alternatively be valued by presence in the longest
15 contig.

Preprocessing 24 can, and often will, also include formatting of the data as specifically appropriate for passage to the analytical algorithms of process 25. Such formatting can and typically will include, *inter alia*,
20 addition of a unique sequence identifier, either derived from the original accession number in genomic sequence database 100, or newly applied, and can further include additional annotation. Formatting can include conversion from one to another sequence listing standard, such as
25 conversion to or from FASTA or the like, depending upon the input expected by the subsequent process.

Preprocessing, which can be optional depending upon the function desired to be identified and the informational requirements of the methods for effecting
30 such identification, is followed by sequence processing 25, where sequences with the desired function are identified within the genomic sequence.

As mentioned above, such functions can include, but are not limited to, encoding protein, regulating
35 transcription, regulating message transport after

transcription into mRNA, regulating message splicing after transcription, of regulating message degradation, and the like. Other functions include directing somatic recombination events, contributing to chromosomal stability
5 or movement, contributing to allelic exclusion or X chromosome inactivation, or the like.

The methods of the present invention are particularly useful for gene discovery, that is, for identifying, from genomic sequence, regions that function
10 to encode genes, and in a particularly useful embodiment, for identifying regions that function to encode genes not hitherto identified by expression-based or directed cloning and sequencing. In conjunction with verification using the novel single exon microarrays of the present invention, as
15 further described below, the methods herein described become powerful gene discovery tools.

Accordingly, in a preferred embodiment of the present invention, process 25 is used to identify putative coding regions. Two preferred approaches in process 25 for
20 identifying sequence that encodes putative genes are gene prediction and comparative sequence analysis.

Gene prediction can be performed using any of a number of algorithmic methods, embodied in one or more software programs, that identify open reading frames (ORFs)
25 using a variety of heuristics, such as GRAIL, DICTION, and GENEFINDER. Comparative sequence analysis similarly can be performed using any of a variety of known programs that identify regions with lower sequence variability.

As further described in Example 1, below, gene
30 finding software programs yield a range of results. For the newly accessioned human genomic sequence input in Example 1, for example, GRAIL identified the greatest percentage of genomic sequence as putative coding region, 2% of the data analyzed; GENEFINDER was second, calling 1%;
35 and DICTION yielded the least putative coding region, with

0.8% of genomic sequence called as coding region.

Increased reliability can be obtained when consensus is required among several such methods. Although discussed herein particularly with respect to exon calling, 5 consensus among methods will in general increase reliability of predicting other functions as well.

Thus, as indicated by query 26, sequence processing 25, optionally with preprocessing 24, can be repeated with a different method, with consensus among such 10 iterations determined and reported in process 27.

Process 27 compares the several outputs for a given input genomic sequence and identifies consensus among the separately reported results. The consensus itself, as well as the sequence meeting that consensus, is then stored 15 in process 29a, displayed in process 29b, and/or output to process 300 for subsequent identification of a subset thereof suitable for assay.

Multiple levels of consensus can be calculated and reported by process 27. For example, as further 20 described in Example 1, *infra*, process 27 can report consensus as between all specific pairs of methods of gene prediction, as consensus among any one or more of the pairs of methods of gene prediction, or as among all of the gene prediction algorithms used. Thus, in Example 1, process 27 25 reported that GRAIL and GENEFINDER programs agreed on 0.7% of genomic sequence, that GRAIL and DICTION agreed on 0.5% of genomic sequence, and that the three programs together agreed on 0.25% of the data analyzed. Put another way, 0.25% of the genomic sequence was identified by all three 30 of the programs as containing putative coding region.

Furthermore, consensus can be required among different approaches to identifying a chosen function.

For example, if the function desired to be identified is coding of protein sequence, and a first used 35 approach to exon calling is gene prediction, the process

can be repeated on the same input sequence, or subset thereof, with another approach, such as comparative sequence analysis. In such a case, where comparative sequence analysis follows gene prediction, the comparison
5 can be performed not only on genomic nucleic acid sequence, but additionally or alternatively can be performed on the predicted amino acid sequence translated from the ORFs prior identified by the gene prediction approach.

Although shown as an iterative process, the
10 multiple analyses required to achieve consensus can be done in series, in parallel, or some combination thereof.

Predicted functional sequence, optionally representing a consensus among a plurality of methods and approaches for determination thereof, is passed to process
15 300 for identification of a subset thereof for functional assay.

In the preferred embodiment of the methods of the present invention, wherein the function sought to be identified is protein coding, process 300 is used to
20 identify a subset thereof suitable for experimental verification by physical and/or bioinformatic approaches.

For example, putative ORFs identified in process 200 can be classified, or binned, bioinformatically into putative genes. This binning can be based *inter alia* upon
25 consideration of the average number of exons/gene in the species chosen for analysis, upon density of exons that have been called on the genomic sequence, and other empirical rules. Thereafter, one or more among the gene-specific ORFs can be chosen for subsequent use in gene
30 expression assay.

Where such subsequent gene expression assay uses amplified nucleic acid, considerations such as desired amplicon length, primer synthesis requirements, putative exon length, sequence GC content, existence of possible
35 secondary structure, and the like can be used to identify

and select those ORFs that appear most likely successfully to amplify. Where subsequent gene expression assay relies upon nucleic acid hybridization, whether or not using amplified product, further considerations involving hybridization stringency can be applied to identify that subset of sequences that will most readily permit sequence-specific discrimination at a chosen hybridization and wash stringency. One particular such consideration is avoidance of putative exons that span repetitive sequence; such sequence can hybridize spuriously to nonspecific message, reducing specific signal in the hybridization.

For bioinformatic assay, there are fewer constraints on the sequences that can be tested experimentally, and in this latter case therefore process 300 can output the entirety of the input sequence.

The subset of sequences identified by process 300 as suitable for use in assay is then used in process 400 to create the physical and/or informational substrate for experimental verification of the predictions made in process 200, and thereafter to assay those substrates.

As mentioned, the methods of the present invention are particularly useful for identifying potential coding regions within genomic sequence. In a preferred embodiment of process 400, therefore, the expression of the sequences predicted to encode protein is verified. The combination of the predictive and experimental methods provides a powerful gene discovery engine.

Thus, in another aspect, the present invention provides methods and apparatus for verifying the expression of putative genes identified within genomic sequence. In particular, the invention provides a novel method of verifying gene expression in which expression of predicted ORFs is measured and confirmed using a novel type of nucleic acid microarray, the genome-derived single exon nucleic acid microarrays of the present invention.

Putative ORFs as predicted by a consensus of gene calling, particularly gene prediction, algorithms in process 200, and as further identified as suitable by process 300, are amplified from genomic DNA using the polymerase chain reaction (PCR). Although PCR is conveniently used, other amplification approaches can also be used.

Amplification schemes can be designed to capture the entirety of each predicted ORF in an amplicon with minimal additional (that is, intronic or intergenic) sequence. Because ORFs predicted from human genomic sequence using the methods of the present invention differ in length, such an approach results in amplicons of varying length.

However, most predicted ORFs are shorter than 500 bp in length, and although amplicons of at least about 100 or 200 base pairs can be immobilized as probes on nucleic acid microarrays, early experimental results using the methods of the present invention have suggested that longer amplicons, at least about 400 or 500 base pairs, are more effective. Furthermore, certain advantages derive from application to the microarray of amplicons of defined size.

Therefore, amplification schemes can alternatively, and preferably, be designed to amplify regions of defined size, preferably at least about 300, 400 or 500 bp, centered about each predicted ORF. Such an approach results in a population of amplicons of limited size diversity, but that typically contain intronic and/or intergenic nucleic acid in addition to putative ORF.

Conversely, somewhat fewer than 10% of ORFs predicted from human genomic sequence according to the methods of the present invention exceed 500 bp in length. Portions of such extended ORFs, preferably at least about 300, 400 or 500 bp in length, can be amplified. However, it has been discovered that the percentage success at

amplifying pieces of such ORFs is low, and that such putative exons are more effectively amplified when larger fragments, at least about 1000 or 1500 bp, and even as large as 2000 bp are amplified.

5 The putative ORFs selected in process 300 are thus input into one or more primer design programs, such as PRIMER3 (available online for use at <http://www-genome.wi.mit.edu/cgi-bin/primer/>), with a goal of amplifying at least about 500 base pairs of genomic
10 sequence centered within or about ORFs predicted to be no more than about 500 bp, or at least about 1000 - 1500 bp of genomic sequence for ORFs predicted to exceed 500 bp in length, and the primers synthesized by standard techniques. Primers with the requisite sequences can be purchased
15 commercially or synthesized by standard techniques.

Conveniently, a first predetermined sequence can be added commonly to the ORF-specific 5' primer and a second, typically different, predetermined sequence commonly added to each 3' ORF-unique primer. This serves
20 to immortalize the amplicon, that is, serves to permit further amplification of any amplicon using a single set of primers complementary respectively to the common 5' and common 3' sequence elements. The presence of these "universal" priming sequences further facilitates later
25 sequence verification, providing a sequence common to all amplicons at which to prime sequencing reactions. The common 5' and 3' sequences further serve to add a cloning site should any of the ORFs warrant further study.

Such predetermined sequence is usefully at least
30 about 10, 12 or 15 nt in length, and usually does not exceed about 25 nt in length. The "universal" priming sequences used in the examples presented *infra* were each 16 nt long.

The genomic DNA to be used as substrate for
35 amplification will come from the eukaryotic species from

which the genomic sequence data had originally been obtained, or a closely related species, and can conveniently be prepared by well known techniques from somatic or germline tissue or cultured cells of the organism. See, e.g., Short Protocols in Molecular Biology : A Compendium of Methods from Current Protocols in Molecular Biology, Ausubel et al. (eds.), 4th edition (April 1999), John Wiley & Sons (ISBN: 047132938X) and Maniatis et al., Molecular Cloning : A Laboratory Manual, 2nd edition (December 1989), Cold Spring Harbor Laboratory Press (ISBN: 0879693096). Many such prepared genomic DNAs are available commercially, with the human genomic DNAs additionally having certification of donor informed consent.

Although the intronic and intergenic material flanking putative coding regions in the amplicons could potentially interfere with hybridizations during microarray experiments, we have found, surprisingly, that differential expression ratios are not significantly affected. Rather, the predominant effect of exon size is to alter the absolute signal intensity, rather than its ratio. Equally surprising, the art had suggested that single exon probes would not provide sufficient signal intensity for high stringency hybridization analyses; we find that such probes not only provide adequate signal, but have substantial advantages, as herein described.

After partial purification, as by size exclusion spin column, with or without confirmation as to amplicon quality as by gel electrophoresis, each amplicon (single exon probe) is disposed in an array upon a support substrate.

Methods for creating microarrays by deposition and fixation of nucleic acids onto support substrates are well known in the art (Reviewed by Schena et al., see above).

Typically, the support substrate will be glass, although other materials, such as amorphous or crystalline silicon or plastics. Such plastics include polymethylacrylic, polyethylene, polypropylene, polyacrylate, polymethylmethacrylate, polyvinylchloride, polytetrafluoroethylene, polystyrene, polycarbonate, polyacetal, polysulfone, celluloseacetate, cellulosenitrate, nitrocellulose, or mixtures thereof, can also be used. Typically, the support will be rectangular, although other shapes, particularly circular disks and even spheres, present certain advantages. Particularly advantageous alternatives to glass slides as support substrates for array of nucleic acids are optical discs, as described in WO 98/12559.

The amplified nucleic acids can be attached covalently to a surface of the support substrate or, more typically, applied to a derivatized surface in a chaotropic agent that facilitates denaturation and adherence by presumed noncovalent interactions, or some combination thereof.

Robotic spotting devices useful for arraying nucleic acids on support substrates can be constructed using public domain specifications (The MGuide, version 2.0, <http://cmgm.stanford.edu/pbrown/mguide/index.html>), or can conveniently be purchased from commercial sources (MicroArray GenII Spotter and MicroArray GenIII Spotter, Molecular Dynamics, Inc., Sunnyvale, CA). Spotting can also be effected by printing methods, including those using ink jet technology.

As is well known in the art, microarrays typically also contain immobilized control nucleic acids. For controls useful in providing measurements of background signal for the genome-derived single exon microarrays of the present invention, a plurality of *E. coli* genes can readily be used. As further described in Example 1, 16 or

32 *E. coli* genes suffice to provide a robust measure of background noise in such microarrays.

As is well known in the art, the amplified product disposed in arrays on a support substrate to create
5 a nucleic acid microarray can consist entirely of natural nucleotides linked by phosphodiester bonds, or alternatively can include either nonnative nucleotides, alternative internucleotide linkages, or both, so long as complementary binding can be obtained in the hybridization.
10 If enzymatic amplification is used to produce the immobilized probes, the amplifying enzyme will impose certain further constraints upon the types of nucleic acid analogs that can be generated.

Although particularly described herein as using
15 high density microarrays constructed on planar substrates, the methods of the present invention for confirming the expression of ORFs predicted from genomic sequence can use any of the known types of microarrays, as herein defined, including lower density planar arrays, and microarrays on
20 nonplanar, nonunitary, distributed substrates.

For example, gene expression can be confirmed using hybridization to lower density arrays, such as those constructed on membranes, such as nitrocellulose, nylon, and positively-charged derivatized nylon membranes.
25 Further, gene expression can also be confirmed using nonplanar, bead-based microarrays such as are described in Brenner et al., *Proc. Natl. Acad. Sci. USA* 97(4):166501670 (2000); U.S. Patent No. 6,057,107; and U.S. Patent No. 5,736,330. In theory, a packed collection of such beads
30 provides in aggregate a higher density of nucleic acid probe than can be achieved with spotting or lithography techniques on a single planar substrate.

Planar microarrays on solid substrates, however, provide certain useful advantages, including high
35 throughput and compatibility with existing readers. For

example, each standard microscope slide can include at least 1000, typically at least 2000, preferably 5000 and upto 10,000 - 50,000 or more nucleic acid probes of discrete sequence. The number of sequences deposited will
5 depend on their required application.

Each putative gene can be represented in the array by a single predicted ORF. Alternatively, genes can be represented by more than one predicted ORF. For purposes of measuring differential splicing, more than one
10 predicted ORF will be provided for a putative gene. And as is well known in the art, each probe of defined sequence, representing a single predicted ORF, can be deposited in a plurality of locations on a single microarray to provide redundancy of signal.

15 The genome-derived single exon microarrays described above differ in several fundamental and advantageous ways from microarrays presently used in the gene expression art, including (1) those created by deposition of mRNA-derived nucleic acids, (2) those created
20 by *in situ* synthesis of oligonucleotide probes, and (3) those constructed from yeast genomic DNA.

Most nucleic acid microarrays that are in use for study of eukaryotic gene expression have as immobilized probes nucleic acids that are derived - either directly or
25 indirectly - from expressed message. As discussed above, it is common, for example, for such microarrays to be derived from cDNA/EST libraries, either from those previously described in the literature, see Lennon *et al.*,
or from the *de novo* construction of "problem specific"
30 libraries targeted at a particular biological question, R.S. Thomas *et al.*, *Cancer Res.* (in press). Such microarrays are herein collectively denominated "EST microarrays".

Such EST microarrays by definition can measure
35 expression only of those genes found in EST libraries,

shown herein to represent only a fraction of expressed genes. Furthermore, such libraries – and thus microarrays based thereupon – are biased by the tissue or cell type of message origin, by the expression levels of the respective
5 genes within the tissues, and by the ability of the message successfully to have been reverse-transcribed and cloned.

Thus, as further discussed in Example 1, the methods of the present invention enable sequences that do not appear in EST or other expression databases to be
10 determined – subsequently arrayed for expression measurements could not, therefore, have been represented as probes on an EST microarray. And as further demonstrated in the examples, *infra*, the remaining population of genes identified from genomic sequence by the methods of the
15 present invention – that is, the one third of sequences that had previously been accessioned in EST or other expression databases – are biased toward genes with higher expression levels.

Representation of a message in an EST and/or cDNA
20 library depends upon the successful reverse transcription, optionally but typically with subsequent successful cloning, of the message. This introduces substantial bias into the population of probes available for arraying in EST microarrays..

25 In contrast, neither reverse transcription nor cloning is required to produce the probes arrayed on the genome-derived single exon microarrays of the present invention. And although the ultimate deposition of a probe on the genome-derived single exon microarray of the present
30 invention depends upon a successful amplification from genomic material, *a priori* knowledge of the sequence of the desired amplicon affords greater opportunity to recover any given probe sequence recalcitrant to amplification than is afforded by the requirement for successful reverse
35 transcription and cloning of unknown message in EST

approaches.

Thus, the genome-derived single exon microarrays of the present invention present a far greater diversity of probes for measuring gene expression, with far less bias, 5 than do EST microarrays presently used in the art.

As a further consequence of their ultimate origin from expressed message, the probes in EST microarrays often contain poly-A (or complementary poly-T) stretches derived from the poly-A tail of mature mRNA. These homopolymeric 10 stretches contribute to cross-hybridization, that is, to a spurious signal occasioned by hybridization to the homopolymeric tail of a labeled cDNA that lacks sequence homology to the gene-specific portion of the probe.

In contrast, the probes arrayed in the genome- 15 derived single exon microarrays of the present invention lack homopolymeric stretches derived from message polyadenylation, and thus can provide more specific signal. Typically, at least about 50, 60 or 75% of the probes on the genome-derived single exon microarrays of the present 20 invention lack homopolymeric regions consisting of A or T, where a homopolymeric region is defined for purposes herein as stretches of 25 or more, typically 30 or more, identical nucleotides.

A further distinction, which also affects the 25 specificity of hybridization, is occasioned by the typical derivation of EST microarray probes from cloned material. Because much of the probe material disposed as probes on EST microarrays is excised or amplified from plasmid, phage, or phagemid vectors, EST microarrays typically 30 include a fair amount of vector sequence, more so when the probes are amplified, rather than excised, from the vector.

In contrast, the vast majority of probes in the genome-derived single exon microarrays of the present invention contain no prokaryotic or bacteriophage vector 35 sequence, having been amplified directly or indirectly from

genomic DNA. Typically, therefore, at least about 50, 60, 70 or 80% or more of individual exon-including probes disposed on a genome-derived single exon microarray of the present invention lack vector sequence, and particularly
5 lack sequences drawn from plasmids and bacteriophage. Preferably, at least about 85, 90 or more than 90% of exon-including probes in the genome-derived single exon microarray of the present invention lack vector sequence. With attention to removal of vector sequences through
10 preprocessing 24, percentages of vector-free exon-including probes can be as high as 95 - 99%. The substantial absence of vector sequence from the genome-derived single exon microarrays of the present invention results in greater specificity during hybridization, since spurious cross-
15 hybridization to a probe vector sequence is reduced.

As a further consequence of excision or amplification of probes from vectors in construction of EST microarrays, the probes arrayed thereon often contain artificial sequence, derived from vector polylinker
20 multiple cloning sites, at both 5' and 3' ends. The probes disposed upon the genome-derived single exon microarrays need have no such artificial sequence appended thereto.

As mentioned above, however, the ORF-specific primers used to amplify putative ORFs can include
25 artificial sequences, typically 5' to the ORF-specific primer sequence, useful for "universal" (that is, independent of ORF sequence) priming of subsequent amplification or sequencing reactions. When such
"universal" 5' and/or 3' priming sequences are appended to
30 the amplification primers, the probes disposed upon the genome-derived single exon microarray will include artificial sequence similar to that found in EST microarrays. However, the genome-derived single exon microarray of the present invention can be made without
35 such sequences, and if so constructed, presents an even

smaller amount of nonspecific sequence that would contribute to nonspecific hybridization.

Yet another consequence of typical use of cloned material as probes in EST microarrays is that such
5 microarrays contain probes that result from cloning artifacts, such as chimeric molecules containing coding region of two separate genes. Derived from genomic material, typically not thereafter cloned, the probes of the genome-derived single exon microarrays of the present
10 invention lack such cloning artifacts, and thus provide greater specificity of signal in gene expression measurements.

A further consequence of the cloned origin of probes on many EST microarrays is that the individual
15 probes often have disparate sizes, which can cause the optimal hybridization stringency to vary among probes on a single microarray. In contrast, as discussed above, the probes arrayed on the genome-derived single exon microarrays of the present invention can readily be
20 designed to have a narrow distribution in sizes, with the range of probe sizes no greater than about 10% of the average size, typically no greater than about 5% of the average probe size.

Because of their origin from fully- or partially-
25 spliced message, probes disposed upon EST arrays will often include multiple exons. The percentage of such exon-spanning probes in an EST microarray can be calculated, on average, based upon the predicted number of exons/gene for the given species and the average length of the immobilized
30 probes. For human genes, the near-complete sequence of human chromosome 22, Dunham et al., *Nature* 402(6761):489-95 (1999), predicts that human genes average 5.5 exons/gene. Even with probes of 200 - 500 bp, the vast majority of human EST microarray probes include more than one exon.

35 In contrast, by virtue of their origin from

algorithmically identified ORFs in genomic sequence, the probes in the genome-derived single exon microarrays of the present invention can consist of individual exons. Thus, in contrast to EST microarrays, at least about 50, 60, 70, 5 75, 80, 85, 95 or 99% of probes deposited in the genome-derived microarray of the present invention consist of, or include, no more than one predicted ORF.

This provides the ability, not readily achieved using EST microarrays, to use the genome-derived single 10 exon microarrays of the present invention to measure tissue-specific expression of individual exons, which in turn allows differential splicing events to be detected and characterized, and in particular, allows the correlation of differential splicing to tissue-specific expression 15 patterns.

Furthermore, the exons that are represented in EST microarrays are often biased toward the 3' or 5' end of their respective genes, since sequencing strategies used for EST identification are so biased. In contrast, no such 20 3' or 5' bias necessarily inheres in the selection of exons for disposition on the genome-derived single exon microarrays of the present invention.

Conversely, the probes provided on the genome-derived single exon microarrays of the present invention 25 typically, but need not necessarily, include intronic and/or intergenic sequence that is absent from EST microarrays, which are derived from mature mRNA. Typically, at least about 50, 60, 70, 80 or 90% of the exon-including probes on the genome-derived single exon 30 microarrays of the present invention include sequence drawn from noncoding regions. As discussed above, the additional presence of noncoding region does not significantly interfere with measurement of gene expression, and provides the additional opportunity to assay prespliced RNA, and 35 thus measure such phenomena such as nuclear export control.

The genome-derived single exon microarrays of the present invention are also quite different from *in situ* synthesis microarrays, where probe size is severely constrained by inadequacies in the photolithographic
5 synthesis process.

Typically, probes arrayed on *in situ* synthesis microarrays are limited to a maximum of about 25 bp. As a well known consequence, hybridization to such chips must be performed at low stringency. In order, therefore, to
10 achieve unambiguous sequence-specific hybridization results, the *in situ* synthesis microarray requires substantial redundancy, with concomitant programmed arraying for each probe of probe analogues with altered (*i.e.*, mismatched) sequence.

15 In contrast, the longer probe length of the genome-derived single exon microarrays of the present invention allows much higher stringency hybridization and wash. Typically, therefore, exon-including probes on the genome-derived single exon microarrays of the present
20 invention average at least about 100, 200, 300, 400 or 500 bp in length. By obviating the need for substantial probe redundancy, this approach permits a higher density of probes for discrete exons or genes to be arrayed on the microarrays of the present invention than can be achieved
25 for *in situ* synthesis microarrays.

A further distinction is that the probes in *in situ* synthesis microarrays typically are covalently linked to the substrate surface. In contrast, the probes disposed on the genome-derived microarray of the present invention
30 typically are, but need not necessarily be, bound noncovalently to the substrate.

Furthermore, the short probe size on *in situ* microarrays causes large percentage differences in the melting temperature of probes hybridized to their
35 complementary target sequence, and thus causes large

percentage differences in the theoretically optimum stringency across the array as a whole.

In contrast, the larger probe size in the microarrays of the present invention create lower percentage differences in melting temperature across the range of arrayed probes.

A further significant advantage of the microarrays of the present invention over *in situ* synthesized arrays is that the quality of each individual probe can be confirmed before deposition. In contrast, the quality of probes cannot be assessed on a probe-by-probe basis for the *in situ* synthesized microarrays presently being used.

The genome-derived single exon microarrays of the present invention are also distinguished over, and present substantial benefits over, the genome-derived microarrays from lower eukaryotes such as yeast. Lashkari et al., *Proc. Natl. Acad. Sci. USA* 94:13057-13062 (1997).

Only about 220 - 250 of the 6100 or so nuclear genes in *Saccharomyces cerevisiae* - that is, only about 4 - 5% - have standard, spliceosomal, introns, Lopez et al., *Nucl. Acids Res.* 28:85-86 (2000); Spingola et al., *RNA* 5(2):221-34 (1999). Furthermore, the entire yeast genome has already been sequenced. These two facts permit the ready amplification and disposition of single-ORF amplicons on such microarray without the requirement for antecedent use of gene prediction and/or comparative sequence analyses.

Thus, a significant aspect of the present invention is the ability to identify and to confirm expression of predicted coding regions in genomic sequence drawn from eukaryotic organisms that have a higher percentage of genes having introns than do yeast such as *Saccharomyces cerevisiae*, particularly in genomic sequence drawn from eukaryotes in which at least about 10, 20 or 50%

of protein-encoding genes have introns. In preferred embodiments, the methods and apparatus of the present invention are used to identify and confirm expression of novel genes from genomic sequence of eukaryotes in which
5 the average number of introns per gene is at least about one, two or three or more.

After the physical substrate is prepared, experimental verification of predicted function is performed.

10 In a preferred embodiment of the present invention, where the function sought to be identified in genomic sequence is protein coding, experimental verification is performed by measuring expression of the putative ORFs, typically through nucleic acid hybridization
15 experiments, and in particularly preferred embodiments, through hybridization to genome-derived single exon microarrays prepared as above- described.

Expression is conveniently measured and expressed for each probe in the microarray as a ratio of the
20 expression measured concurrently in a plurality of mRNA sources, according to techniques well known in the microarray art, Reviewed in Schena et al., and as further described in Example 2, below. The mRNA source for the reference against which specific expression is measured can
25 be drawn from a homogeneous mRNA source, such as a single cultured cell-type, or alternatively can be heterogeneous, as from a pool of mRNA derived from multiple tissues and/or cell types, as further described in Example 2, *infra*.

mRNA can be prepared by standard techniques, see
30 Ausubel et al. and Maniatis et al., or purchased commercially. The mRNA is then typically reverse-transcribed in the presence of labeled nucleotides: the index source (that in which expression is desired to be measured) is reverse transcribed in the presence of
35 nucleotides labeled with a first label, typically a

fluorophore (fluorochrome; fluor; fluorescent dye); the reference source is reverse transcribed in the presence of a second label, typically a fluorophore, typically fluorometrically-distinguishable from the first label. As
5 further described in Example 2, *infra*, Cy3 and Cy5 dyes prove particularly useful in these methods. After partial purification of the index and reference targets, hybridization to the probe array is conducted according to standard techniques, typically under a coverslip.

10 After wash, microarrays are conveniently scanned using a commercial microarray scanning device, such as a Gen3 Scanner (Molecular Dynamics, Sunnyvale, CA). Data on expression is then passed, with or without interim storage, to process 500, where the results for each probe are
15 related to the original sequence.

Often, hybridization of target material to the genome-derived single exon microarray will identify certain of the probes thereon as of particular interest. Thus, it is often desirable that the user be able readily to obtain
20 sufficient quantities of an individual probe, either for subsequent arrayed deposition upon an additional support substrate, often as part of a microarray having a plurality of probes so identified, or alternatively or additionally as a solitary solid-phase or solution-phase probe, for
25 further use.

Thus, in another aspect, the present invention provides compositions and kits for the ready production of nucleic acids identical in sequence to, or substantially identical in sequence to, probes on the genome-derived
30 single exon microarrays of the present invention.

In this aspect, a small quantity of each probe is disposed, typically without attachment to substrate, in a spatially-addressable ordered set, typically one per well of a microtiter dish. Although a 96 well microtiter plate
35 can be used, greater efficiency is obtained using higher

density arrays, such as are provided by microtiter plates having 384, 864, 1536, 3456, 6144, or 9600 wells, and although microtiter plates having physical depressions (wells) are conveniently used, any device that permits
5 addressable withdrawal of reagent from fluidly-noncommunicating areas can be used.

In this aspect of the invention, therefore, a fluidly noncommunicating addressable ordered set of individual probes, corresponding to those on a genome-
10 derived single exon microarray, is provided, with each probe in sufficient quantity to permit amplification, such as by PCR. As earlier mentioned, the ORF-specific 5' primers used for genomic amplification can have a first common sequence added thereto, and the ORF-specific 3'
15 primers used for genomic amplification can have a second, different, common sequence added thereto, thus permitting, in this preferred embodiment, the use of a single set of 5' and 3' primers to amplify any one of the probes from the amplifiable ordered set.

20 Each discrete amplifiable probe can also be packaged with amplification primers, solutes, buffers, etc., and can be provided in dry (e.g., lyophilized) form or wet, in the latter case typically with addition of agents that retard evaporation.

25 In another aspect of the present invention, a genome-derived single-exon microarray is packaged together with such an ordered set of amplifiable probes corresponding to the probes, or one or more subsets of probes, thereon. In alternative embodiments, the ordered
30 set of amplifiable probes is packaged separately from the genome-derived single exon microarray.

In some embodiments, the microarray and/or ordered probe set are further packaged with recordable media that provide probe identification and addressing
35 information, and that can additionally contain annotation

information, such as gene expression data. Such recordable media can be packaged with the microarray, with the ordered probe set, or with both.

If the microarray is constructed on a substrate
5 that incorporates recordable media, such as is described in international patent application no. WO 98/12559, then separate packaging of the genome-derived single exon microarray and the bioinformatic information is not required.

10 The amount of amplifiable probe material should be sufficient to permit at least one amplification sufficient for subsequent hybridization assay.

Although the use of high density genome-derived microarrays on solid planar substrates is presently a
15 preferred approach for the physical confirmation and characterization of the expression of sequences predicted to encode protein, other types of microarrays (as herein defined) can also be used.

Furthermore, as earlier mentioned, experimental
20 verification of the function predicted from genomic sequence in process 200 can be bioinformatic, rather than, or additional to, physical verification.

For example, where the function desired to be identified is protein coding, the predicted ORFs can be
25 compared bioinformatically to sequences known or suspected of being expressed.

Thus, the sequences output from process 300 (or process 200), can be used to query expression databases, such as EST databases, SNP ("single nucleotide
30 polymorphism") databases, known cDNA and mRNA sequences, SAGE ("serial analysis of gene expression") databases, and more generalized sequence databases that allow query for expressed sequences. Such query can be done by any sequence query algorithm, such as BLAST ("basic local
35 alignment search tool"). The results of such query -

including information on identical sequences and information on nonidentical sequences that have diffuse or focal regions of sequence homology to the query sequence – can then be passed directly to process 500, or used to
5 inform analyses subsequently undertaken in process 200, process 300, or process 400.

Experimental data, whether obtained by physical or bioinformatic assay in process 400, is passed to process 500 where it is usefully related to the sequence data
10 itself, a process colloquially termed "annotation". Such annotation can be done using any technique that usefully relates the functional information to the sequence, as, for example, by incorporating the functional data into the record itself, by linking records in a hierarchical or
15 relational database, by linking to external databases, or by a combination thereof. Such database techniques are well within the skill in the art.

The annotated sequence data can be stored locally, uploaded to genomic sequence database 100, and/or
20 displayed 800.

The methods and apparatus of the present invention rapidly produce functional information from genomic sequence. Coupled with the escalating pace at which sequence now accumulates, the rapid pace of sequence
25 annotation produces a need for methods of displaying the information in meaningful ways.

FIG. 3 shows visual display 80 presenting a single genomic sequence annotated according to the present invention. Because of its nominal resemblance to artistic
30 works of Piet Mondrian, visual display 80 is alternatively described herein as a "Mondrian".

Each of the visual elements of display 80 is aligned with respect to the genomic sequence being annotated (hereinafter, the "annotated sequence"). Given
35 the number of nucleotides typically represented in an

annotated sequence, representation of individual nucleotides would rarely be readable in hard copy output of display 80. Typically, therefore, the annotated sequence is schematized as rectangle 89, extending from the left
5 border of display 80 to its right border. By convention herein, the left border of rectangle 89 represents the first nucleotide of the sequence and the right border of rectangle 89 represents the last nucleotide of the sequence.

10 As further discussed below, however, the Mondrian visual display of annotated sequence can serve as a convenient graphical user interface for computerized representation, analysis, and query of information stored electronically. For such use, the individual nucleotides
15 can conveniently be linked to the X axis coordinate of rectangle 89. This permits the annotated sequence at any point within rectangle 89 readily to be viewed, either automatically - for example, by time-delayed appearance of a small overlaid window upon movement of a cursor or other
20 pointer over rectangle 89 - or through user intervention, as by clicking a mouse or other pointing device at a point in rectangle 89.

Visual display 80 is generated after user specification of the genomic sequence to be displayed.
25 Such specification can consist of or include an accession number for a single clone (e.g., a single BAC accessioned into GenBank), wherein the starting and stopping nucleotides are thus absolutely identified, or alternatively can consist of or include an anchor or
30 fulcrum point about which a chosen range of sequence is anchored, thus providing relative endpoints for the sequence to be displayed. For example, the user can anchor such a range about a given chromosomal map location, gene name, or even a sequence returned by query for similarity
35 or identity to an input query sequence. When visual

display 80 is used as a graphical user interface to computerized data, additional control over the first and last displayed nucleotide will typically be dynamically selectable, as by use of standard zooming and/or selection
5 tools.

Field 81 of visual display 80 is used to present the output from process 200, that is, to present the bioinformatic prediction of those sequences having the desired function within the genomic sequence. Functional
10 sequences are typically indicated by at least one rectangle 83 (83a, 83b, 83c), the left and right borders of which respectively indicate, by their X-axis coordinates, the starting and ending nucleotides of the region predicted to have function.

15 Where a single bioinformatic method or approach identifies a plurality of regions having the desired function, a plurality of rectangles 83 is disposed horizontally in field 81. Where multiple methods and/or approaches are used to identify function, each such method
20 and/or approach can be represented by its own series of horizontally disposed rectangles 83, each such horizontally disposed series of rectangles offset vertically from those representing the results of the other methods and approaches.

25 Thus, rectangles 83a in FIG. 3 represent the functional predictions of a first method of a first approach for predicting function, rectangles 83b represent the functional predictions of a second method and/or second approach for predicting that function, and rectangles 83c
30 represent the predictions of a third method and/or approach.

Where the function desired to be identified is protein coding, field 81 is used to present the bioinformatic prediction of sequences encoding protein.
35 For example, rectangles 83a can represent the results from

GRAIL or GRAIL II, rectangles 83b can represent the results from GENEFINDER, and rectangles 83c can represent the results from DICTION.

Optionally, and preferably, rectangles 83 collectively representing predictions of a single method and/or approach are identically colored and/or textured, and are distinguishable from the color and/or texture used for a different method and/or approach.

Alternatively, or in addition, the color, hue, density, or texture of rectangles 83 can be used further to report a measure of the bioinformatic reliability of the prediction. For example, many gene prediction programs will report a measure of the reliability of prediction. Thus, increasing degrees of such reliability can be indicated, e.g., by increasing density of shading. Where display 80 is used as a graphical user interface, such measures of reliability, and indeed all other results output by the program, can additionally or alternatively be made accessible through linkage from individual rectangles 83, as by time-delayed window ("tool tip" window), or by pointer (e.g., mouse)-activated link.

As earlier described, increased predictive reliability can be achieved by requiring consensus among methods and/or approaches to determining function. Thus, field 81 can include a horizontal series of rectangles 83 that indicate one or more degrees of consensus in predictions of function.

Although FIG. 3 shows three series of horizontally disposed rectangles in field 81, display 80 can include as few as one such series of rectangles and as many as can discriminably be displayed, depending upon the number of methods and/or approaches used to predict a given function.

Furthermore, field 81 can be used to show predictions of a plurality of different functions.

However, the increased visual complexity occasioned by such display makes more useful the ability of the user to select a single function for display. When display 80 is used as a graphical user interface for computer query and analysis, such function can usefully be indicated and user-selectable, as by a series of graphical buttons or tabs (not shown in FIG. 3).

Rectangle 89 is shown in FIG. 3 as including interposed rectangle 84. Rectangle 84 represents the portion of annotated sequence for which predicted functional information has been assayed physically, with the starting and ending nucleotides of the assayed material indicated by the X axis coordinates of the left and right borders of rectangle 84. Rectangle 85, with optional inclusive circles 86 (86a, 86b, and 86c) displays the results of such physical assay.

Although a single rectangle 84 is shown in FIG. 3, physical assay is not limited to just one region of annotated genomic sequence. It is expected that an increasing percentage of regions predicted to have function by process 200 will be assayed physically, and that display 80 will accordingly, for any given genomic sequence, have an increasing number of rectangles 84 and 85, representing an increased density of sequence annotation.

Where the function desired to be identified is protein coding, rectangle 84 identifies the sequence of the probe used to measure expression. In embodiments of the present invention where expression is measured using genome-derived single exon microarrays, rectangle 84 identifies the sequence included within the probe immobilized on the support surface of the microarray. As noted *supra*, such probe will often include a small amount of additional, synthetic, material incorporated during amplification and designed to permit reamplification of the probe, which sequence is typically not shown in display 80.

Rectangle 87 is used to present the results of bioinformatic assay of the genomic sequence. For example, where the function desired to be identified is protein coding, process 400 can include bioinformatic query of expression databases with the sequences predicted in process 200 to encode exons. And as earlier discussed, because bioinformatic assay presents fewer constraints than does physical assay, often the entire output of process 200 can be used for such assay, without further subsetting thereof by process 300. Therefore, rectangle 87 typically need not have separate indicators therein of regions submitted for bioinformatic assay; that is, rectangle 87 typically need not have regions therein analogous to rectangles 84 within rectangle 89.

Rectangle 87 as shown in FIG. 3 includes smaller rectangles 880 and 88. Rectangles 880 indicate regions that returned a positive result in the bioinformatic assay, with rectangles 88 representing regions that did not return such positive results. Where the function desired to be predicted and displayed is protein coding, rectangles 880 indicate regions of the predicted exons that identify sequence with significant similarity in expression databases, such as EST, SNP, SAGE databases, with rectangles 88 indicating genes novel over those identified in existing expression data bases.

Rectangles 880 can further indicate, through color, shading, texture, or the like, additional information obtained from bioinformatic assay.

For example, where the function assayed and displayed is protein coding, the degree of shading of rectangles 880 can be used to represent the degree of sequence similarity found upon query of expression databases. The number of levels of discrimination can be as few as two (identity, and similarity, where similarity has a user-selectable lower threshold). Alternatively, as

many different levels of discrimination can be indicated as can visually be discriminated.

Where display 80 is used as a graphical user interface, rectangles 880 can additionally provide links directly to the sequences identified by the query of expression databases, and/or statistical summaries thereof. As with each of the precedingly-discussed uses of display 80 as a graphical user interface, it should be understood that the information accessed via display 80 need not be resident on the computer presenting such display, which often will be serving as a client, with the linked information resident on one or more remotely located servers.

Rectangle 85 displays the results of physical assay of the sequence delimited by its left and right borders.

Rectangle 85 can consist of a single rectangle, thus indicating a single assay, or alternatively, and increasingly typically, will consist of a series of rectangles (85a, 85b, 85c) indicating separate physical assays of the same sequence.

Where the function assayed is gene expression, and where gene expression is assayed as herein described using simultaneous two-color fluorescent detection of hybridization to genome-derived single exon microarrays, individual rectangles 85 can be colored to indicate the degree of expression relative to control. Conveniently, shades of green can be used to depict expression in the sample over control values, and shades of red used to depict expression less than control, corresponding to the spectra of the Cy3 and Cy5 dyes conventionally used for respective labeling thereof. Additional functional information can be provided in the form of circles 86 (86a, 86b, 86c), where the diameter of the circle can be used to indicate expression intensity. As discussed *infra*, such

relative expression (expression ratios) and absolute expression (signal intensity) can be expressed using normalized values.

Where display 80 is used as a graphical user interface, rectangle 85 can be used as a link to further information about the assay. For example, where the assay is one for gene expression, each rectangle 85 can be used to link to information about the source of the hybridized mRNA, the identity of the control, raw or processed data from the microarray scan, or the like.

FIG. 4 is rendition of display 80 representing gene prediction and gene expression for a hypothetical BAC, showing conventions used in the Examples presented *infra*. BAC sequence ("Chip seq.") 89 is presented, with the physically assayed region thereof (corresponding to rectangle 84 in FIG. 3) shown in white. Algorithmic gene predictions are shown in field 81, with predictions by GRAIL shown, predictions by GENEFINDER, and predictions by DICTION shown. Within rectangle 87, regions of sequence that, when used to query expression databases, return identical or similar sequences ("EST hit") are shown as white rectangles (corresponding to rectangles 880 in FIG. 3), gray indicates low homology, and black indicates unknowns (where black and gray would correspond to rectangles 88 in FIG. 3).

Although FIGS. 3 and 4 show a single stretch of sequence, uninterrupted from left to right, longer sequences are usefully represented by vertical stacking of such individual Mondrians, as shown in FIGS. 9 and 10.

Single Exon Probes Useful For Measuring Gene Expression

The methods and apparatus of the present invention rapidly produce functional information from genomic sequence. Where the function to be identified is

protein coding, the methods and apparatus of the present invention rapidly identify and confirm the expression of portions of genomic sequence that function to encode protein. As a direct result, the methods and apparatus of
5 the present invention rapidly yield large numbers of single-exon nucleic acid probes, the majority from previously unknown genes, each of which is useful for measuring and/or surveying expression of a specific gene in one or more tissues or cell types.

10 It is, therefore, another aspect of the present invention to provide genome-derived single exon nucleic acid probes useful for gene expression analysis, and particularly for gene expression analysis by microarray.

Using the methods and genome-derived single-exon
15 microarrays of the present invention, we have for example readily identified a large number of unique ORFs from human genomic sequence. Using single exon probes that encompass these ORFs, we have demonstrated, through microarray hybridization analysis, the expression of 12,821 of these
20 ORFs in brain.

As would immediately be appreciated by one of skill in the art, each single exon probe having demonstrable expression in brain is currently available for use in measuring the level of its ORF's expression in
25 brain.

Diseases of the brain and nervous system are a significant cause of human morbidity and mortality. Increasingly, genetic factors are being found that contribute to predisposition, onset, and/or aggressiveness
30 of most, if not all, of these diseases. Although mutations in single genes have been identified as causative for some diseases of the brain and nervous system, for the most part these disorders are believed to have polygenic etiologies.

For example, over the past few decades
35 Alzheimer's disease (AD), once considered a rare disorder,

has become recognized as a major public health problem; over 4,000,000 people in the United States are now estimated to suffer with various stages of this progressive, degenerative brain disorder.

5 Although there is no agreement on the exact incidence or prevalence of Alzheimer's disease, in part due to varying diagnostic criteria and difficulties of differential diagnosis among dementias, the studies are consistent in pointing to an exponential rise in prevalence
10 of this disease with age. After age 65, the percentage of affected people approximately doubles with every decade of life, regardless of definition. Among people age 85 or older, studies suggest that 25 to 35 percent have dementia, including Alzheimer's disease; one study reports that 47.2
15 percent of people over age 85 have Alzheimer's disease, exclusive of other dementias.

 Alzheimer's disease progressively destroys memory, reason, judgment, language, and, eventually, the ability to carry out even the simplest of tasks. Anatomic
20 changes associated with Alzheimer's disease begin in the entorhinal cortex, proceed to the hippocampus, and then gradually spread to other regions, particularly the cerebral cortex. Chief among such anatomic changes are the presence of characteristic extracellular plaques and
25 internal neurofibrillary tangles.

 Alzheimer's disease has been suspected to have a multifactorial genetic etiological component for almost half a century. Sjogren et al., *Acta Psychiat. Neurol. Scand.* 82(suppl.): 1-152 (1952).

30 At least four genes have been identified to date that contribute to development of Alzheimer's disease: AD1 is caused by mutations in the amyloid precursor gene (APP); AD2 is associated with the APOE4 allele on chromosome 19; AD3 is caused by mutation in a chromosome 14 gene encoding
35 a 7-transmembrane domain protein, presenilin-1 (PSEN1), and

AD4 is caused by mutation in a gene on chromosome 1 that encodes a similar 7-transmembrane domain protein, presenilin-2 (PSEN2).

There is strong evidence, however, for additional, as yet uncharacterized, AD loci on other chromosomes.

For example, Daw et al., Am. J. Hum. Genet. 66: 196-204 (2000), estimated the number of additional quantitative trait loci (QTLs) and their contribution to the variance in age at onset of AD, and reported that 4 loci make a contribution to the variance in age at onset of late-onset AD similar to or greater in magnitude than that made by apoE, with one locus making a contribution several times greater than that of apoE. These results suggest that several genes not yet localized may play a larger role than does apoE in late-onset AD.

In accord, three groups recently announced the possible existence of an AD susceptibility gene on chromosome 10. Bertram et al., Science 290(5500):2302-2303 (2000); Ertekin-Taner et al., Science 290(5500):2303-2304 (2000); and Myers et al., Science 290(5500):2304-2305 (2000).

As another example, multiple sclerosis (MS) affects about 350,000 Americans, with approximately 200 new cases diagnosed each week, with an estimated annual monetary cost in the U.S. alone of \$2.5 billion.

Clinically, MS is an unpredictable disorder, with symptoms, presentation and course falling broadly into one of several clinical patterns. In relapsing-remitting (RR) MS, the disease first manifests as a series of attacks followed by complete or partial remissions, with symptoms returning later after a period of stability. In primary-progressive (PP) MS, there is a gradual clinical decline with no distinct remissions, although there may be

temporary plateaus or minor relief from symptoms.

Secondary-progressive (SP) MS begins with a relapsing-remitting course followed by a later primary-progressive course. Rarely, patients may have a progressive-relapsing

5 (PR) course in which the disease takes a progressive path punctuated by acute attacks. PP, SP, and PR MS are sometimes lumped together and called chronic progressive MS. The waxing and waning course characteristic of RR, SP and PR MS makes differential diagnosis difficult.

10 Anatomically, MS attacks are associated with focal inflammation in areas of the white matter of the central nervous system (CNS), accompanied or followed by demyelination in these areas, termed plaques. Destruction of the myelin sheath slows or blocks neurological
15 transmission, leading to diminished or lost function.

Clinical manifestations depend upon the location of the plaques and severity of demyelination, and range from fatigue, the most common symptom of MS, to visual
20 impairment, due to inflammation of the optic nerve, termed optic neuritis, to numbness and paresthesias, to focal muscular weakness, ataxia, and bladder incontinence.

Increasing evidence suggests that genotype contributes to susceptibility to MS.

As early as 1965, McAlpine, in Multiple
25 Sclerosis: A Reappraisal (McAlpine, ed.), Williams and Wilkins Co. pp. 61-74 (1965), concluded that the risk to a first-degree relative of a patient with multiple sclerosis is at least 15 times that for a member of the general
30 population, but could discern no definite genetic pattern of inheritance.

Subsequently, many studies associated MS with HLA (MHC) haplotype. Haines et al., Hum. Molec. Genet.
7:1229-1234 (1998), studying a data set of 98 multiplex MS families, confirmed earlier reports that genetic linkage to
35 the MHC can be explained by association with the HLA-DR2

allele, but suggested that MHC association explains only between 17% and 62% of the genetic etiology of MS.

From a review of genomic screens, Dyment et al., Hum. Molec. Genet. 6: 1693-1698 (1997), concluded that a number of genes with interacting effects are likely and that no single region has a major influence on familial risk. Chataway et al., Brain 121: 1869-1887 (1998), reporting a follow-up on U.K. studies using a systematic genome screen to determine the genetic basis of MS, stated that a gene of major effect had been excluded from 95% of the genome and one with a moderate role from 65%, results thus suggesting that multiple sclerosis depends on independent or epistatic effects of several genes, each with small individual effects, rather than a very few genes of major biologic importance.

As a yet further example, schizophrenia has long been recognized to have complex, likely polygenic, genetic contributions.

Schizophrenia is a common psychiatric disorder, occurring in 1 to 1.5 percent of the population worldwide, and is characterized by variable constellations of symptoms drawn from a universe of behavioral abnormalities. Although there are accepted alternative diagnostic criteria, primary criteria for diagnosis require two or more of the following, each present for a significant portion of time during a 1-month period (or less if successfully treated): (1) delusions; (2) hallucinations; (3) disorganized speech (e.g., frequent derailment or incoherence); (4) grossly disorganized or catatonic behavior; (5) negative symptoms, i.e., affective flattening, alogia, or avolition. (Diagnostic and Statistic Manual of Mental Disorders DSM-IV-TR, American Psychiatric Association (2000)). Only one such symptom is required if delusions are bizarre or hallucinations consist of a voice keeping up a running commentary on the

person's behavior or thoughts, or consist of two or more voices conversing with each other.

Three-quarters of persons with schizophrenia develop the disease between 16 and 25 years of age: onset is uncommon after age 30, rare after age 40. In the 16 to 25 year old age group, schizophrenia affects more men than women; in the 25-30 year old group, the incidence is higher in women than in men. Studies have shown that some persons with schizophrenia recover completely, and many others improve to the point where they can live independently, often with the maintenance of drug therapy. However, approximately 15 percent of people with schizophrenia respond only moderately to medication and require extensive support throughout their lives, while another 15 percent simply do not respond to existing treatment.

Schizophrenia has long been known to have a significant genetic component. Studies have consistently demonstrated that the risk to relatives of a proband with schizophrenia is higher than the risk to relatives of controls. Moldin, in Genetics and Mental Disorders: Report of the NIMH Genetics Workgroup (NIH publication 98-4268, (1998), reviewed family and twin studies published between 1920 and 1987 and found the recurrence risk ratios to be 48 for monozygotic twins, 11 for first-degree relatives, 4.25 for second-degree relatives, and 2 for third-degree relatives. He also found that concordance rates for monozygotic twins averaged 46%, even when reared in different families, whereas the concordance rates for dizygotic twins averaged only 14%. The prevalence of schizophrenia is known to be higher in biologic than in adoptive relatives of schizophrenic adoptees.

The mode of inheritance is unclear, however. Susceptibility has been mapped to many loci, including chromosomes 1q21-q22, 5, 6p23, 8p22-p21, 11q, 13q14-q21, 13q32, 15q15, 15q14, 18p, and 22q11. Chromosome

19 has also been implicated in schizophrenia, at 2
different sites, as have sites on the X chromosome. Wei et
al., Nature Genet. 25:376-377 (2000) report more
specifically that the NOTCH4 locus is associated with
5 susceptibility to schizophrenia.

In general, however, it is believed that
development of schizophrenia involves multiple loci.

For example, Williams et al., Hum. Molec. Genet.
8:1729-1739 (1999) undertook a systematic search for
10 linkage in 196 affected sib pairs (ASPs) with
schizophrenia. Using 229 microsatellite markers at an
average intermarker distance of 17.26 cM, followed in a
second stage by a further 54 markers allowing the regions
identified in stage 1 to be typed at an average spacing of
15 5.15 cM, Williams et al. considered results on chromosomes
4p, 18q, and Xcen as suggestive; however, given the scores,
Williams et al. interpreted their results as suggesting
that common genes of major effect (susceptibility ratio
more than 3) are unlikely to exist for schizophrenia.

20 Similarly, Shaw et al., Am. J. Med. Genet.
81(5):364-76 (1998), in a genome-wide search for
schizophrenia susceptibility genes, found that twelve
chromosomes (1, 2, 4, 5, 8, 10, 11, 12, 13, 14, 16, and
22) had at least one region with a nominal P value <0.05 ,
25 that two of these chromosomes had a nominal P value <0.01
(chromosomes 13 and 16), and that five chromosomes (1, 2,
4, 11, and 13) had at least one marker with a lod score
>2.0, suggesting the existence of multiple loci that
contribute to schizophrenia susceptibility.

30 As yet another example, multiple genes are
thought to predispose to epilepsy.

Epilepsy is characterized by recurrent,
paroxysmal disorders of cerebral function (seizures); that
is, by sudden, brief attacks of altered consciousness,
35 motor activity, sensory phenomena, or inappropriate

behavior. The risk of developing epilepsy is 1% in the period from birth to age 20, and 3% at age 75.

Epilepsy is caused by excessive discharge of cerebral neurons. Clinical manifestations depend on the type and location of discharge. In partial seizures, for example, the excess neuronal discharge is contained within one region of the cerebral cortex. Simple partial seizures consist of motor, sensory, or psychomotor phenomena without loss of consciousness; the specific phenomenon reflects the affected area of the brain. In generalized seizures, the discharge bilaterally and diffusely involves the entire cortex. Sometimes a focal lesion of one part of a hemisphere activates the entire cerebrum bilaterally so rapidly that it produces a generalized tonic-clonic seizure before a focal sign appears.

Epilepsy is a family of disorders. Those that are idiopathic are believed to have multiple genetic contributions. For example, idiopathic generalized epilepsy (IGE) is characterized by recurring generalized seizures in the absence of detectable brain lesions and/or metabolic abnormalities. Twin and family studies suggest that genetic factors play a key part in its etiology. Although a mutation in the CACNB4 gene can cause the disorder, linkage to 8q24, Zara et al., Hum. Molec. Genet. 4: 1201-1207(1995), 3q26 and 14q23, Sander et al., Hum. Molec. Genet. 9:1465-1472 (2000), and 2q36 has been also demonstrated, with a multilocus model appearing to fit best the observed familial patterns.

Polygenic contributions to the etiology of various neurologic cancers have similarly been described.

For example, gliomas account for 45% of intracranial tumors, and multiple loci have been implicated in its development, with losses of chromosome 17p, increase in copy number of chromosome 7, structural abnormalities of

chromosomes 9p and 19q, and genes on chromosome 10 among the suspects.

Other significant diseases of brain and nervous tissue are also believed to have a genetic, typically
5 polygenic, etiologic component. These diseases include, for example, Parkinson's disease, dementia with Lewy bodies, frontotemporal dementia, corticobasal ganglionic degeneration, progressive supranuclear palsy, prion
10 diseases (Creutzfeld-Jakob, Gerstmann-Straussler-Shenker, familial fatal insomnia), Tourette's Syndrome, corticobasal degeneration, multiple system atrophy, striatonigral degeneration, Shy-Drager syndrome, olivopontocerebellar atrophy, spinocerebellar ataxia, Friedreich ataxia, ataxia-telangiectasia, amyotrophic lateral sclerosis, bulbosplinal
15 atrophy (Kennedy's syndrome), spinal muscular atrophy, neuronal storage diseases (sphingolipid, mucopolysaccharide, mucolipid), leukodystrophy, Krabbe disease, metachromic leukodystrophy, adrenoleukodystrophy, Pelizaeus-Merzbacher disease, Canavan disease,
20 mitochondrial encephalomyopathy, Leigh disease, neurofibromatosis (Type I and Type II), tuberous sclerosis, paraneoplastic syndrome, subacute cerebellar degeneration, subacute sensory neuropathy, opsoclonus/myoclonus, retinal degeneration, stiff-man syndrome and Von Hippel-Lindau
25 disease.

Many neurologic cancers other than gliomas have also been shown or suspected to have genetic bases or contributions. Among these cancers are astrocytoma, fibrillary astrocytoma, pilocytic astrocytoma,
30 pleomorphic xanthoastrocytoma, oligodendroglioma, ependymoma, gangliocytoma, ganglioglioma, medulloblastoma, primary brain germ cell tumor, pineocytoma, pineoblastoma, and meningioma.

Other disorders of brain and central nervous
35 system that likely have genetic components include the

various forms of neural deafness, catatonia, depression, bipolar (manic-depressive) disorder, Wilson's Disease, Pick disease, neuromyelitis optica (Devic disease), central pontine myelinolysis, Marchiafava-Bignami disease, 5 Guillain-Barre syndrome, sleep disorders (insomnia, myoclonus, narcolepsy, cataplexy, sleep apnea), amnesia, aphasias (including Broca's aphasia and Wernicke's aphasia), cortical blindness, visual agnosia, auditory agnosia, and Kluver-Bucy syndrome.

10 The human genome-derived single exon nucleic acid probes and microarrays of the present invention are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of human brain, particularly those diseases with polygenic etiology. With each of the single 15 exon probes described herein shown to be expressed at detectable levels in human brain, and with about 2/3 of the probes identifying novel genes, the single exon microarrays of the present invention provide exceptionally high informational content for such studies.

20 For example, diagnosis (including differential diagnosis among clinically indistinguishable disorders), staging, and/or grading of a disease can be based upon the quantitative relatedness of a patient gene expression profile to one or more reference expression profiles known 25 to be characteristic of a given neurologic disease, or to specific grades or stages thereof.

In one embodiment, the patient gene expression profile is generated by hybridizing nucleic acids obtained directly or indirectly from transcripts expressed in the 30 patient's brain (or other CNS tissues, including cultured tissues) to the genome-derived single exon microarray of the present invention. Reference profiles are obtained similarly by hybridizing nucleic acids from individuals with known disease. Methods for quantitatively relating 35 gene expression profiles, without regard to the function of

the protein encoded by the gene, are disclosed in WO 99/58720, incorporated herein by reference in its entirety.

In another approach, the genome-derived single exon probes and microarrays of the present invention can be
5 used to interrogate genomic DNA, rather than pools of expressed message; this latter approach permits predisposition to and/or prognosis of neurologic disease to be assessed through the massively parallel determination of altered copy number, deletion, or mutation in the patient's
10 genome of exons known to be expressed in human brain. The algorithms set forth in WO 99/58720 can be applied to such genomic profiles without regard to the function of the protein encoded by the interrogated gene.

The utility is specific to the probe; at
15 sufficiently high hybridization stringency, which stringencies are well known in the art - see Ausubel et al. and Maniatis et al. - each probe reports the level of expression of message specifically containing that ORF.

It should be appreciated, however, that the
20 probes of the present invention, for which expression in the brain has been demonstrated are useful for both measurement in the brain and for survey of expression in other tissues.

Significant among such advantages is the presence
25 of probes for novel genes.

As mentioned above and further detailed in Examples 1 and 2, the methods described enable ORFs which are not present in existing expression databases to be identified. And the fewer the number of tissues in which
30 the ORF can be shown to be expressed, the more likely the ORF will prove to be part of a novel gene: as further discussed in Example 2, ORFs whose expression was measurable in only a single of the tested tissues were represented in existing expression databases at a rate of
35 only 11%, whereas 36% of ORFs whose expression was

measurable in 9 tissues were present in existing expression databases, and fully 45% of those ORFs expressed in all ten tested tissues were present in existing expressed sequence databases.

5 Either as tools for measuring gene expression or tools for surveying gene expression, the genome-derived single exon probes of the present invention have significant advantages over the cDNA or EST-based probes that are currently available for achieving these utilities.

10 The genome-derived single exon probes of the present invention are useful in constructing genome-derived single exon microarrays; the genome-derived single exon microarrays, in turn, are useful devices for measuring and for surveying gene expression in the human.

15 Gene expression analysis using microarrays - conventionally using microarrays having probes derived from expressed message - is well-established as useful in the biological research arts (see Lockhart et al. *Nature* 405, 827-836).

20 Microarrays have been used to determine gene expression profiles in cells in response to drug treatment (see, for example, Kaminski et al., "Global Analysis of Gene Expression in Pulmonary Fibrosis Reveals Distinct Programs Regulating Lung Inflammation and Fibrosis," *Proc. Natl. Acad. Sci. USA* 97(4):1778-83 (2000); Bartosiewicz et al., "Development of a Toxicological Gene Array and Quantitative Assessment of This Technology," *Arch. Biochem. Biophys.* 376(1):66-73 (2000)), viral infection (see for example, Geiss et al., "Large-scale Monitoring of Host Cell Gene Expression During HIV-1 Infection Using cDNA Microarrays," *Virology* 266(1):8-16 (2000)) and during cell processes such as differentiation, senescence and apoptosis (see, for example, Shelton et al., "Microarray Analysis of Replicative Senescence," *Curr. Biol.* 9(17):939-45 (1999);
35 Voehringer et al., "Gene Microarray Identification of Redox

and Mitochondrial Elements That Control Resistance or Sensitivity to Apoptosis," *Proc. Natl. Acad. Sci. USA* 97(6):2680-5 (2000)).

Microarrays have also been used to determine
5 abnormal gene expression in diseased tissues (see, for example, Alon et al., "Broad Patterns of Gene Expression Revealed by Clustering Analysis of Tumor and Normal Colon Tissues Probed by Oligonucleotide Arrays," *Proc. Natl. Acad. Sci. USA* 96(12):6745-50 (1999); Perou et al.,
10 "Distinctive Gene Expression Patterns in Human Mammary Epithelial Cells and Breast Cancers, *Proc. Natl. Acad. Sci. USA* 96(16):9212-7 (1999); Wang et al., "Identification of Genes Differentially Over-expressed in Lung Squamous Cell Carcinoma Using Combination of cDNA Subtraction and
15 Microarray Analysis," *Oncogene* 19(12):1519-28 (2000); Whitney et al., "Analysis of Gene Expression in Multiple Sclerosis Lesions Using cDNA Microarrays," *Ann. Neurol.* 46(3):425-8 (1999)), in drug discovery screens (see, for example, Scherf et al., "A Gene Expression Database for the
20 Molecular Pharmacology of Cancer," *Nat. Genet.* 24(3):236-44 (2000)) and in diagnosis to determine appropriate treatment strategies (see, for example, Sgroi et al., "In vivo Gene Expression Profile Analysis of Human Breast Cancer Progression," *Cancer Res.* 59(22):5656-61 (1999)).

25 In microarray-based gene expression screens of pharmacological drug candidates upon cells, each probe provides specific useful data. In particular, it should be appreciated that even those probes that show no change in expression are as informative as those that do change,
30 serving, in essence, as negative controls.

For example, where gene expression analysis is used to assess toxicity of chemical agents on cells, the failure of the agent to change a gene's expression level is evidence that the drug likely does not affect the pathway
35 of which the gene's expressed protein is a part.

Analogously, where gene expression analysis is used to assess side effects of pharmacological agents – whether in lead compound discovery or in subsequent screening of lead compound derivatives – the inability of the agent to alter a gene's expression level is evidence that the drug does not affect the pathway of which the gene's expressed protein is a part.

WO 99/58720 provides methods for quantifying the relatedness of a first and second gene expression profile and for ordering the relatedness of a plurality of gene expression profiles. The methods so described permit useful information to be extracted from a greater percentage of the individual gene expression measurements from a microarray than methods previously used in the art.

Other uses of microarrays are described in Gerhold et al., *Trends Biochem. Sci.* 24(5):168-173 (1999) and Zweiger, *Trends Biotechnol.* 17(11):429-436 (1999); Schena et al.

The invention particularly provides genome-derived single-exon probes known to be expressed in brain.

The individual single exon probes can be provided in the form of substantially isolated and purified nucleic acid, typically, but not necessarily, in a quantity sufficient to perform a hybridization reaction.

Such nucleic acid can be in any form directly hybridizable to the message that contains the probe's ORF, such as double stranded DNA, single-stranded DNA complementary to the message, single-stranded RNA complementary to the message, or chimeric DNA/RNA molecules so hybridizable. The nucleic acid can alternatively or additionally include either nonnative nucleotides, alternative internucleotide linkages, or both, so long as complementary binding can be obtained. For example, probes can include phosphorothioates, methylphosphonates, morpholino analogs, and peptide nucleic acids (PNA), as are

described, for example, in U.S. Patent Nos. 5,142,047; 5,235,033; 5,166,315; 5,217,866; 5,184,444; 5,861,250.

Usefully, however, such probes are provided in a form and quantity suitable for amplification, where the amplified product is thereafter to be used in the hybridization reactions that probe gene expression. Typically, such probes are provided in a form and quantity suitable for amplification by PCR or by other well known amplification technique. One such technique additional to PCR is rolling circle amplification, as is described, *inter alia*, in U.S. Patent Nos. 5,854,033 and 5,714,320 and international patent publications WO 97/19193 and WO 00/15779. As is well understood, where the probes are to be provided in a form suitable for amplification, the range of nucleic acid analogues and/or internucleotide linkages will be constrained by the requirements and nature of the amplification enzyme.

Where the probe is to be provided in form suitable for amplification, the quantity need not be sufficient for direct hybridization for gene expression analysis, and need be sufficient only to function as an amplification template, typically at least about 1, 10 or 100 pg or more.

Each discrete amplifiable probe can also be packaged with amplification primers, either in a single composition that comprises probe template and primers, or in a kit that comprises such primers separately packaged therefrom. As earlier mentioned, the ORF-specific 5' primers used for genomic amplification can have a first common sequence added thereto, and the ORF-specific 3' primers used for genomic amplification can have a second, different, common sequence added thereto, thus permitting, in this embodiment, the use of a single set of 5' and 3' primers to amplify any one of the probes. The probe composition and/or kit can also include buffers, enzyme,

etc., required to effect amplification.

As mentioned earlier, when intended for use on a genome-derived single exon microarray of the present invention, the genome-derived single exon probes of the present invention will typically average at least about 5 100, 200, 300, 400 or 500 bp in length, including (and typically, but not necessarily centered about) the ORF. Furthermore, when intended for use on a genome-derived single exon microarray of the present invention, the 10 genome-derived single exon probes of the present invention will typically not contain a detectable label.

When intended for use in solution phase hybridization, however – that is, for use in a hybridization reaction in which the probe is not first 15 bound to a support substrate (although the target may indeed be so bound) – length constraints that are imposed in microarray-based hybridization approaches will be relaxed, and such probes will typically be labeled.

In such case, the only functional constraint that 20 dictates the minimum size of such probe is that each such probe must be capable of specifically identifying in a hybridization reaction the exon from which it is drawn. In theory, a probe of as little as 17 nucleotides is capable of uniquely identifying its cognate sequence in the human 25 genome. For hybridization to expressed message – a subset of target sequence that is much reduced in complexity as compared to genomic sequence – even fewer nucleotides are required for specificity.

Therefore, the probes of the present invention 30 can include as few as 20, 25 or 50 bp or ORF, or more. In particular embodiments, the ORF sequences are given in SEQ ID NOS. 12,822 – 25,434, respectively, for probe SEQ ID NOS. 1 – 12,821. The minimum amount of ORF required to be included in the probe of the present invention in order to 35 provide specific signal in either solution phase or

microarray-based hybridizations can readily be determined for each of ORF SEQ ID NOS. 12,822 - 25,434 individually by routine experimentation using standard high stringency conditions.

5 Such high stringency conditions are described, *inter alia*, in Ausubel et al. and Maniatis et al. For microarray-based hybridization, standard high stringency conditions can usefully be 50% formamide, 5X SSC, 0.2 µg/µl poly(dA), 0.2 µg/µl human c_{ot}1 DNA, and 0.5 % SDS, in a
10 humid oven at 42°C overnight, followed by successive washes of the microarray in 1X SSC, 0.2% SDS at 55°C for 5 minutes, and then 0.1X SSC, 0.2% SDS, at 55°C for 20 minutes. For solution phase hybridization, standard high stringency conditions can usefully be aqueous hybridization
15 at 65°C in 6X SSC. Lower stringency conditions, suitable for cross-hybridization to mRNA encoding structurally- and functionally-related proteins, can usefully be the same as the high stringency conditions but with reduction in temperature for hybridization and washing to room
20 temperature (approximately 25°C).

When intended for use in solution phase hybridization, the maximum size of the single exon probes of the present invention is dictated by the proximity of other expressed exons in genomic DNA: although each single
25 exon probe can include intergenic and/or intronic material contiguous to the ORF in the human genome, each probe of the present invention will include portions of only one expressed exon.

Thus, each single exon probe will include no more
30 than about 25 kb of contiguous genomic sequence, more typically no more than about 20 kb of contiguous genomic sequence, more usually no more than about 15 kb, even more usually no more than about 10 kb. Usually, probes that are maximally about 5 kb will be used, more typically no more
35 than about 3 kb.

It will be appreciated that the Sequence Listing appended hereto presents, by convention, only that strand of the probe and ORF sequence that can be directly translated reading from 5' to 3' end. As would be well understood by one of skill in the art, single stranded probes must be complementary in sequence to the ORF as present in an mRNA; it is well within the skill in the art to determine such complementary sequence. It will further be understood that double stranded probes can be used in both solution-phase hybridization and microarray-based hybridization if suitably denatured.

Thus, it is an aspect of the present invention to provide single-stranded nucleic acid probes that have sequence complementary to those described herein above and below, and double-stranded probes one strand of which has sequence complementary to the probes described herein.

The probes can, but need not, contain intergenic and/or intronic material that flanks the ORF, on one or both sides, in the same linear relationship to the ORF that the intergenic and/or intronic material bears to the ORF in genomic DNA. The probes do not, however, contain nucleic acid derived from more than one expressed ORF.

And when intended for use in solution hybridization, the probes of the present invention can usefully have detectable labels. Nucleic acid labels are well known in the art, and include, *inter alia*, radioactive labels, such as ^3H , ^{32}P , ^{33}P , ^{35}S , ^{125}I , ^{131}I ; fluorescent labels, such as Cy3, Cy5, Cy5.5, Cy7, SYBR[®]

Green and other labels described in Haugland, *Handbook of Fluorescent Probes and Research Chemicals*, 7th ed., Molecular Probes Inc., Eugene, OR (2000), or fluorescence resonance energy transfer tandem conjugates thereof; labels suitable for chemiluminescent and/or enhanced chemiluminescent detection; labels suitable for ESR and NMR detection; and labels that include one member

of a specific binding pair, such as biotin, digoxigenin, or the like.

The probes, either in quantity sufficient for hybridization or sufficient for amplification, can be provided in individual vials or containers.

Alternatively, such probes can usefully be packaged as a plurality of such individual genome-derived single exon probes.

When provided as a collection of plural individual probes, the probes are typically made available in amplifiable form in a spatially-addressable ordered set, typically one per well of a microtiter dish. Although a 96 well microtiter plate can be used, greater efficiency is obtained using higher density arrays.

If, as earlier mentioned, the ORF-specific 5' primers used for genomic amplification had a first common sequence added thereto, and the ORF-specific 3' primers used for genomic amplification had a second, different, common sequence added thereto, a single set of 5' and 3' primers can be used to amplify all of the probes from the amplifiable ordered set.

Such collections of genome-derived single exon probes can usefully include a plurality of probes chosen for the common attribute of expression in the human brain.

In such defined subsets, typically at least 50, 60, 75, 80, 85, 90 or 95% or more of the probes will be chosen by their expression in the defined tissue or cell type.

The single exon probes of the present invention, as well as fragments of the single exon probes comprising selectively hybridizable portions of the probe ORF, can be used to obtain the full length cDNA that includes the ORF by (i) screening of cDNA libraries; (ii) rapid amplification of cDNA ends ("RACE"); or (iii) other conventional means, as are described, *inter alia*, in

Ausubel et al. and Maniatis et al.

It is another aspect of the present invention to provide genome-derived single exon nucleic acid microarrays useful for gene expression analysis, where the term
5 "microarray" has the meaning given in the definitional section of this description, *supra*.

The invention particularly provides genome-derived single-exon nucleic acid microarrays comprising a plurality of probes known to be expressed in human brain.
10 In preferred embodiments, the present invention provides human genome-derived single exon microarrays comprising a plurality of probes drawn from the group consisting of SEQ ID NOS.: 1 - 12,821.

When used for gene expression analysis, the
15 genome-derived single exon microarrays provide greater physical informational density than do the genome-derived single exon microarrays that have lower percentages of probes known to be expressed commonly in the tested tissue. At a fixed probe density, for example, a given microarray
20 surface area of the defined subset genome-derived single exon microarray can yield a greater number of expression measurements. Alternatively, at a given probe density, the same number of expression measurements can be obtained from a smaller substrate surface area. Alternatively, at a
25 fixed probe density and fixed surface area, probes can be provided redundantly, providing greater reliability in signal measurement for any given probe. Furthermore, with a higher percentage of probes known to be expressed in the assayed tissue, the dynamic range of the detection means
30 can be adjusted to reveal finer levels discrimination among the levels of expression.

Although particularly described with respect to their utility as probes of gene expression, particularly as probes to be included on a genome-derived single exon
35 microarray, each of the nucleic acids having SEQ ID NOS.: 1

- 12,821 contains an open-reading frame, set forth respectively in SEQ ID NOS.: 12,822 - 25,434, that encodes a protein domain. Thus, each of SEQ ID NOS. 1 - 12,821 can be used, or that portion thereof in SEQ ID NOS. 12,822 -
5 25,434 used, to express a protein domain by standard *in vitro* recombinant techniques. See Ausubel et al. and Maniatis et al.

Additionally, kits are available commercially that readily permit such nucleic acids to be expressed as
10 protein in bacterial cells, insect cells, or mammalian cells, as desired (e.g., HAT[™] Protein Expression & Purification System, ClonTech Laboratories, Palo Alto, CA; Adeno-X[™] Expression System, ClonTech Laboratories, Palo Alto, CA; Protein Fusion & Purification (pMAL[™]) System, New
15 England Biolabs, Beverley, MA)

Furthermore, shorter peptides can be chemically synthesized using commercial peptide synthesizing equipment and well known techniques. Procedures are described, *inter alia*, in Chan et al. (eds.), Fmoc Solid Phase Peptide
20 Synthesis: A Practical Approach (Practical Approach Series, (Paper)), Oxford Univ. Press (March 2000) (ISBN: 0199637245); Jones, Amino Acid and Peptide Synthesis (Oxford Chemistry Primers, No 7) , Oxford Univ. Press (August 1992) (ISBN: 0198556683); and Bodanszky, Principles
25 of Peptide Synthesis (Springer Laboratory), Springer Verlag (December 1993) (ISBN: 0387564314).

It is, therefore, another aspect of the invention to provide peptides comprising an amino acid sequence translated from SEQ ID NOS.: 12,822 - 25,434. Such amino
30 acid sequences are set out in SEQ ID NOS: 25,435 - 37,811. Any such recombinantly-expressed or synthesized peptide of at least 8, and preferably at least about 15, amino acids, can be conjugated to a carrier protein and used to generate antibody that recognizes the peptide. Thus, it is a
35 further aspect of the invention to provide peptides that

have at least 8, preferably at least 15, consecutive amino acids.

The following examples are offered by way of illustration and not by way of limitation.

EXAMPLE 1

Preparation of Single Exon Microarrays from ORFs Predicted in Human Genomic Sequence

10

Bioinformatics Results

All human BAC sequences in fewer than 10 pieces that had been accessioned in a five month period immediately preceding this study were downloaded from GenBank. This corresponds to ~2200 clones, totaling ~350 MB of sequence, or approximately 10% of the human genome.

After masking repetitive elements using the program CROSS_MATCH, the sequence was analyzed for open reading frames using three separate gene finding programs. The three programs predict genes using independent algorithmic methods developed on independent training sets: GRAIL uses a neural network, GENEFINDER uses a hidden Markoff model, and DICTION, a program proprietary to Genetics Institute, operates according to a different heuristic. The results of all three programs were used to create a prediction matrix across the segment of genomic DNA.

The three gene finding programs yielded a range of results. GRAIL identified the greatest percentage of genomic sequence as putative coding region, 2% of the data analyzed. GENEFINDER was second, calling 1%, and DICTION yielded the least putative coding region, with 0.8% of genomic sequence called as coding region.

The consensus data were as follows. GRAIL and GENEFINDER agreed on 0.7% of genomic sequence, GRAIL and

DICTION agreed on 0.5% of genomic sequence, and the three programs together agreed on 0.25% of the data analyzed. That is, 0.25% of the genomic sequence was identified by all three of the programs as containing putative coding
5 region.

ORFs predicted by any two of the three programs ("consensus ORFs") were assorted into "gene bins" using two criteria: (1) any 7 consecutive exons within a 25 kb window were placed together in a bin as likely contributing to a
10 single gene, and (2) all ORFs within a 25 kb window were placed together in a bin as likely contributing to a single gene if fewer than 7 exons were found within the 25 kb window.

15 PCR

The largest ORF from each gene bin that did not span repetitive sequence was then chosen for amplification, as were all consensus ORFs longer than 500 bp. This method approximated one exon per gene; however, a number of genes
20 were found to be represented by multiple elements.

Previously, we had determined that DNA fragments fewer than 250 bp in length do not bind well to the amino-modified glass surface of the slides used as support substrate for construction of microarrays; therefore,
25 amplicons were designed in the present experiments to approximate 500 bp in length.

Accordingly, after selecting the largest ORF per gene bin, a 500 bp fragment of sequence centered on the ORF was passed to the primer picking software, PRIMER3
30 (available online for use at <http://www-genome.wi.mit.edu/cgi-bin/primer/>). A first additional sequence was commonly added to each ORF-unique 5' primer, and a second, different, additional sequence was commonly added to each ORF-unique 3' primer, to permit
35 subsequent reamplification of the amplicon using a single

set of "universal" 5' and 3' primers, thus immortalizing the amplicon. The addition of universal priming sequences also facilitates sequence verification, and can be used to add a cloning site should some ORFs be found to warrant
5 further study.

The ORFs were then PCR amplified from genomic DNA, verified on agarose gels, and sequenced using the universal primers to validate the identity of the amplicon to be spotted in the microarray.

10 Primers were supplied by Operon Technologies (Alameda, CA). PCR amplification was performed by standard techniques using human genomic DNA (Clontech, Palo Alto, CA) as template. Each PCR product was verified by SYBR® green (Molecular Probes, Inc., Eugene, OR) staining of
15 agarose gels, with subsequent imaging by Fluorimager (Molecular Dynamics, Inc., Sunnyvale, CA). PCR amplification was classified as successful if a single band appeared.

The success rate for amplifying ORFs of interest
20 directly from genomic DNA using PCR was approximately 75%. FIG. 5 graphs the distribution of predicted ORF (exon) length and distribution of amplified PCR products, with ORF length shown in red and PCR product length shown in blue (which may appear black in the figure). Although the range
25 of ORF sizes is readily seen to extend to beyond 900 bp, the mean predicted exon size was only 229 bp, with a median size of 150 bp (n=9498). With an average amplicon size of 475 ± 25 bp, approximately 50% of the average PCR
amplification product contained predicted coding region,
30 with the remaining 50% of the amplicon containing either intron, intergenic sequence, or both.

Using a strategy predicated on amplifying about 500 bp, it was found that long exons had a higher PCR failure rate. To address this, the bioinformatics process
35 was adjusted to amplify 1000, 1500 or 2000 bp fragments

from exons larger than 500 bp. This improved the rate of successful amplification of exons exceeding 500 bp, constituting about 9.2% of the exons predicted by the gene finding algorithms.

5 Approximately 75% of the probes disposed on the array (90% of those that successfully PCR amplified) were sequence-verified by sequencing in both the forward and reverse direction using MegaBACE sequencer (Molecular Dynamics, Inc., Sunnyvale, CA), universal primers, and
10 standard protocols.

 Some genomic clones (BACs) yielded very poor PCR and sequencing results. The reasons for this are unclear, but may be related to the quality of early draft sequence or the inclusion of vector and host contamination in some
15 submitted sequence data.

 Although the intronic and intergenic material flanking coding regions could theoretically interfere with hybridization during microarray experiments, subsequent empirical results demonstrated that differential expression
20 ratios were not significantly affected by the presence of noncoding sequence. The variation in exon size was similarly found not to affect differential expression ratios significantly; however, variation in exon size was observed to affect the absolute signal intensity (data not
25 shown).

 The 350 MB of genomic DNA was, by the above-described process, reduced to 9750 discrete probes, which were spotted in duplicate onto glass slides using commercially available instrumentation (MicroArray GenII
30 Spotter and/or MicroArray GenIII Spotter, Molecular Dynamics, Inc., Sunnyvale, CA). Each slide additionally included either 16 or 32 *E. coli* genes, the average hybridization signal of which was used as a measure of background biological noise.

35 Each of the probe sequences was BLASTed against

the human EST data set, the NR data set, and SwissProt GenBank (May 7, 1999 release 2.0.9).

One third of the probe sequences (as amplified) produced an exact match (BLAST Expect ("E") values less than 1×10^{-100}) to either an EST (20% of sequences) or a known mRNA (13% of sequences). A further 22% of the probe sequences showed some homology to a known EST or mRNA (BLAST E values from 1×10^{-5} to 1×10^{-99}). The remaining 45% of the probe sequences showed no significant sequence homology to any expressed, or potentially expressed, sequences present in public databases.

All of the probe sequences (as amplified) were then analyzed for protein similarities with the SwissProt database using BLASTX, Gish *et al.*, *Nature Genet.* 3:266 (1993). The predicted functional breakdowns of the 2/3 of probes identical or homologous to known sequences are presented in Table 1.

Table 1

Function of Predicted ORFs As Deduced From Comparative Sequence Analysis			
Total	V6 chip	V7 chip	Function Predicted from Comparative Sequence Analysis
211	96	115	Receptor
120	43	77	Zinc Finger
30	11	19	Homeobox
25	9	16	Transcription Factor
17	11	7	Transcription
118	57	61	Structural
95	39	56	Kinase
36	18	18	Phosphatase
83	31	52	Ribosomal

45	19	26	Transport
21	17	14	Growth Factor
17	12	5	Cytochrome
50	33	17	Channel

As can be seen, the two most common types of genes were transcription factors and receptors, making up 2.2% and 1.8% of the arrayed elements, respectively.

5

EXAMPLE 2

Gene Expression Measurements From Genome-Derived Single Exon Microarrays

10

The two genome-derived single exon microarrays prepared according to Example 1 were hybridized in a series of simultaneous two-color fluorescence experiments to (1) 15 Cy3-labeled cDNA synthesized from message drawn individually from each of brain, heart, liver, fetal liver, placenta, lung, bone marrow, HeLa, BT 474, or HBL 100 cells, and (2) Cy5-labeled cDNA prepared from message pooled from all ten tissues and cell types, as a control in 20 each of the measurements. Hybridization and scanning were carried out using standard protocols and Molecular Dynamics equipment.

Briefly, mRNA samples were bought from commercial sources (Clontech, Palo Alto, CA and Amersham Pharmacia 25 Biotech (APB)). Cy3-dCTP and Cy5-dCTP (both from APB) were incorporated during separate reverse transcriptions of 1 µg of polyA⁺ mRNA performed using 1 µg oligo(dT)12-18 primer and 2 µg random 9mer primers as follows. After heating to 70°C, the RNA:primer mixture was snap cooled on ice. After 30 snap cooling on ice, added to the RNA to the stated final concentration was: 1X Superscript II buffer, 0.01 M DTT,

100 μ M dATP, 100 μ M dGTP, 100 μ M dTTP, 50 μ M dCTP, 50 μ M
Cy3-dCTP or Cy5-dCTP 50 μ M, and 200 U Superscript II
enzyme. The reaction was incubated for 2 hours at 42°C.
After 2 hours, the first strand cDNA was isolated by adding
5 1 U Ribonuclease H, and incubating for 30 minutes at 37°C.
The reaction was then purified using a Qiagen PCR cleanup
column, increasing the number of ethanol washes to 5.
Probe was eluted using 10 mM Tris pH 8.5.

Using a spectrophotometer, probes were measured
10 for dye incorporation. Volumes of both Cy3 and Cy5 cDNA
corresponding to 50 pmoles of each dye were then dried in a
Speedvac, resuspended in 30 μ l hybridization solution
containing 50% formamide, 5X SSC, 0.2 μ g/ μ l poly(dA), 0.2
 μ g/ μ l human c_{ot}1 DNA, and 0.5 % SDS.

15 Hybridizations were carried out under a
coverslip, with the array placed in a humid oven at 42°C
overnight. Before scanning, slides were washed in 1X SSC,
0.2% SDS at 55°C for 5 minutes, followed by 0.1X SSC, 0.2%
SDS, at 55°C for 20 minutes. Slides were briefly dipped in
20 water and dried thoroughly under a gentle stream of
nitrogen.

Slides were scanned using a Molecular Dynamics
Gen3 scanner, as described. Schena (ed.), Microarray
Biochip: Tools and Technology, Eaton Publishing
25 Company/BioTechniques Books Division (2000) (ISBN:
1881299376).

Although the use of pooled cDNA as a reference
permitted the survey of a large number of tissues, it
attenuates the measurement of relative gene expression,
30 since every highly expressed gene in the tissue/cell type-
specific fluorescence channel will be present to a level of
at least 10% in the control channel. Because of this fact,
both signal and expression ratios (the latter hereinafter,
"expression" or "relative expression") for each probe were
35 normalized using the average ratio or average signal,

respectively, as measured across the whole slide.

Data were accepted for further analysis only when signal was at least three times greater than biological noise, the latter defined by the average signal produced by the *E. coli* control genes.

The relative expression signal for these probes was then plotted as function of tissue or cell type, and is presented in FIG. 6.

FIG. 6 shows the distribution of expression across a panel of ten tissues. The graph shows the number of sequence-verified products that were either not expressed ("0"), expressed in one or more but not all tested tissues ("1" - "9"), and expressed in all tissues tested ("10").

Of 9999 arrayed elements on the two microarrays (including positive and negative controls and "failed" products), 2353 (51%) were expressed in at least one tissue or cell type. Of the gene elements showing significant signal - where expression was scored as "significant" if the normalized Cy3 signal was greater than 1, representing signal 5-fold over biological noise (0.2) - 39% (991) were expressed in all 10 tissues. The next most common class (15%) consisted of gene elements expressed in only a single tissue.

The genes expressed in a single tissue were further analyzed, and the results of the analyses are compiled in FIG. 7.

FIG. 7A is a matrix presenting the expression of all verified sequences that showed expression greater than 3 in at least one tissue. Each clone is represented by a column in the matrix. Each of the 10 tissues assayed is represented by a separate row in the matrix, and relative expression of a clone in that tissue is indicated at the respective node by intensity of green shading, with the intensity legend shown in panel B. The top row of the

matrix ("EST Hit") contains "bioinformatic" rather than "physical" expression data – that is, presents the results returned by query of EST, NR and SwissProt databases using the probe sequence. The legend for "bioinformatic expression" (i.e., degree of homology returned) is presented in panel C. Briefly, white is known, black is novel, with gray depicting nonidentical with significant homology (white: E values < 1e-100; gray: E values from 1e-05 to 1e-99; black: E values > 1e-05).

As FIG. 7 readily shows, heart and brain were demonstrated to have the greatest numbers of genes that were shown to be uniquely expressed in the respective tissue. In brain, 200 uniquely expressed genes were identified; in heart, 150. The remaining tissues gave the following figures for uniquely expressed genes: liver, 100; lung, 70; fetal liver, 150; bone marrow, 75; placenta, 100; HeLa, 50; HBL, 100; and BT474, 50.

It was further observed that there were many more "novel" genes among those that were up-regulated in only one tissue, as compared with those that were down-regulated in only one tissue. In fact, it was found that ORFs whose expression was measurable in only a single of the tested tissues were represented in sequencing databases at a rate of only 11%, whereas 36% of the ORFs whose expression was measurable in 9 of the tissues were present in public databases. As for those ORFs expressed in all ten tissues, fully 45% were present in existing expressed sequence databases. These results are not unexpected, since genes expressed in a greater number of tissues have a higher likelihood of being, and thus of having been, discovered by EST approaches.

Comparison of Signal from Known and Unknown Genes

The normalized signal of the genes found to have high homology to genes present in the GenBank human EST

database were compared to the normalized signal of those genes not found in the GenBank human EST database. The data are shown in FIG. 8.

FIG. 8 shows the normalized Cy3 signal intensity for all sequence-verified products with a BLAST Expect ("E") value of greater than $1e-30$ (designated "unknown") upon query of existing EST, NR and SwissProt databases, and shows in blue the normalized Cy3 signal intensity for all sequence-verified products with a BLAST Expect value of less than $1e-30$ ("known"). Note that biological background noise has an averaged normalized Cy3 signal intensity of 0.2.

As expected, the most highly expressed of the ORFs were "known" genes. This is not surprising, since very high signal intensity correlates with very commonly-expressed genes, which have a higher likelihood of being found by EST sequence.

However, a significant point is that a large number of even the high expressers were "unknown". Since the genomic approach used to identify genes and to confirm their expression does not bias exons toward either the 3' or 5' end of a gene, many of these high expression genes will not have been detected in an end-sequenced cDNA library.

The significant point is that presence of the gene in an EST database is *not* a prerequisite for incorporation into a genome-derived microarray, and further, that arraying such "unknown" exons can help to assign function to as-yet undiscovered genes.

Verification of Gene Expression

To ascertain the validity of the approach described above to identify genes from raw genomic sequence, expression of two of the probes was assayed using reverse transcriptase polymerase chain reaction (RT PCR)

and northern blot analysis.

Two microarray probes were selected on the basis of exon size, prior sequencing success, and tissue-specific gene expression patterns as measured by the microarray experiments. The primers originally used to amplify the two respective ORFs from genomic DNA were used in RT PCR against a panel of tissue-specific cDNAs (Rapid-Scan gene expression panel 24 human cDNAs) (OriGene Technologies, Inc., Rockville, MD).

Sequence AL079300_1 was shown by microarray hybridization to be present in cardiac tissue, and sequence AL031734_1 was shown by microarray experiment to be present in placental tissue (data not shown). RT-PCR on these two sequences confirmed the tissue-specific gene expression as measured by microarrays, as ascertained by the presence of a correctly sized PCR product from the respective tissue type cDNAs.

Clearly, all microarray results cannot, and indeed should not, be confirmed by independent assay methods, or the high throughput, highly parallel advantages of microarray hybridization assays will be lost. However, in addition to the two RT-PCR results presented above, the observation that 1/3 of the arrayed genes exist in expression databases provides powerful confirmation of the power of our methodology – which combines bioinformatic prediction with expression confirmation using genome-derived single exon microarrays – to identify novel genes from raw genomic data.

To verify that the approach further provides correct characterization of the expression patterns of the identified genes, a detailed analysis was performed of the microarrayed sequences that showed high signal in brain.

For this latter analysis, sequences that showed high (normalized) signal in brain, but which showed very low (normalized) signal (less than 0.5, determined to be

biological noise) in all other tissues, were further studied. There were 82 sequences that fit these criteria, approximately 2% of the arrayed elements. The 10 sequences showing the highest signal in brain in microarray
 5 hybridizations are detailed in Table 2, along with assigned function, if known or reasonably predicted.

Table 2

Function of the Most Highly Expressed Genes Expressed Only in Brain				
Microarray Sequence Name	Normal Signal	Expressi on Ratio	Homology to EST present in GenBank	Gene Function as described by GenBank
AP000217-1	5.2	+7.7	High	S-100 protein, b-chain, Ca ²⁺ binding protein expressed in central nervous system
AP000047-1	2.3		High	Unknown Function
AC006548-9	1.7		High	Similar to mouse membrane glyco-protein M6, expressed in central nervous system

AC007245-5	1.5		High	Similar to amphiphysin, a synaptic vesicle-associated protein. Ref 21
L44140-4	1.2	+2.0	High	Endothelial actin-binding protein found in nonmuscle filamin
AC004689-9	1.2	+3.5	High	Protein Phosphatase PP2A, neuronal/ downregulates activated protein kinases
AL031657-1	1.2	+3.0	High	Unknown function/ Contains the anhyrin motif, a common protein sequence motif
AC009266-2	1.1	+3.7	Low	Low homology to the Synaptotagmin I protein in rat/present at low levels throughout rat brain
AP000086-1	1.0	+2.7	Low	Unknown, very poor homology to collagen

AC004689-3	1.0		High	Protein Phosphatase PP2A, neuronal/ downregulates activated protein kinases
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Of the ten sequences studied by these latter confirmatory approaches, eight were previously known. Of these eight, six had previously been reported to be
5 important in the central nervous system or brain. The exon giving the highest signal (AP00217-1) was found to be the gene encoding an S100B Ca^{2+} binding protein, reported in the literature to be highly and uniquely expressed in the central nervous system. Heizmann, *Neurochem. Res.* 9:1097
10 (1997).

A number of the brain-specific probe sequences (including AC006548-9, AC009266-2) did not have homology to any known human cDNAs in GenBank but did show homology to rat and mouse cDNAs. Sequences AC004689-9 and AC004689-3
15 were both found to be phosphatases present in neurons (Millward et al., *Trends Biochem. Sci.* 24(5):186-191 (1999)). Two microarray sequences, AP000047-1 and AP000086-1 have unknown function, with AP000086-1 being absent from GenBank. Functionality can now be narrowed
20 down to a role in the central nervous system for both of these genes, showing the power of designing microarrays in this fashion.

Next, the function of the chip sequences with the highest (normalized) signal intensity in brain, regardless
25 of expression in other tissues, was assessed. In this latter analysis, we found expression of many more common genes, since the sequences were not limited to those expressed only in brain. For example, looking at the 20 highest signal intensity spots in brain, 4 were similar to

tubulin (AC00807905; AF146191-2; AC007664-4; AF14191-2), 2
were similar to actin (AL035701-2; AL034402-1), and 6 were
found to be homologous to glyceraldehyde-3-phosphate
dehydrogenase (GAPDH) (AL035604-1; Z86090-1; AC006064-L,
5 AC006064-K; AC035604-3; AC006064-L). These genes are often
used as controls or housekeeping genes in microarray
experiments of all types.

Other interesting genes highly expressed in brain
were a ferritin heavy chain protein, which is reported in
10 the literature to be found in brain and liver (Joshi et
al., *J. Neurol. Sci.* 134(Suppl):52-56 (1995)), a result
duplicated with the array. Other highly expressed chip
sequences included a translation elongation factor 1 α
(AC007564-4), a DEAD-box homolog (AL023804-4), and a Y-
15 chromosome RNA-binding motif (Chai et al., *Genomics*
49(2):283-89 (1998)) (AC007320-3). A low homology analog
(AP00123-1/2) to a gene, DSCR1, thought to be involved in
trisomy 21 (Down's syndrome), showed high expression in
both brain and heart, in agreement with the literature
20 (Fuentes et al., *Mol. Genet.* 4(10):1935-44 (1995)).

As a further validation of the approach, we
selected the BAC AC006064 to be included on the array.
This BAC was known to contain the GAPDH gene, and thus
could be used as a control for the ORF selection process.
25 The gene finding and exon selection algorithms resulted in
choosing 25 exons from BAC AC006064 for spotting onto the
array, of which four were drawn from the GAPDH gene. Table
3 shows the comparison of the average expression ratio for
the 4 exons from BAC006064 compared with the average
30 expression ratio for 5 different dilutions of a
commercially available GAPDH cDNA (Clontech).

Table 3

Comparison of Expression Ratio, for each tissue, of GAPDH		
	AC006064 (n = 4)	Control (n = 5)
Bone Marrow	-1.81 \pm 0.11	-1.85 \pm 0.08
Brain	-1.41 \pm 0.11	-1.17 \pm 0.05
BT474	1.85 \pm 0.09	1.66 \pm 0.12
Fetal Liver	-1.62 \pm 0.07	-1.41 \pm 0.05
HBL100	1.32 \pm 0.05	2.64 \pm 0.12
Heart	1.16 \pm 0.09	1.56 \pm 0.10
HeLa	1.11 \pm 0.06	1.30 \pm 0.15
Liver	-1.62 \pm 0.22	-2.07 \pm
Lung	-4.95 \pm 0.93	-3.75 \pm 0.21
Placenta	-3.56 \pm 0.25	-3.52 \pm 0.43

Each tissue shows excellent agreement between the experimentally chosen exons and the control, again demonstrating the validity of the present exon mining approach. In addition, the data also show the variability of expression of GAPDH within tissues, calling into question its classification as a housekeeping gene and utility as a housekeeping control in microarray experiments.

EXAMPLE 3

Representation of Sequence and Expression Data as a "Mondrian"

15

For each genomic clone processed for microarray as above-described, a plethora of information was accumulated, including full clone sequence, probe sequence within the clone, results of each of the three gene finding programs, EST information associated with the probe

20

sequences, and microarray signal and expression for multiple tissues, challenging our ability to display the information.

Accordingly, we devised a new tool for visual
5 display of the sequence with its attendant annotation which, in deference to its visual similarity to the paintings of Piet Mondrian, is hereinafter termed a "Mondrian". FIGS. 3 and 4 present the key to the information presented on a Mondrian.

10 FIG. 9 presents a Mondrian of BAC AC008172 (bases 25,000 to 130,000 shown), containing the carbamyl phosphate synthetase gene (AF154830.1). Purple background within the region shown as field 81 in FIG. 3 indicates all 37 known exons for this gene.

15 As can be seen, GRAIL II successfully identified 27 of the known exons (73%), GENEFINDER successfully identified 37 of the known exons (100%), while DICTION identified 7 of the known exons (19%).

Seven of the predicted exons were selected for
20 physical assay, of which 5 successfully amplified by PCR and were sequenced. These five exons were all found to be from the same gene, the carbamyl phosphate synthetase gene (AF154830.1).

The five exons were arrayed, and gene expression
25 measured across 10 tissues. As is readily seen in the Mondrian, the five chip sequences on the array show identical expression patterns, elegantly demonstrating the reproducibility of the system.

FIG. 10 is a Mondrian of BAC AL049839. We
30 selected 12 exons from this BAC, of which 10 successfully sequenced, which were found to form between 5 and 6 genes. Interestingly, 4 of the genes on this BAC are protease inhibitors. Again, these data elegantly show that exons selected from the same gene show the same expression
35 patterns, depicted below the red line. From this figure,

it is clear that our ability to find known genes is very good. A novel gene is also found from 86.6 kb to 88.6 kb, upon which all the exon finding programs agree. We are confident we have two exons from a single gene since they
5 show the same expression patterns and the exons are proximal to each other. Backgrounds in the following colors indicate a known gene (top to bottom):
red = kallistatin protease inhibitor (P29622);
purple = plasma serine protease inhibitor (P05154);
10 turquoise = α 1 anti-chymotrypsin (P01011); mauve = 40S ribosomal protein (P08865). Note that chip sequence 8 and 12 did not sequence verify.

15 EXAMPLE 4

Genome-Derived Single Exon Probes Useful For Measuring Human Gene Expression

The protocols set forth in Examples 1 and 2,
20 *supra*, were applied to additional human genomic sequence as it became newly available in GenBank to identify unique exons in the human genome that could be shown to be expressed at significant levels in brain tissue.

These unique exons are within longer probe
25 sequences. Each probe was completely sequenced on both strands prior to its use on a genome-derived single exon microarray; sequencing confirms the exact chemical structure of each probe. An added benefit of sequencing is that it placed us in possession of a set of single base-
30 incremented fragments of the sequenced nucleic acid, starting from the sequencing primer 3' OH. (Since the single exon probes were first obtained by PCR amplification from genomic DNA, we were of course additionally in possession of an even larger set of single base incremented
35 fragments of each of the 12,821 single exon probes, each

fragment corresponding to an extension product from one of the two amplification primers.)

The structures of the 12,821 unique single exon probes are clearly presented in the Sequence Listing as SEQ ID Nos.: 1 - 12,821. The 16 nt 5' primer sequence and 16 nt 3' primer sequence present on the amplicon are not included in the sequence listing. The sequences of the exons present within each of these probes is presented in the Sequence Listing as SEQ ID NOs.: 12,822 - 25,434, respectively. It will be noted that some amplicons have more than one exon, some exons are contained in more than one amplicon.

As detailed in Example 2, expression was demonstrated by disposing the amplicons as single exon probes on nucleic acid microarrays and then performing two-color fluorescent hybridization analysis; significant expression is based on a statistical confidence that the signal is significantly greater than negative biological control spots. The negative biological control is formed from spotted DNA sequences from a different species. Here, 32 sequences from E.Coli were spotted in duplicate to give a total of 64 spots.

For each hybridisation (each slide, each colour) the median value of the signal from all of the spots is determined. The normalised signal value is the arithmetic mean of the signal from duplicate spots divided by the population median.

Control spots are eliminated if there is more than a five-fold difference between each one of the duplicate spots raw signals.

The median of the signal from the remaining control spots is calculated and all subsequent calculations are done with normalised signals.

Control spots having a signal of greater than median + 2.4 (the value 2.4 is roughly 12 times the

observed standard deviation of control spot populations) are eliminated. Spots with such high signals are considered to be "outliers".

The mean and standard deviation of the modified
5 control spot populations are calculated.

The mean + 3x the standard deviation (mean + (3*SD)) is used as the signal threshold qualifier for that particular hybridisation. Thus, individual thresholds are determined for each channel and each hybridisation.

10 This means that, assuming that the data is distributed normally, there is a 99% confidence that any signal exceeding the threshold is significant.

The probes and their expression data are presented in Table 4, set forth respectively in Example 5.
15 Example 5 presents the subset of probes that is significantly expressed in the human heart and thus presents the subset of probes that was recognized to be useful for measuring expression of their cognate genes in human brain tissue.

20 The sequence of each of the exon probes identified by SEQ ID NOS.: 12,822 - 25,434 was individually used as a BLAST (or, for SWISSPROT, BLASTX) query to identify the most similar sequence in each of dbEST, SwissProt (BLASTX), and NR divisions of GenBank. Because
25 the query sequences are themselves derived from genomic sequence in GenBank, only nongenic hits from NR were scored.

The smallest in value of the BLAST (or BLASTX) expect ("E") scores for each query sequence across the
30 three database divisions was used as a measure of the "expression novelty" of the probe's ORF. Table 4 is sorted in descending order based on this measure, reported as "Most Similar (top) Hit BLAST E Value". Those sequences for which no "Hit E Value" is listed are those exons which were
35 found to have no similar sequences.

As sorted, Table 4 thus lists its respective probes (by "AMPLICON SEQ ID NO.:" and additionally by the SEQ ID NO:. of the exon contained within the probe:"EXON SEQ ID NO.:") from least similar to sequences known to be expressed (*i.e.*, highest BLAST E value), at the beginning of the table, to most similar to sequences known to be expressed (*i.e.*, lowest BLAST E value), at the bottom of the table.

Table 4 further provides, for each listed probe, the accession number of the database sequence that yielded the "Most Similar (top) Hit BLAST E Value", along with the name of the database in which the database sequence is found ("Top Hit Database Source").

Table 4 further provides SEQ ID NOS. corresponding to the predicted amino acid sequences where they have been determined for the probe and exon nucleotide sequences. These are set out as PEPTIDE SEQ ID NOS.:. The peptide sequences for a given exon are predicted as follows: Since each chip exon is a consensus sequence drawn from predictions from various exon finding programs (*i.e.* Grail, GeneFinder and GenScan), the multiple initial ORFs are first determined in a uniform way according to each prediction. In particular, the reading frame for predicting the first amino acid in the peptide sequence always starts with the first base of any codon and ends with the last base of non-termination codon. Next, for each strand of the exon, initial ORFs are merged into one or more final ORFs in an exhaustive process based on the following criteria: 1) the merging ORFs must be overlapping, and 2) the merging ORFs must be in the same frame.

The Sequence Listing, which is a superset of all of the data presented in Table 4, further includes, for each probe, the most similar hit, with accession number and BLAST E value, from the each of the three queried databases.

Table 4 further lists, for each probe, a portion of the descriptor for the top hit ("Top Hit Descriptor") as provided in the sequence database. For those ORFs that are similar in sequence, but nonidentical to known sequences (e.g., those with BLAST E values between about $1e-05$ and $1e-100$), the descriptor reveals the likely function of the protein encoded by the probe's ORF.

Using BLAST E value cutoffs of $1e-05$ (i.e., 1×10^{-5}) and $1e-100$ (i.e., 1×10^{-100}) as evidence of similarity to sequences known to be expressed is of course arbitrary: in Example 2, *supra*, a BLAST E value of $1e-30$ was used as the boundary when only two classes were to be defined for analysis (unknown, $>1e-30$; known $<1e-30$) (see also FIG. 8). Furthermore, even when the "Most Similar (Top) Hit BLAST E Value" is low, e.g., less than about $1e-100$ — which is probative evidence that the query sequence has previously been shown to be expressed — the top hit is highly unlikely exactly to match the probe sequence.

First, such expression entries typically will not have the intronic and/or intergenic sequence present within the single exon probes listed in the Table. Second, even the ORF itself is unlikely in such cases to be present identically in the databases, since most of the EST and mRNA clones in existing databases include multiple exons, without any indication of the location of exon boundaries.

As noted, the data presented in Table 4 represent a proper subset of the data present within the attached sequence listing. For each amplicon probe (SEQ ID NOs.: 1 - 12,821) and probe exon (SEQ ID NOs.: 12,822 - 25,434, respectively), the sequence listing further provides, through iterated annotation fields $<220>$ and $<223>$:

(a) the accession number of the BAC from which the sequence was derived ("MAP TO"), thus providing a link to the chromosomal map location and other information about the genomic milieu of the probe sequence;

(b) the most similar sequence provided by BLAST query of the EST database, with accession number and BLAST E value for the "hit";

(c) the most similar sequence provided by BLAST query of the GenBank NR database, with accession number and BLAST E value for the "hit"; and

(d) the most similar sequence provided by BLASTX query of the SWISSPROT database, with accession number and BLAST E value for the "hit".

10

EXAMPLE 5

Genome-Derived Single Exon Probes Useful For Measuring Expression of Genes in Human Brain

15

Table 4 (536 pages) presents expression, homology, and functional information for the genome-derived single exon probes that are expressed significantly in human brain.

20

CLAIMS

1. A spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived
5 from human brain comprising a plurality single exon nucleic probes, said probes comprising any one of the nucleotide sequences set out in SEQ ID NOs: 1 - 12,821 or a complementary sequence, or a portion of such a sequence.
- 10 2. A spatially-addressable set of single exon nucleic acid probes as claimed in claim 1 wherein each of said plurality of probes is separately and addressably amplifiable.
3. A spatially-addressable set of single exon nucleic acid
15 probes as claimed in claim 1 wherein each of said plurality of probes is separately and addressably isolatable from said plurality.
4. A spatially-addressable set of single exon nucleic acid
20 probes as claimed in any of claims 1 to 3 wherein said probes comprise any one of the nucleotide sequences set out in SEQ ID NOS.: 12,822 - 25,434.
5. A spatially-addressable set of single exon nucleic acid
25 probes as claimed in any of claims 1 to 4, wherein each of said plurality of probes is amplifiable using at least one common primer.
6. A spatially-addressable set of single exon nucleic acid
30 probes as claimed in any of claims 1 to 5 wherein the set comprises between 50 - 20,000 single exon nucleic acid probes.
7. A spatially-addressable set of single exon nucleic acid
35 probes as claimed in any of claims 1 to 6, wherein the

average length of the single exon nucleic acid probes is between 200 and 500 bp.

8. A spatially-addressable set of single exon nucleic acid probes as claimed in any of claims 1 to 7, wherein at least 50% of said single exon nucleic acid probes lack prokaryotic and bacteriophage vector sequence.

9. A spatially-addressable set of single exon nucleic acid probes as claimed in any of claims 1 to 8, wherein at least 50% of said single exon nucleic acid probes lack homopolymeric stretches of A or T.

10. A spatially-addressable set of single exon nucleic acid probes as claimed in any of claims 1 - 9 characterised in that said set of probes is addressably disposed upon a substrate.

11. A spatially-addressable set of single exon nucleic acid probes as claimed in claim 10 wherein said substrate is selected from glass, amorphous silicon, crystalline silicon and plastic.

12. A microarray comprising a spatially addressable set of single exon nucleic acid probes as claimed in any of claims 1 - 11.

13. A single exon nucleic acid probe for measuring human gene expression in a sample derived from human brain comprising a nucleotide sequence as set out in any of SEQ ID NOs.: 1 - 12,821 or a complementary sequence or a fragment thereof wherein said probe hybridizes at high stringency to a nucleic acid molecule expressed in the human brain.

14. A single exon nucleic acid probe as claimed in claim 13 comprising a nucleotide sequence as set out in any of SEQ ID NOs.: 12,822 - 25,434 or a complementary sequence or a fragment thereof.
- 5
15. A single exon nucleic acid probe for measuring human gene expression in a sample derived from human brain which is a nucleic acid molecule having a sequence encoding a peptide comprising a peptide sequence as set out in any of
10 SEQ ID NOs.: 25,435 - 37,811, or a complementary sequence or a fragment thereof wherein said probe hybridizes at high stringency to a nucleic acid expressed in the human brain.
16. A single exon nucleic acid probe as claimed in any one
15 of claims 13 to 15 wherein said single exon nucleic acid probe comprises between 15 and 25 contiguous nucleotides of said SEQ ID NO.
17. A single exon nucleic acid probe as claimed in any one
20 of claims 13 to 15, wherein said probe is between 3 - 25 kb in length.
18. A single exon nucleic acid probe as claimed in any one
25 of claims 13 - 17, wherein said probe is DNA, RNA or PNA.
19. A single exon nucleic acid probe as claimed in any one of claims 13 - 18, wherein said probe is detectably labeled.
- 30 20. A single exon nucleic acid probe as claimed in any one of claims 13 - 19, wherein said probe lacks prokaryotic and bacteriophage vector sequence.
- 35 21. A single exon nucleic acid probe as claimed in any one of claims 13 - 20, wherein said probe lacks homopolymeric

stretches of A or T.

22. A method of measuring gene expression in a sample derived from human brain, comprising:

5 contacting the microarray of claim 12, with a first collection of detectably labeled nucleic acids, said first collection of nucleic acids derived from mRNA of human brain; and then
10 measuring the label detectably bound to each probe of said microarray.

23. A method of identifying exons in a eukaryotic genome, comprising:

15 algorithmically predicting at least one exon from genomic sequence of said eukaryote; and then detecting specific hybridization of detectably labeled nucleic acids to a single exon probe,
20 wherein said detectably labeled nucleic acids are derived from mRNA from the brain of said eukaryote, said probe is a single exon probe having a fragment identical in sequence to, or complementary in sequence to, said predicted exon, said probe is included within a microarray according to claim 12, and said fragment is selectively hybridizable at high stringency.

25 24. A method of assigning exons to a single gene, comprising:

30 identifying a plurality of exons from genomic sequence according to the method of claim 23; and then measuring the expression of each of said exons in a plurality of tissues and/or cell types using hybridization to single exon microarrays having a probe with said exon,
35 wherein a common pattern of expression of said exons in

said plurality of tissues and/or cell types indicates that the exons should be assigned to a single gene.

25. A nucleic acid sequence as set out in any of SEQ ID
5 NOs: 1 - 25,434 which encodes a peptide.
26. A peptide encoded by a sequence as set out in any of
SEQ ID Nos: 1 - 25,434.
- 10 27. A peptide comprising a sequence as set out in any of
SEQ ID NOs: 25,435 - 37,811.

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Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
437	13223	25868	6.47				
869	13638	26308	15.92				
1022	13782		2.15				
1279	14029	26698	10.88				
1488	14235	26921	1.22				
1488	14235	26922	1.22				
1609	14355	27044	3.19				
1633	14379	27066	6.1				
1718	14461	27180	3.31				
1743	14485	27184	1.44				
1750	14492	27192	6.78				
1884	14621	27331	1.44				
1971	14707	27425	2.14				
2162	14892	27627	2.7				
2277	15003	27743	2.91				
2578	15292	28028	1				
2578	15292	28029	1				
3181	15944	28595	2.83				
3442	16198	28848	1.42				
3505	16261	28915	12.04				
3549	16304		1				
3549	16402	29042	1.87				
3928	16678		1.03				
4173	16913	29543	1.52				
4230	16971	29595	6.4				
4248	16989	29613	0.97				
4248	16989	29614	0.97				
4303	17042		1.07				
4361	17099	29734	0.76				
4784	17516	30138	0.99				
4983	17706	30310	5.38				
4995	17718	30323	1.3				
5176	17965	30500	1.57				
5176	17985	30501	1.57				

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Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5336	18139		4.3				
5510	18308		6.14				
5593	18139		3.97				
5948	18443	31356	0.6				
5654	18449	31362	3.28				
5932	25082	31673	1.62				
5958	18740	31999	1.75				
6322	19092		1.27				
6454	19222	32220	1.1				
6454	19222	32221	1.1				
7025	19717	32774	1				
7025	19717	32775	1				
7311	19994	33071	1.76				
7311	19994	33072	1.76				
7712	20376		0.61				
7980	20655	33780	1.4				
8384	21077	34214	1.49				
8799	21451	34598	0.59				
8799	21451	34599	0.59				
9434	22112	35287	2.67				
9606	22318	35515	0.77				
9792	22433	35638	1.24				
9922	22570	35767	0.94				
10328	22975	36194	0.62				
10328	22975	36195	0.62				
10582	23277		2.53				
10749	25131	36878	1.34				
10952	23629		2.2				
11030	23701	36968	1.84				
11332	24023	37328	2.02				
11485	24086		2.47				
12313	24735		1.52				
12609	24916	31006	2.36				
5961	18743	31703	17.79	9.9E+000 AJ239028.1	NT		Homo sapiens LSS gene, partial, exons 15, 16, 17 and 18

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Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7805	20600	33730	1.74	9.8E+00	U52716.1	NT	Haemophilus influenzae Rd section 31 of 163 of the complete genome
9643	22295	35489	0.44	9.8E+00	Y18930.1	NT	Sulfobolus solfataricus 281 kb genomic DNA fragment, strain P2
9643	22295	35490	0.44	9.8E+00	Y18930.1	NT	Sulfobolus solfataricus 281 kb genomic DNA fragment, strain P2
6801	19639	32684	0.73	9.6E+00	AF05630.1	NT	Gallus gallus ornithine transcarbamylase (OTC) gene, exon 1
6801	19639	32685	0.73	9.6E+00	AF05630.1	NT	Gallus gallus ornithine transcarbamylase (OTC) gene, exon 1
10321	22968	36187	1.17	9.6E+00	AF242432.1	NT	Mus musculus Naip3 gene, exon 1; neuronal apoptosis inhibitory protein 1 (Naip1) and general transcription factor 1H polypeptide 2 (Gt2h2) genes, complete cds
10321	22968	36188	1.17	9.6E+00	AF242432.1	NT	Mus musculus Naip3 gene, exon 1; neuronal apoptosis inhibitory protein 1 (Naip1) and general transcription factor 1H polypeptide 2 (Gt2h2) genes, complete cds
2671	15381	28119	1	9.4E+00	L11433.1	NT	Dengue virus type 3 membrane protein (prMM)/envelope glycoprotein (E) polyprotein mRNA, partial cds
2671	15381	28120	1	9.4E+00	L11433.1	NT	Dengue virus type 3 membrane protein (prMM)/envelope glycoprotein (E) polyprotein mRNA, partial cds
2824	16690	28334	2.87	9.4E+00	AB043785.1	NT	Mus musculus A73 gene for antithrombin, complete cds
7997	20692	33820	0.91	9.3E+00	AF130980.1	NT	Homo sapiens ectodysplasin-A receptor protein (EDAR) gene, exons 2, 3, and 4
8901	21592	34733	3.06	9.3E+00	P11210	SWISSPROT	IMMEDIATE-EARLY PROTEIN 1 (IE1) (IMMEDIATE-EARLY PHOSPHOPROTEIN PP89)
5214	18022	30645	2.46	9.1E+00	AF085609.1	NT	Leuciscus cephalus orientalis cytochrome b (cyt b) gene, partial cds; mitochondrial gene for mitochondrial product
5214	18022	30646	2.46	9.1E+00	AF085609.1	NT	Leuciscus cephalus orientalis cytochrome b (cyt b) gene, partial cds; mitochondrial gene for mitochondrial product
8330	21997		0.83	9.0E+00	P08241	SWISSPROT	RHODOPSIN
5946	18727	31685	5.55	8.9E+00	BE971806.1	EST_HUMAN	601651038R1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:3934592 3'
6287	19080	32041	2.28	8.7E+00	AB019788.1	NT	Cynops pyrrhogaster CpTbx3 premature mRNA, partial cds
6287	19080	32042	2.28	8.7E+00	AB019788.1	NT	Cynops pyrrhogaster CpTbx3 premature mRNA, partial cds
430	13216	25861	2.3	8.4E+00	5031804	NT	Homo sapiens insulin receptor substrate 1 (IRS1) mRNA
6355	20426	33545	3.58	8.1E+00	AJ131719.1	NT	Zea mays mRNA for legumain-like protease (see2a)
11122	23791		2	8.0E+00	P41820	SWISSPROT	BREFELDIN A RESISTANCE PROTEIN
8051	20745		0.89	7.6E+00	Z21489.1	NT	African swine fever virus NP1450L gene encoding RNA polymerase largest subunit
7246	19931		1.9	7.5E+00	AL445065.1	NT	Thermoplasma acidophilum complete genome, segment 3/5
8259	20953	34090	1.61	7.5E+00	P35441	SWISSPROT	THROMBOSPONDIN 1 PRECURSOR
8259	20953	34091	1.61	7.5E+00	P35441	SWISSPROT	THROMBOSPONDIN 1 PRECURSOR
5711	18504	31428	2.66	7.4E+00	BF700517.1	EST_HUMAN	602128876F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4286506 5'
8651	21343	34487	2.7	7.4E+00	P04929	SWISSPROT	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR
8651	21343	34488	2.7	7.4E+00	P04929	SWISSPROT	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR

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Single Exon Probes Expressed In Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2977	15743	28390	3.56	7.2E+00	L12051.1	NT	Lycopodium esculentum Mill. GTPase (SAR2) mRNA, complete cds
2977	15743	28391	3.56	7.2E+00	L12051.1	NT	Lycopodium esculentum Mill. GTPase (SAR2) mRNA, complete cds
6931	19667	32713	0.71	7.2E+00	BE179090.1	EST_HUMAN	RCO-H10613-200300-031-a07 HT0613 Homo sapiens cDNA
7049	19740	32800	1.28	7.1E+00	P28166	SWISSPROT	ZINC-FINGER PROTEIN 1 (ZINC-FINGER HOMEODOMAIN PROTEIN 1)
7049	19740	32801	1.28	7.1E+00	P28166	SWISSPROT	ZINC-FINGER PROTEIN 1 (ZINC-FINGER HOMEODOMAIN PROTEIN 1)
9498	22151		6.63	7.1E+00	AL161595.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 91
11359	24047	37350	3.28	7.1E+00	P05850	SWISSPROT	HYPOTHETICAL 17.3 KDA PROTEIN IN MRDA-PHPB INTERGENIC REGION
9882	22532	35729	3.37	7.0E+00	P48610	SWISSPROT	ARGININE KINASE (AK)
11215	23878	37165	1.51	7.0E+00	O22469	SWISSPROT	WD-40 REPEAT PROTEIN MS13
8181	20875	34011	1.92	6.9E+00	P35679	SWISSPROT	60S RIBOSOMAL PROTEIN L4 (L2)
10249	22897	36107	1.38	6.9E+00	P44834	SWISSPROT	DNA MISMATCH REPAIR PROTEIN MUTS
10267	22915	36125	0.47	6.9E+00	P34226	SWISSPROT	SKI5 PROTEIN
7808	20503	33623	1.53	6.8E+00	W03412.1	EST_HUMAN	zao7c11.11 Soeres melanocyte 2Nblm Homo sapiens cDNA clone IMAGE:291860 5'
7808	20503	33624	1.53	6.8E+00	W03412.1	EST_HUMAN	zao7c11.11 Soeres melanocyte 2Nblm Homo sapiens cDNA clone IMAGE:291860 5'
9031	21721		1.29	6.8E+00	P36307	SWISSPROT	OUTER CAPSID PROTEIN VP4 (HEMAGGLUTININ) (OUTER LAYER PROTEIN VP4) [CONTAINS:
10109	22757	35969	3.24	6.8E+00	Q03570	SWISSPROT	OUTER CAPSID PROTEIN VP4 (HEMAGGLUTININ) (OUTER LAYER PROTEIN VP4) [CONTAINS:
5202	18010		0.72	6.6E+00	Q09028	SWISSPROT	HYPOTHETICAL 157.0 KDA PROTEIN C38C10.5 IN CHROMOSOME III
6450	19218	32216	0.61	6.6E+00	BF672121.1	EST_HUMAN	CATECHOL-O-METHYLTRANSFERASE, SOLUBLE FORM (S-COMT)
9974	22822	35827	2.36	6.6E+00	Q9ZE07	SWISSPROT	602152573F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4283427 5'
9974	22822	35828	2.36	6.6E+00	Q9ZE07	SWISSPROT	URIDYLATE KINASE (UK) (URIDINE MONOPHOSPHATE KINASE) (UMP KINASE)
11073	23743		1.97	6.6E+00	Q10309	SWISSPROT	URIDYLATE KINASE (UK) (URIDINE MONOPHOSPHATE KINASE) (UMP KINASE)
9079	21768	34931	7	6.5E+00	P03374	SWISSPROT	PROBABLE CATION-TRANSPORTING ATPASE C8C3.05C
10203	22851	36067	0.48	6.5E+00	BE866001.1	EST_HUMAN	ENV POLYPROTEIN [CONTAINS: COAT PROTEIN GP52, COAT PROTEIN GP36]
9842	22294	35488	1.55	6.2E+00	AY010901.1	EST_HUMAN	601678435F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3960969 5'
10460	23106	36337	0.5	6.2E+00	8754621	NT	Schizaphyllum commune unknown mRNA
6938	19871	32717	1.46	6.0E+00	BE780163.1	EST_HUMAN	Mus musculus mannose 2, alpha B1 (Man2b1), mRNA
8716	23367	35565	0.46	6.0E+00	AP000006.1	NT	601468031F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3871303 5'
10411	23057	36274	0.67	6.0E+00	AE001862.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 1166001-1485000 nt, position (617)
10411	23057	36275	0.67	6.0E+00	AE001862.1	NT	Deinococcus radiodurans R1 section 1 of 2 of the complete chromosome 2
						NT	Deinococcus radiodurans R1 section 1 of 2 of the complete chromosome 2
						NT	Mus musculus mixed lineage kinase 3 (Mlk3) and two pore domain K+ channel subunit (Kcnk6) genes, complete cds
6428	19196	32193	7.32	5.9E+00	AF155142.1	NT	
3514	16270		0.99	5.8E+00	7661557	NT	Homo sapiens DESC1 protein (DESC1), mRNA
7061	19752	32816	0.95	5.7E+00	AF302046.1	NT	Mus musculus immunoglobulin scavenger receptor (gSR) mRNA, complete cds

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7081	19752	32817	0.95	5.7E+00	AF302046.1	NT	Mus musculus immunoglobulin scavenger receptor IgSR mRNA, complete cds
7468	20142		1.13	5.6E+00	P75080	SWISSPROT	DNA POLYMERASE III, ALPHA CHAIN POLC-TYPE (POLII)
11456	23223	36458	2.99	5.6E+00	Q55276	SWISSPROT	LYCOPENE BETA CYCLASE
8157	19934	31901	0.69	5.5E+00	P47447	SWISSPROT	HEAT-INDUCIBLE TRANSCRIPTION REPRESSOR HRCA
10678	23369		1.28	5.5E+00	AF175425.1	NT	Mus musculus DNA methyltransferase (Dnmt1) gene, exons 30, 31, and 32
11454	23221	36455	3.09	5.5E+00	P11990	SWISSPROT	PNEUMOLYSIN (THIOL-ACTIVATED CYTOLYSIN)
8830	19492	32514	1.14	5.4E+00	X02212.1	NT	Chicken alpha-cardiac actin gene
8830	19492	32515	1.14	5.4E+00	X02212.1	NT	Chicken alpha-cardiac actin gene
7769	20465		1.54	5.4E+00	Q91062	SWISSPROT	VITELLOGENIN PRECURSOR (VTG) [CONTAINS: LIPOVITELLIN LV-1N; LIPOVITELLIN LV-1C; LIPOVITELLIN LV-2]
8698	21390	34534	0.83	5.4E+00	P40379	SWISSPROT	REP1 PROTEIN
8698	21390	34535	0.83	5.4E+00	P40379	SWISSPROT	REP1 PROTEIN
9936	22584	35784	1.83	5.4E+00	Q17094	SWISSPROT	RHODOPSIN
9936	22584	35785	1.83	5.4E+00	Q17094	SWISSPROT	RHODOPSIN
4734	17468	30102	1.32	5.3E+00	L43128.1	NT	Bovine immunodeficiency-like virus surface envelope gene, 5' end of cds
7978	20673		3.23	5.3E+00	P54098	SWISSPROT	DNA POLYMERASE GAMMA (MITOCHONDRIAL DNA POLYMERASE CATALYTIC SUBUNIT)
8882	21573		0.49	5.3E+00	AB034990.1	NT	Homo sapiens HIRPUD1 gene for stress protein Hrp, complete cds
11828	24225	37548	3.2	5.3E+00	Q27905	SWISSPROT	PROBABLE ANTIBACTERIAL PEPTIDE POLYPROTEIN PRECURSOR
6371	18177		0.91	5.2E+00	BE184840.1	EST_HUMAN	QV4-HT0691-270400-186409 HT0691 Homo sapiens cDNA
10271	22919		0.95	5.2E+00	AF248070.1	NT	Drosophila orientacea R1B retrotransposable element reverse transcriptase gene, partial cds
11150	23817		2	5.2E+00	Q10136	SWISSPROT	HYPOPHYSICAL 61.1 KD PROTEIN C23E2.03C IN CHROMOSOME 1
8861	21552	34698	0.9	5.1E+00	Q16005	SWISSPROT	RHODOPSIN
9725	22376	35577	1.19	5.1E+00	P09182	SWISSPROT	COLICIN N IMMUNITY PROTEIN (MICROCIN N IMMUNITY PROTEIN)
6193	18969	31944	0.72	5.0E+00	BF310443.1	EST_HUMAN	601894910F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4124114 5'
10094	22742		0.59	5.0E+00	BF308561.1	EST_HUMAN	601890420F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4131509 5'
10330	22977	36197	3.07	5.0E+00	AF162445.2	NT	Canis familiaris skeletal muscle chloride channel ClC-1 (CLCN1) mRNA, complete cds
11280	23922	37214	8.95	5.0E+00	Z83860.1	NT	Mycobacterium tuberculosis H37RV complete genome; segment 103/162
10132	22780		0.71	4.9E+00	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RefSeq gene, and sodium phosphate transporter (NPT3) gene, complete cds
4039	16784		10.86	4.8E+00	AF185255.1	NT	Eunice australis histone H3 (H3) gene, partial cds
8054	20748	33879	0.47	4.8E+00	BF367909.1	EST_HUMAN	RC3-GN0042-100800-011-c10 GN0042 Homo sapiens cDNA
8439	21131		5.28	4.8E+00	AW750067.1	EST_HUMAN	PMO-BT0547-310100-002-504 BT0547 Homo sapiens cDNA
283	13090	25731	1.86	4.7E+00	BF240552.1	EST_HUMAN	601875654F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4095716 5'

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
284	13080	25731	1.89	4.7E+00	BF240552.1	EST_HUMAN	601875654F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4099716 5'
3268	16030	28679	2.38	4.7E+00	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
9085	21783	34948	1.18	4.6E+00	BE646437.1	EST_HUMAN	7e86g10.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:3292098 3' similar to TR:O75140 O75140
9095	21783	34949	1.18	4.6E+00	BE646437.1	EST_HUMAN	KIAA0645 PROTEIN, contains element PTR5 repetitive element ;
10287	22935		0.61	4.6E+00	AF240786.1	NT	7e86g10.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:3292098 3' similar to TR:O75140 O75140
11054	23724		2.31	4.6E+00	D63999.1	NT	KIAA0645 PROTEIN, contains element PTR5 repetitive element ;
11605	24204	37528	2.59	4.5E+00	AE001044.1	NT	KIAA0645 PROTEIN, contains element PTR5 repetitive element ;
11762	24353	37685	1.78	4.5E+00	BF669841.1	EST_HUMAN	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
3035	15801	28447	0.98	4.4E+00	BF530893.1	EST_HUMAN	Synechocystis sp. PCC6803 complete genome, 18/27, 2287260-2392728
3035	15801	28448	0.98	4.4E+00	BF530893.1	EST_HUMAN	Arohaeoglobus fulgidus section 63 of 172 of the complete genome
6109	18886		1.66	4.4E+00	X13414.1	NT	602123238F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4280216 5'
6027	18807		0.68	4.3E+00	AF059679.1	NT	602072585F1 NCI_CGAP_Brn87 Homo sapiens cDNA clone IMAGE:4215284 5'
7338	20019	33097	2.03	4.3E+00	Y13402.1	NT	602072585F1 NCI_CGAP_Brn87 Homo sapiens cDNA clone IMAGE:4215284 5'
7515	20188	33280	0.65	4.3E+00	AE001222.1	NT	Murine I gene for MHC class II (a) associated invariant chain
10769	23453	36696	7.64	4.3E+00	AF240786.1	NT	Homo sapiens neutrophil collagenase (CLGNA) gene, promoter region and 5'UTR
5430	18229		3.44	4.2E+00	P16444	SWISSPROT	Treponema pallidum section 38 of 87 of the complete genome
5507	18305	31208	0.87	4.2E+00	P51926	SWISSPROT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
6874	19591	32627	2.62	4.2E+00	P13983	SWISSPROT	MICROSOMAL DIPEPTIDASE PRECURSOR (MDP) (DEHYDROPEPTIDASE-I) (RENAL DIPEPTIDASE) (RDP)
6874	19591	32628	2.62	4.2E+00	P13983	SWISSPROT	LAF-4 PROTEIN (LYMPHOID NUCLEAR PROTEIN)
8859	21550	34697	4.68	4.2E+00	AI809013.1	EST_HUMAN	EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN)
9818	22489	35672	1.06	4.2E+00	P31368	SWISSPROT	EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN)
10049	22697		0.48	4.2E+00	P40886	SWISSPROT	wf67g03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2360692 3'
5846	29079	31569	0.56	4.1E+00	O09185	SWISSPROT	NUBBIN PROTEIN (TWIN PROTEIN) (POU DOMAIN PROTEIN 1) (PDM-1) (DPOU-19) (DOCT1)
5846	29079	31570	0.56	4.1E+00	O09185	SWISSPROT	HEXOSE TRANSPORTER HXT8
7012	19704	32760	0.84	4.1E+00	BE25668.1	EST_HUMAN	CELLULAR TUMOR ANTIGEN P83
7111	19799	32863	0.65	4.1E+00	BF247939.1	EST_HUMAN	CELLULAR TUMOR ANTIGEN P83
7559	20229	33332	8.73	4.1E+00	O23810	SWISSPROT	CELLULAR TUMOR ANTIGEN P83
7681	20345		0.62	4.1E+00	AB041523.1	NT	CELLULAR TUMOR ANTIGEN P83
7683	20347	33459	4.32	4.1E+00	P28964	SWISSPROT	CELLULAR TUMOR ANTIGEN P83
							601110727F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3351534 5'
							601859030F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4069758 5'
							YY1 PROTEIN PRECURSOR
							Palinopten yessensis mRNA for calcineurin A, complete cds
							GENE 68 PROTEIN

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7683	20347	33460	4.32	4.1E+00	P28964	SWISSPROT	GENE 68 PROTEIN
7817	20512	33638	2.53	4.1E+00	U57503.1	NT	Pan troglodytes novel repetitive solo LTR element in the RNU2 locus
9440	22118	35285	0.57	4.1E+00	P11253	SWISSPROT	50S RIBOSOMAL PROTEIN L4
9571	22224	35409	2.46	4.1E+00	BF692425.1	EST_HUMAN	602247938F1 NIH_MGC 62 Homo sapiens cDNA clone IMAGE:4333209 5'
10205	22853		0.48	4.1E+00	P46414	SWISSPROT	CYCLIN-DEPENDENT KINASE INHIBITOR 1B (CYCLIN-DEPENDENT KINASE INHIBITOR P27)
10800	23483		3.06	4.1E+00	P09716	SWISSPROT	HYPOTHETICAL PROTEIN HVLF1
10892	23572		11.89	4.1E+00	BE885880.1	EST_HUMAN	601507510F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3909051 5'
3533	16289		0.95	4.0E+00	P38229	SWISSPROT	GLC7-INTERACTING PROTEIN 1
5372	16500	32524	0.77	4.0E+00	O62653	SWISSPROT	SUCRASE-ISOMALTASE, INTESTINAL [CONTAINS: SUCRASE; ISOMALTASE]
5372	16500	32525	0.77	4.0E+00	O62653	SWISSPROT	SUCRASE-ISOMALTASE, INTESTINAL [CONTAINS: SUCRASE; ISOMALTASE]
6838	19500	32524	0.75	4.0E+00	O62653	SWISSPROT	SUCRASE-ISOMALTASE, INTESTINAL [CONTAINS: SUCRASE; ISOMALTASE]
6838	19500	32525	0.75	4.0E+00	O62653	SWISSPROT	SUCRASE-ISOMALTASE, INTESTINAL [CONTAINS: SUCRASE; ISOMALTASE]
7089	19778	32843	1.44	4.0E+00	O33010	SWISSPROT	CELL DIVISION PROTEIN FTSY HOMOLOG
8772	21464	34611	0.45	4.0E+00	Q14157	SWISSPROT	HYPOTHETICAL PROTEIN KIA0144
8843	22494	35695	0.44	4.0E+00	O61309	SWISSPROT	NITRIC-OXIDE SYNTHASE (NOS, TYPE I) (NEURONAL NOS) (N-NOS) (NNOS)
10065	22713	35931	0.63	4.0E+00	AE002132.1	NT	Ureaplasma urealyticum section 33 of 59 of the complete genome
11453	23220	36454	1.53	4.0E+00	P14546	SWISSPROT	CYTOCHROME C OXIDASE POLYPEPTIDE III
11537	24137	37444	2.27	4.0E+00	P07564	SWISSPROT	GENOME POLYPROTEIN [CONTAINS: CAPSID PROTEIN C (CORE PROTEIN); MATRIX PROTEIN (ENVELOPE GLYCOPROTEIN M); MAJOR ENVELOPE PROTEIN E; NONSTRUCTURAL PROTEINS NS1, NS2A, NS2B, NS4A AND NS4B; HELICASE (NS3); RNA-DIRECTED RNA POLYMERASE (NS5)]
11537	24137	37445	2.27	4.0E+00	P07564	SWISSPROT	GENOME POLYPROTEIN [CONTAINS: CAPSID PROTEIN C (CORE PROTEIN); MATRIX PROTEIN (ENVELOPE GLYCOPROTEIN M); MAJOR ENVELOPE PROTEIN E; NONSTRUCTURAL PROTEINS NS1, NS2A, NS2B, NS4A AND NS4B; HELICASE (NS3); RNA-DIRECTED RNA POLYMERASE (NS5)]
3494	16250	28904	4.61	3.9E+00	X64518.1	NT	N. tabacum chitinase gene 50 for class I chitinase C
4287	17026		8.24	3.9E+00	AF055466.1	NT	Mus musculus seminal vesicle secretory protein 89 (MSVSP89) gene, promoter region
5572	18369	31279	2.91	3.9E+00	BE814357.1	EST_HUMAN	MRO-BN0070-300500-028-h05 BN0070 Homo sapiens cDNA
5572	18369	31280	2.91	3.9E+00	BE814357.1	EST_HUMAN	MRO-BN0070-300500-028-h05 BN0070 Homo sapiens cDNA
6591	19354	32367	0.55	3.9E+00	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
6774	19518	32546	4.62	3.9E+00	P39299	SWISSPROT	HYPOTHETICAL TRANSCRIPTIONAL REGULATOR IN AIDS-RPSF INTERGENIC REGION

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Single Exon Probes Expressed in Brain

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7262	19948	33022	4.3	3.9E+00	M23907.1	NT	Human MHC class II lymphocyte antigen (DP-w4-beta-1) gene, exon 2
8216	20910	34048	1.88	3.9E+00	X05865.1	NT	Xlaevis mRNA for M4 muscarinic receptor
11365	23178	36403	3.3	3.9E+00	Y18000.1	NT	Homo sapiens NF2 gene
2635	15347		0.9	3.8E+00	AE001562.1	NT	Helicobacter pylori, strain J99 section 123 of 132 of the complete genome
6287	19070	32054	0.96	3.8E+00	G57630	SWISSPROT	HYPOTHETICAL PROTEIN MJ0385
6673	19590	32628	0.66	3.8E+00	AI493849.1	EST_HUMAN	qz5107 x1 NCL CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2030437 3'
8331	21024	34161	1.1	3.8E+00	D44725.1	EST_HUMAN	HUMSUPY135 Human brain cDNA Homo sapiens cDNA clone 148
9694	22345		0.62	3.8E+00	AJ390361.1	NT	Streptococcus oralis partial xpi gene for xanthine phosphoribosyltransferase, strain NC1C7864
4001	16748	29379	12.29	3.7E+00	AL161539.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 39
7069	19757		1.03	3.7E+00	AL445065.1	NT	Thermoplasma acidophilum complete genome, segment 3/5
8609	21301		0.55	3.7E+00	4503950	NT	Homo sapiens glucokinase (hexokinase 4, maturity onset diabetes of the young 2) (GCK), nuclear gene encoding mitochondrial protein, mRNA
9078	21765	34928	0.7	3.7E+00	U43541.1	NT	Mus musculus laminin beta 2 gene, exons 17-33, and complete cds
11408	24057	37363	2.23	3.7E+00	BF669279.1	EST_HUMAN	602120551F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4277748 5'
11408	24057	37364	2.23	3.7E+00	BF669279.1	EST_HUMAN	602120551F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4277748 5'
579	13359	25986	5.19	3.6E+00	AV761055.1	EST_HUMAN	AV761055 MDS Homo sapiens cDNA clone MDSBLUE10 5'
4745	17477		1.06	3.6E+00	AL161472.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 2
5174	17983	30498	0.74	3.6E+00	BF316316.1	EST_HUMAN	601901866F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4131016 5'
8450	21142	34280	0.95	3.6E+00	D12367.1	EST_HUMAN	HUM000TB08 Liver HepG2 cell line. Homo sapiens cDNA clone tb08
8450	21142	34281	0.95	3.6E+00	D12367.1	EST_HUMAN	HUM000TB08 Liver HepG2 cell line. Homo sapiens cDNA clone tb08
8543	21235	34378	3.83	3.6E+00	AE004447.1	NT	Pseudomonas aeruginosa PA01, section 8 of 529 of the complete genome
8543	21235	34379	3.83	3.6E+00	AE004447.1	NT	Pseudomonas aeruginosa PA01, section 8 of 529 of the complete genome
10759	23444						Escherichia coli glycerophosphate dehydrogenase (gldD) gene, partial cds; and the translation start site has been verified (gldE), the translation start site has been verified (gldG), and repressor protein (gldR) genes, complete cds
3241	16003	26652	4.07	3.6E+00	M96795.1	NT	Cryptosporidium felis heat shock protein 70 (HSP70) gene, partial cds
5911	18695		1.1	3.5E+00	AF221538.1	NT	Borrelia burgdorferi (strain 25015) outer surface protein (ospC) gene, partial cds
6118	18896	31864	1.17	3.5E+00	L42898.1	EST_HUMAN	Y940c08.r1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:34840 5'
8383	21076		0.56	3.5E+00	P24657	SWISSPROT	THROMBOXANE-A SYNTHASE (TXA SYNTHASE) (TXS)
8930	21621	34763	1.02	3.5E+00	AA190998.1	EST_HUMAN	zp86b04.s1 Stratagene HeLa cell s3 937216 Homo sapiens cDNA clone IMAGE:627055 3' similar to contains Alu repetitive element; contains element MSR1 repetitive element
8930	21621	34764	1.02	3.5E+00	AA190998.1	EST_HUMAN	zp86b04.s1 Stratagene HeLa cell s3 937216 Homo sapiens cDNA clone IMAGE:627055 3' similar to contains Alu repetitive element; contains element MSR1 repetitive element
9393	22055	35227	0.96	3.5E+00	AL161553.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 53

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Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10417	23063	36283	0.46	3.5E+00	AJ133723.1	NT	Bos taurus mRNA for Ran-binding protein 2, partial
1501	14247	26933	2.94	3.4E+00	AF254577.1	NT	Brassica napus RPB5d mRNA, complete cds
7261	18945	33021	2.84	3.4E+00	P04052	SWISSPROT	DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT
7801	20267	33374	0.69	3.4E+00	P04052	SWISSPROT	DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT
8577	21269		0.7	3.4E+00	J65406.1	NT	Human alternatively spliced potassium channels ROM-K1, ROM-K2, ROM-K3, ROM-K4, ROM-K5, and ROM-K6 (KCNJ1) gene, complete cds
8972	21662	34813	0.67	3.4E+00	AJ28042.1	NT	Homo sapiens 999 kb contig between AML1 and CBR1 on chromosome 21q22, segment 2/3
9010	21700	34850	0.54	3.4E+00	AJ250567.1	NT	Homo sapiens partial TM4SF2 gene for tetraspanin protein, exon 6
10764	22812	36030	2.97	3.4E+00	AF013167.1	NT	Saccharomyces cerevisiae MSS1 gene, complete cds
11519	24119	37429	1.89	3.4E+00	L77570.1	NT	Homo sapiens DiGeorge syndrome critical region, centromeric end
5977	18759	31722	1.57	3.3E+00	Q09669	SWISSPROT	PUTATIVE IRON ALCOHOL DEHYDROGENASE
5977	18759	31723	1.57	3.3E+00	Q09669	SWISSPROT	PUTATIVE IRON ALCOHOL DEHYDROGENASE
7784	20489	33611	0.79	3.3E+00	AF111188.2	NT	Homo sapiens serine palmitoyl transferase, subunit II gene, complete cds; and unknown genes
10361	23008	36223	0.9	3.3E+00	AP001511.1	NT	Bacillus halodurans genomic DNA, section 5/14
10361	23008	36224	0.9	3.3E+00	AP001511.1	NT	Bacillus halodurans genomic DNA, section 5/14
488	13273	25908	1.64	3.2E+00	X89422.1	NT	D. rerio zp-50 POU gene
4004	13273	25908	0.9	3.2E+00	X89422.1	NT	D. rerio zp-50 POU gene
4679	17413	30048	1.08	3.2E+00	4502404	NT	Homo sapiens carcinoembryonic antigen-related cell adhesion molecule 1 (biliary glycoprotein) (CEACAM1), mRNA
5481	18280	31176	1.06	3.2E+00	P54924	SWISSPROT	SQUALENE-HOPENE CYCLASE
5481	18280	31177	1.06	3.2E+00	P54924	SWISSPROT	SQUALENE-HOPENE CYCLASE
5515	18313	31214	2.7	3.2E+00	P12783	SWISSPROT	PHOSPHOGLYCERATE KINASE, CYTOSOLIC
5515	18313	31215	2.7	3.2E+00	P12783	SWISSPROT	PHOSPHOGLYCERATE KINASE, CYTOSOLIC
6214	18988	31964	1.78	3.2E+00	P18931	SWISSPROT	NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4
6214	18988	31965	1.78	3.2E+00	P18931	SWISSPROT	NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4
7505	20176	33270	0.7	3.2E+00	P04275	SWISSPROT	VON WILLEBRAND FACTOR PRECURSOR (VWF)
7672	20336	33448	2.65	3.2E+00	Y13655.1	NT	Chlamydomonas reinhardtii chloroplast DNA for rps9, ycf4, ycf3, rps18 genes
7672	20336	33449	2.65	3.2E+00	Y13655.1	NT	Chlamydomonas reinhardtii chloroplast DNA for rps9, ycf4, ycf3, rps18 genes
8928	21619		4.51	3.2E+00	P13061	SWISSPROT	S. cerevisiae threonine deaminase (LV1) gene, complete cds
9430	22108	35283	0.87	3.2E+00	M36383.1	NT	PERIPLASMIC (NIFE) HYDROGENASE SMALL SUBUNIT (NIFE HYDROGENYLASE SMALL CHAIN)
10041	22669	35907	2.03	3.2E+00	A5016081.2	NT	Oryzias latipes OIG06 gene for guanylyl cyclase C, complete cds
11948	24500		2.44	3.2E+00	L33836.1	NT	Sus scrofa choline acetyltransferase gene, promoter region
5785	18576	31505	2.46	3.1E+00	Q10135	SWISSPROT	HYPOTHETICAL 142.5 KD PROTEIN C23E2.02 IN CHROMOSOME 1
7287	19970	33047	0.83	3.1E+00	P52178	SWISSPROT	TRIOSE PHOSPHATE/PHOSPHATE TRANSLOCATOR, NON-GREEN PLASTID PRECURSOR (CTPT)

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7927	20293		0.94	3.1E+00	AF303225.1	NT	Bacillus alcalophilus pectate lyase (pelE) gene, complete cds
7986	20681	33807	0.48	3.1E+00	P40985	SWISSPROT	PROBABLE UBQUITIN-PROTEIN LIGASE HUL4
8500	21192	34333	4.36	3.1E+00	P49894	SWISSPROT	TYPE I IODOTHYRONINE DEIODINASE (TYPE I 5'DEIODINASE) (DIOI) (TYPE 1 DI) (5DI)
8500	21192	34334	4.36	3.1E+00	P49894	SWISSPROT	TYPE I IODOTHYRONINE DEIODINASE (TYPE I 5'DEIODINASE) (DIOI) (TYPE 1 DI) (5DI)
9158	21889		3.85	3.1E+00	Q14957	SWISSPROT	GLUTAMATE (NMDA) RECEPTOR SUBUNIT EPSILON 3 PRECURSOR (N-METHYL D-ASPARTATE RECEPTOR SUBTYPE 2C) (NR2C) (NMDAR2C)
9796	22447	35652	0.59	3.1E+00	7524759	NT	Chlorella vulgaris chloroplast, complete genome
9888	22538		0.63	3.1E+00	Q10125	SWISSPROT	HYPOTHETICAL 56.3 KD PROTEIN F52C9.5 IN CHROMOSOME III
10234	22882	36095	5.52	3.1E+00	P49365	SWISSPROT	DEOXYHYPUISINE SYNTHASE (DHS)
11440	23207		2.66	3.1E+00	P33515	SWISSPROT	GENOME POLYPEPTIDE [CONTAINS: CAPSID PROTEIN C (CORE PROTEIN); MATRIX PROTEIN (ENVELOPE PROTEIN M); MAJOR ENVELOPE PROTEIN E; NONSTRUCTURAL PROTEINS NS1, NS2A, NS2B, NS4A AND NS4B; HELICASE (NS3); RNA-DIRECTED RNA POLYMERASE (NS5)]
11463	24066		3.28	3.1E+00	S56660.1	NT	retinoid acid nuclear receptor isoform beta 2 [mice, embryonal carcinoma cell line, PCC7-MZ1, mRNA, 2971 nt]
2842	15610	28259	1.09	3.0E+00	8923984	NT	Homo sapiens hypothetical protein PRO0889 (PRO0889), mRNA
5254	18060	30689	1.32	3.0E+00	X53096.1	NT	S.aureus genes encoding Sau961 DNA methyltransferase and Sau961 restriction endonuclease
6461	19228	32228	0.83	3.0E+00	X56037.1	NT	Corynebacterium glutamicum thrC gene for threonine synthase (EC 4.2.99.2)
6461	19228	32229	0.83	3.0E+00	X56037.1	NT	Corynebacterium glutamicum thrC gene for threonine synthase (EC 4.2.99.2)
7055	19746		8.09	3.0E+00	P18406	SWISSPROT	CYR61 PROTEIN PRECURSOR (3CH61)
7096	19765		0.6	3.0E+00	Q13201	SWISSPROT	ENDOTHELIAL CELL MULTIMERIN PRECURSOR
8805	21497		1.2	3.0E+00	X67838.1	NT	B.napus DNA for myrosinase
10192	22840	36055	0.62	3.0E+00	Q58605	SWISSPROT	S-ADENOSYLMETHIONINE SYNTHETASE (METHIONINE ADENOSYL TRANSFERASE) (ADOMET SYNTHETASE)
10544	23240	36474	1.57	3.0E+00	Q16181	SWISSPROT	CDC10 PROTEIN HOMOLOG
10931	23611	36860	6.44	3.0E+00	P51842	SWISSPROT	RETINAL GUANYLYL CYCLASE 2 PRECURSOR (GUANYLYL CYCLASE 2F, RETINAL) (RETGC-2) (ROD OUTER SEGMENT MEMBRANE GUANYLYL CYCLASE 2) (ROS-GC2) (GUANYLYL CYCLASE F) (GC-F)
10931	23611	36861	6.44	3.0E+00	P51842	SWISSPROT	RETINAL GUANYLYL CYCLASE 2 PRECURSOR (GUANYLYL CYCLASE 2F, RETINAL) (RETGC-2) (ROD OUTER SEGMENT MEMBRANE GUANYLYL CYCLASE 2) (ROS-GC2) (GUANYLYL CYCLASE F) (GC-F)
11578	24177	37492	2.72	3.0E+00	P34194	SWISSPROT	NADH-LUBIQUINONE OXIDOREDUCTASE CHAIN 4
2004	14740	27464	2.28	2.9E+00	AE002225.2	NT	Chlamydomonas reinhardtii AR39, section 53 of 94 of the complete genome
6809	19470	32463	1.74	2.9E+00	Z36879.1	NT	F.pringlei gdcA gene for P-protein of the glycine cleavage system
7110	19798	32861	5.21	2.9E+00	Q14514	SWISSPROT	BRAIN-SPECIFIC ANGIOGENESIS INHIBITOR 1 PRECURSOR

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7110	19798	32862	5.21	2.9E+00	O14514	SWISSPROT	BRAIN-SPECIFIC ANGIOGENESIS INHIBITOR 1 PRECURSOR
7356	20037	33115	6.84	2.9E+00	P46589	SWISSPROT	ADHERENCE FACTOR (ADHESION AND AGGREGATION MEDIATING SURFACE ANTIGEN)
7767	20463	33587	0.67	2.9E+00	P05844	SWISSPROT	STRUCTURAL POLYPEPTIDE [CONTAINS: MAJOR STRUCTURAL PROTEIN VP2; NONSTRUCTURAL PROTEIN VP4; MINOR STRUCTURAL PROTEIN VP3]
7767	20463	33588	0.67	2.9E+00	P05844	SWISSPROT	STRUCTURAL POLYPEPTIDE [CONTAINS: MAJOR STRUCTURAL PROTEIN VP2; NONSTRUCTURAL PROTEIN VP4; MINOR STRUCTURAL PROTEIN VP3]
7996	20691	33819	1.03	2.9E+00	BF344171.1	EST_HUMAN	602017413F1 NCI_CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4163059 5'
1440	14187	26872	4.4	2.8E+00	AF186398.1	NT	Buxus harlandii malic acid dehydrogenase K (malK) gene, partial cds; chloroplast gene for chloroplast product
1629	14375		2.74	2.8E+00	AL161562.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 52
7207	19892	32968	5.72	2.8E+00	8393724	NT	Mus musculus endomucin (LOC53423), mRNA
9513	22168		0.54	2.8E+00	BE565182.1	EST_HUMAN	601342756F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3684807 5'
10588	19892	32968	1.32	2.8E+00	8393724	NT	Mus musculus endomucin (LOC53423), mRNA
224	13036	25672	13.51	2.7E+00	8679306	NT	Mus musculus per-hexamer repeat gene 3 (Phxr3), mRNA
224	13036	25673	13.51	2.7E+00	8679306	NT	Mus musculus per-hexamer repeat gene 3 (Phxr3), mRNA
5464	18263	31154	1.17	2.7E+00	L14005.1	NT	Homo sapiens apoA polymorphism Kringle IV gene, exons 1 and 2
8045	20739		0.6	2.7E+00	U15947.1	NT	Ipomoea purpurea chalcone synthase (CHS) gene including complete 5'UTR and complete cds
8667	21558		1.83	2.7E+00	AL116499.1	NT	Bolivis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
9332	20403	33519	0.73	2.7E+00	AW088191.1	EST_HUMAN	xc88e12.x1 NCI_CGAP_Brn35 Homo sapiens cDNA clone IMAGE:2591374 3' similar to gb:U17733
10397	23043		1.75	2.7E+00	BE083527.1	EST_HUMAN	THYMOSIN BETA-4 (HUMAN);
4626	17361	28994	5.15	2.6E+00	AF088749.1	NT	CMO-BT0281-031199-087-h04 BT0281 Homo sapiens cDNA
5460	18259	31149	1.88	2.6E+00	6756601	NT	Mus musculus sphingosine kinase (SPHK1b) mRNA, complete cds
5460	18259	31150	1.88	2.6E+00	6756601	NT	Mus musculus SRY-box containing gene 13 (Sox13), mRNA
5738	18528		0.59	2.6E+00	Y17062.1	NT	Mus musculus SRY-box containing gene 13 (Sox13), mRNA
7454	25424		0.82	2.6E+00	AJ224639.1	NT	Mycobacterium fortuitum furA II gene
7600	20266		6.04	2.6E+00	AF235502.1	NT	Homo sapiens Surf-5 and Surf-6 genes
7958	20653	33776	1.13	2.6E+00	AJ132180.1	NT	Mus musculus SH2-containing Inositol 5-phosphatase (Ship) gene, exons 16 through 27, and complete cds
7958	20653	33777	1.13	2.6E+00	AJ132180.1	NT	faba bean necrotic yellows virus C2-Eg gene, isolate Egyptian EV1-93
9557	22210	35395	2.83	2.6E+00	AL161540.2	NT	faba bean necrotic yellows virus C2-Eg gene, isolate Egyptian EV1-93
10253	22901		1.67	2.6E+00	9056193	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 40
10953	23630	36878	1.32	2.6E+00	AF143875.1	NT	Mus musculus cleavage and polyadenylation specificity factor 3 (Cpsf3), mRNA
12560	25304		3.17	2.6E+00	11419220	NT	Hantavirus Z10 segment M G1/G2 glycoprotein (Z10) gene, complete cds
1448	14195	26878	3.73	2.6E+00	AJ271844.1	NT	Homo sapiens ATP-binding cassette, sub-family B (MDR/TAP), member 4 (ABCB4), mRNA
						NT	Aspergillus nidulans recQ gene for DNA helicase, exons 1-4

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1448	14195	28879	3.73	2.5E+00	AJ271844.1	NT	Aspergillus nidulans recQ gene for DNA helicase, exons 1-4
5723	18515	31434	2.22	2.5E+00	P13485	SWISSPROT	TEICHOIC ACID BIOSYNTHESIS PROTEIN F
5723	18515	31435	2.22	2.5E+00	P13485	SWISSPROT	TEICHOIC ACID BIOSYNTHESIS PROTEIN F
6367	18515	31434	1.63	2.5E+00	P13485	SWISSPROT	TEICHOIC ACID BIOSYNTHESIS PROTEIN F
6367	18515	31435	1.63	2.5E+00	P13485	SWISSPROT	TEICHOIC ACID BIOSYNTHESIS PROTEIN F
6830	19392	32406	0.64	2.5E+00	D30052.1	NT	Vibrio cholerae ctaA gene and ctaB gene for cholera toxins, complete cds
7659	20323	33431	0.99	2.5E+00	AW949158.1	EST_HUMAN	QV4-FT0005-110500-206-g07 FT0005 Homo sapiens cDNA
7700	20363	33477	0.58	2.5E+00	4502902	NT	Homo sapiens clathrin, heavy polypeptide-like 1 (CLTCL1) mRNA
9001	21691	34841	1.53	2.5E+00	D50307.1	NT	Rice DNA for aldolase C-1, complete cds
9752	22403	35608	0.67	2.5E+00	BE29758.1	EST_HUMAN	601175779F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3531090 5'
11528	24128		1.34	2.5E+00	P40170	SWISSPROT	DNAJ PROTEIN
11943	24498		3.08	2.5E+00	AF280665.1	NT	Mus musculus EIF4H gene, partial cds; LIMK1 gene, complete cds; and ELN gene, partial cds
3012	15778	28428	1.13	2.4E+00	M24282.1	NT	Chicken alpha-3 collagen type VI mRNA, 3' end
4849	17579	30203	6.09	2.4E+00	P02843	SWISSPROT	Homo sapiens double C2-like domains, alpha (DOC2A) mRNA
5920	18705	31657	4.16	2.4E+00	P02843	SWISSPROT	VITELLOGENIN I PRECURSOR (YOLK PROTEIN 1)
7280	19984	33040	0.78	2.4E+00	BF687502.1	EST_HUMAN	602120856F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4278012 5'
7280	19984	33041	0.78	2.4E+00	BF687502.1	EST_HUMAN	602120856F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4278012 5'
8039	20734	33865	2.4	2.4E+00	P26842	SWISSPROT	CD27L RECEPTOR PRECURSOR (T-CELL ACTIVATION ANTIGEN CD27) (T14)
8039	20734	33866	2.4	2.4E+00	P26842	SWISSPROT	CD27L RECEPTOR PRECURSOR (T-CELL ACTIVATION ANTIGEN CD27) (T14)
8110	20804		2.63	2.4E+00	AE001486.1	NT	Helicobacter pylori, strain J99 section 47 of 132 of the complete genome
8549	21241		1.61	2.4E+00	AW875126.1	EST_HUMAN	RC2-PT0004-031299-011-405 PT0004 Homo sapiens cDNA
8727	21419	34563	7.38	2.4E+00	P24091	SWISSPROT	ENDOCHITINASE B PRECURSOR (CHN-B)
9938	22586	35788	2.56	2.4E+00	P13673	SWISSPROT	SKIN GRANULE PROTEIN PRECURSOR
9938	22586	35789	2.56	2.4E+00	P13673	SWISSPROT	SKIN GRANULE PROTEIN PRECURSOR
10007	22855	35868	1.88	2.4E+00	X02511.1	NT	H.sapiens CTGF gene and promoter region
10143	22791		6.55	2.4E+00	P09099	SWISSPROT	XYLOLOSE KINASE (XYLOKINASE)
10220	22868	36079	1.62	2.4E+00	BE326702.1	EST_HUMAN	hr63f06.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3133187 3'
10220	22868	36080	1.62	2.4E+00	BE326702.1	EST_HUMAN	hr63f06.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3133187 3'
10490	23136	36384	0.87	2.4E+00	Q51481	SWISSPROT	DENITRIFICATION REGULATORY PROTEIN NIRQ
11331	24022	37327	2.16	2.4E+00	AF156652.2	NT	Frederia x enenase cytosolic ascorbate peroxidase (ApxSC) gene, ApxSC-c allele, complete cds
1231	13980	26650	13.6	2.3E+00	Z46724.1	NT	G.domesticus artificial single chain antibody gene (L3)
4102	16845		1.35	2.3E+00	AJ401081.1	NT	Bos taurus partial cytb gene for cytochrome b

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5744	18538			0.95	N86246.1	EST_HUMAN	J7340F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone J7340 5' similar to PROLYL-CARBOXYPEPTIDASE
7354	20035	33113	2.47	2.3E+00	6978564	NT	Rattus norvegicus ATPase, Ca++ transporting, ubiquitous (ATP2a3), mRNA
7495	25425	33455	3.07	2.3E+00	P07199	SWISSPROT	MAJOR CENTROMERE AUTOANTIGEN B (CENTROMERE PROTEIN B) (CENP-B)
7679	20343	33455	1.01	2.3E+00	X60285.1	NT	M.mazai dnaK and dnaJ genes homologues coding for DnaK and DnaJ
9008	21698	34849	0.54	2.3E+00	5835317	NT	Polyporus ornamentalis mitochondrion, complete genome
9088	21757	34919	1.8	2.3E+00	Q11127	SWISSPROT	ALPHA-(1,3)-FUCOSYLTRANSFERASE (GALACTOSIDE 3-L-FUCOSYLTRANSFERASE)
10704	23395	36632	3.83	2.3E+00	Q07076	SWISSPROT	FUCOSYLTRANSFERASE 4 (FUCT-IV)
11782	24373	37703	3.03	2.3E+00	BF641987.1	EST_HUMAN	ANNEXIN VII (SYNEXIN)
11782	24373	37704	3.03	2.3E+00	BF641987.1	EST_HUMAN	602089121F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4068173 5'
12157	24642	31089	6.84	2.3E+00	BE895237.1	EST_HUMAN	602089121F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4068173 5'
3998	16746	28378	0.95	2.2E+00	AF020528.1	NT	601433673F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3918643 5'
4278	17017	28644	5.01	2.2E+00	D67071.1	NT	Magnaporthe oryzae Class IV chitin synthase (chs4) gene, complete cds
4278	17017	28645	5.01	2.2E+00	D67071.1	NT	Rat gene for regucalcin, exon1 (non-coding exon)
							Rat gene for regucalcin, exon1 (non-coding exon)
5258	18084	30692	12.73	2.2E+00	O88307	SWISSPROT	SORTILIN-RELATED RECEPTOR PRECURSOR (SORTING PROTEIN-RELATED RECEPTOR CONTAINING LDLR CLASS A REPEATS) (MSORLA) (SORLA-1) (LOW-DENSITY LIPOPROTEIN RECEPTOR RELATIVE WITH 11 LIGAND-BINDING REPEATS) (LDLR RELATIVE WITH 11 LIGAND-BINDING REPEATS) (LR11) (>)
5258	18084	30693	12.73	2.2E+00	O88307	SWISSPROT	SORTILIN-RELATED RECEPTOR PRECURSOR (SORTING PROTEIN-RELATED RECEPTOR CONTAINING LDLR CLASS A REPEATS) (MSORLA) (SORLA-1) (LOW-DENSITY LIPOPROTEIN RECEPTOR RELATIVE WITH 11 LIGAND-BINDING REPEATS) (LDLR RELATIVE WITH 11 LIGAND-BINDING REPEATS) (LR11) (>)
5763	18554	31478	1.03	2.2E+00	BE927220.1	EST_HUMAN	RC3-CT0254-300800-022-e06 CT0254 Homo sapiens cDNA
5763	18554	31479	1.03	2.2E+00	BE927220.1	EST_HUMAN	RC3-CT0254-300800-022-e06 CT0254 Homo sapiens cDNA
5971	18753	31714	9.84	2.2E+00	BE250383.1	EST_HUMAN	600943401T1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2959777 3'
6261	19035	32010	3.87	2.2E+00	Q00335	SWISSPROT	MINOR VIRION STRUCTURAL PROTEIN MU-2
6502	19267	32288	3.16	2.2E+00	P51459	SWISSPROT	INSULIN-LIKE GROWTH FACTOR II PRECURSOR (IGF-II) (SOMATOMEDIN A)
6861	17938		3.94	2.2E+00	AA594574.1	EST_HUMAN	rib5b02.s1 NCI_CGAP_Cot10 Homo sapiens cDNA clone IMAGE:1056379 3'
7217	19902	32975	0.9	2.2E+00	AA137027.1	EST_HUMAN	zn97f04.r1 Stratiene fetal retina 937202 Homo sapiens cDNA clone IMAGE:566143 5'
7507	20178	33272	19.2	2.2E+00	AA449012.1	EST_HUMAN	zn05g10.r1 Soares_tad1_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:786634 5'
7589	20257	33365	0.72	2.2E+00	P54918	SWISSPROT	ALANINE RACEMASE
8001	20868	33823	0.58	2.2E+00	BE301580.1	EST_HUMAN	bb17h12.x1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:2963207 3' similar to gb:D45836 Mouse mRNA for nuclear pore-targeting-complex component of (MOUSE);

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Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8001	20696	33824	0.58	2.2E+00	BE301560.1	EST_HUMAN	bb17h12.x1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:2963207 3' similar to gb:D45836 Mouse
8241	21920		11.02	2.2E+00	BE741678.1	EST_HUMAN	mRNA for nuclear pore-targeting-complex component of (MOUSE);
8468	25124		2.28	2.2E+00	Q04706	SWISSPROT	601594733F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3948561 5'
9853	22601	35804	1.1	2.2E+00	A1290373.1	EST_HUMAN	TRANSPONSON TY1 PROTEIN A
9953	22601	35805	1.1	2.2E+00	A1290373.1	EST_HUMAN	qm69b03.x1 Soares_placenta_8to9weeks_2NbHP8to9W Homo sapiens cDNA clone IMAGE:1893965 3'
9956	22644	35856	2.68	2.2E+00	BF246782.1	EST_HUMAN	similar to gb:Y00433 GLUTATHIONE PEROXIDASE (HUMAN);
10353	23000	36217	3.11	2.2E+00	AF183416.1	EST_HUMAN	qm69b03.x1 Soares_placenta_8to9weeks_2NbHP8to9W Homo sapiens cDNA clone IMAGE:1893965 3'
11418	23185	36415	3.47	2.2E+00	P07911	NT	similar to gb:Y00433 GLUTATHIONE PEROXIDASE (HUMAN);
11616	24214	37539	5.89	2.2E+00	P10407	SWISSPROT	601855591F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4075391 5'
556	15545	25867	8.3	2.1E+00	AF132612.2	NT	Homo sapiens ovarian granulosa cell 13.0 kDa protein hGR74 homolog mRNA, complete cds
3575	16330		1.08	2.1E+00	AW449366.1	EST_HUMAN	UROMODULIN PRECURSOR (TAMM-HORSFALL URINARY GLYCOPROTEIN) (THP)
6041	18821		0.89	2.1E+00	P75357	SWISSPROT	EARLY E1A 28 KD PROTEIN
6710	19625	32689	3.95	2.1E+00	O70159	SWISSPROT	Mus musculus pre-T cell receptor alpha gene, enhancer region and upstream region
6946	19428	32443	5.72	2.1E+00	N29575.1	EST_HUMAN	UIH-B13-ald-e-08-Q-UJ.st NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2734550 3'
8395	21088		1.97	2.1E+00	AU123630.1	EST_HUMAN	HYPOTHETICAL PROTEIN MG302 HOMOLOG
1174	13927	26591	1.44	2.0E+00	AF180527.1	NT	ALPHA-2-HS-GLYCOPROTEIN PRECURSOR (FETUIN-A)
1174	13927	26592	1.44	2.0E+00	AF180527.1	NT	Y008a10.s1 Soares_melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:270618 3' similar to gb:M55654
1312	14090	26735	0.97	2.0E+00	AF204927.1	NT	TRANSCRIPTION INITIATION FACTOR TFIIID (HUMAN);
1569	14316		2.61	2.0E+00	P25582	SWISSPROT	AU123630 NT2RM2 Homo sapiens cDNA clone NT2RM2000871 5'
2145	14875	27609	5.98	2.0E+00	Z78279.1	NT	Homo sapiens p22Dokdel (DOKDEL) mRNA, complete cds
2145	14875	27610	5.98	2.0E+00	Z78279.1	NT	Homo sapiens p22Dokdel (DOKDEL) mRNA, complete cds
4080	16824	29450	2.2	2.0E+00	AW664496.1	EST_HUMAN	Oryctolagus cuniculus Na ⁺ /K ⁺ -ATPase beta 1 subunit mRNA, complete cds
4080	16824	29451	2.2	2.0E+00	AW664496.1	EST_HUMAN	PUTATIVE RRNA METHYLTRANSFERASE SPB1
7449	20125		0.92	2.0E+00	P07566	SWISSPROT	R.norvegicus mRNA for collagen alpha1 type I
7923	20618	33745	3.17	2.0E+00	AB008676.1	NT	R.norvegicus mRNA for collagen alpha1 type I
7923	20618	33746	3.17	2.0E+00	AB008676.1	NT	hir13c05.x1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2972168 3' similar to gb:X01877
7923	20618	33747	3.17	2.0E+00	AB008676.1	NT	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, LIVER (HUMAN);
							hir13c05.x1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2972168 3' similar to gb:X01877
							GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, LIVER (HUMAN);
							STRUCTURAL POLYPROTEIN [CONTAINS: NUCLEOCAPSID PROTEIN C; MEMBRANE
							GLYCOPROTEINS E1 AND E2]
							Escherichia coli 0157 DNA, map position at 46 min., complete cds
							Escherichia coli 0157 DNA, map position at 46 min., complete cds
							Escherichia coli 0157 DNA, map position at 46 min., complete cds

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Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8620	21512	34656	3.15	2.0E+00	F31800.1	EST_HUMAN	HSPD22703 HM3 Homo sapiens cDNA clone s4000117B08
12481	25265	30720	7.27	2.0E+00	5834843	NT	Gallus gallus mitochondrion, complete genome
5511	18309	31209	4.77	1.9E+00	6754389	NT	Mus musculus inositol 1,4,5-triphosphate receptor 1 (Itpr1), mRNA
5511	18309	31210	4.77	1.9E+00	6754389	NT	Mus musculus inositol 1,4,5-triphosphate receptor 1 (Itpr1), mRNA
6009	18790	31753	1.32	1.9E+00	BE989695.1	EST_HUMAN	601679636F1 NIH_MGC_78 Homo sapiens cDNA clone IMAGE:3949881 5'
6558	19321		0.75	1.9E+00	AW845689.1	EST_HUMAN	MRO-CT0063-071089-002-g02 CT0063 Homo sapiens cDNA
6650	19412		2.46	1.9E+00	Q63627	SWISSPROT	CTD-BINDING SR-LIKE PROTEIN RA4
8358	21051	34190	2.18	1.9E+00	P02467	SWISSPROT	COLLAGEN ALPHA 2(I) CHAIN PRECURSOR
8358	21051	34191	2.18	1.9E+00	P02467	SWISSPROT	COLLAGEN ALPHA 2(I) CHAIN PRECURSOR
8557	21249		2.94	1.9E+00	BF380208.1	EST_HUMAN	CM3-MT0114-010900-323-h12 MT0114 Homo sapiens cDNA
8792	21484		1.33	1.9E+00	O51781	SWISSPROT	ARGININE DEIMINASE (ADI) (ARGININE DIHYDROLASE) (AD)
9530	22183	35367	0.59	1.9E+00	AA689125.1	EST_HUMAN	ab94a04.s1 Stragene lung (#837210) Homo sapiens cDNA clone IMAGE:854574 3' similar to contains Alu repetitive element contains element L1 L1 repetitive element
10462	23108	36339	0.62	1.9E+00	AF248269.1	NT	Homo sapiens gag-pro-pol precursor protein gene, partial cds
3089	15854	28496	1.3	1.8E+00	P21004	SWISSPROT	PROTEIN B8 PRECURSOR
3118	15883	28522	1.57	1.8E+00	U04356.1	NT	Synechococcus sp. PCC7942 copper transporting P-ATPase (ctaA) and ATP synthase epsilon subunit (atpE) genes, complete cds
3118	15883	28523	1.57	1.8E+00	U04356.1	NT	Synechococcus sp. PCC7942 copper transporting P-ATPase (ctaA) and ATP synthase epsilon subunit (atpE) genes, complete cds
5777	18588		1.91	1.8E+00	P18502	SWISSPROT	HEDGEHOG RECEPTOR (PATCHED PROTEIN)
6013	18784	31757	1.32	1.8E+00	BF311999.1	EST_HUMAN	601897854F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4127384 5'
6305	19077		1.12	1.8E+00	BF68327.1	EST_HUMAN	602198470F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4298272 5'
6841	19403	32418	1.64	1.8E+00	BF305652.1	EST_HUMAN	601893489F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4139038 5'
6958	19440	32455	1.79	1.8E+00	P21249	SWISSPROT	MAJOR ANTIGEN
8016	20711	33841	0.93	1.8E+00	P11369	SWISSPROT	RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ; ENDONUCLEASE]
8016	20711	33842	0.93	1.8E+00	P11369	SWISSPROT	RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ; ENDONUCLEASE]
8368	21061	34201	0.44	1.8E+00	P48634	SWISSPROT	LARGE PROLINE-RICH PROTEIN BAT2 (HLA-B-ASSOCIATED TRANSCRIPT 2)
8368	21061	34202	0.44	1.8E+00	P48634	SWISSPROT	LARGE PROLINE-RICH PROTEIN BAT2 (HLA-B-ASSOCIATED TRANSCRIPT 2)
8368	21061	34203	0.44	1.8E+00	P48634	SWISSPROT	LARGE PROLINE-RICH PROTEIN BAT2 (HLA-B-ASSOCIATED TRANSCRIPT 2)
8753	21445	34593	1.98	1.8E+00	O43281	SWISSPROT	EMBRYONAL FYN-ASSOCIATED SUBSTRATE (HEFS)
9073	21762	34924	0.77	1.8E+00	R31042.1	EST_HUMAN	yt72c08.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:135278 5'
9161	21831	34994	0.76	1.8E+00	AW880004.1	EST_HUMAN	QV0-OT0030-070300-148-a03 OT0030 Homo sapiens cDNA

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9749	22400	35605	0.75	1.8E+00	P27050	SWISSPROT	CHITINASE D PRECURSOR
10183	22831		3.2	1.8E+00	AF111849.1	NT	Homo sapiens PRO530 mRNA, complete cds
10452	23098		0.63	1.8E+00	P44325	SWISSPROT	CYTIDINE DEAMINASE (CYTIDINE AMINOHYDROLASE) (CDA)
12276	25236		5.28	1.8E+00	AF314254.1	NT	Chlamydomonas reinhardtii alternative oxidase 1 (AOX1) gene, nuclear gene encoding mitochondrial protein
12359	24763		3.9	1.8E+00	9508404	NT	Rattus norvegicus Actin-related protein complex 1b (Arpc1b), mRNA
1086	13844	26502	2.21	1.7E+00	Q60114	SWISSPROT	LEVANSUCRASE (BETA-D-FRUCTOFURANOSYL TRANSFERASE) (SUCROSE 6-FRUCTOSYL TRANSFERASE)
2269	14995	27734	2.28	1.7E+00	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21 C080
2372	15094	27833	2.56	1.7E+00	AI141087.1	EST_HUMAN	oz43h05.x1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:1678137 3'
4426	17162	28792	0.81	1.7E+00	Q60114	SWISSPROT	LEVANSUCRASE (BETA-D-FRUCTOFURANOSYL TRANSFERASE) (SUCROSE 6-FRUCTOSYL TRANSFERASE)
5525	18323	31225	1.77	1.7E+00	BE063546.1	EST_HUMAN	CM0-BT0282-171299-127-e05 BT0282 Homo sapiens cDNA
5525	18323	31224	1.77	1.7E+00	BE063546.1	EST_HUMAN	CM0-BT0282-171299-127-e05 BT0282 Homo sapiens cDNA
5927	18711	31686	3.28	1.7E+00	Q91TR8	SWISSPROT	COUP TRANSCRIPTION FACTOR 1 (COUP-TF1) (COUP-TF I)
7118	19806	32871	1.11	1.7E+00	Q03703	SWISSPROT	HYPOTHETICAL 38.0 KD PROTEIN IN CAT2-AMD1 INTERGENIC REGION
7118	19806	32872	1.11	1.7E+00	Q03703	SWISSPROT	HYPOTHETICAL 38.0 KD PROTEIN IN CAT2-AMD1 INTERGENIC REGION
7753	20449	33573	0.91	1.7E+00	AF021335.1	NT	Mus musculus T cell receptor gamma locus, TCR gamma 2 and gamma 4 gene clusters
7932	20827	33755	1.13	1.7E+00	6755715	NT	Mus musculus T cell receptor gamma locus, TCR gamma 2 and gamma 4 gene clusters
7961	20656	33781	0.59	1.7E+00	BF530680.1	EST_HUMAN	602071917F1 NCJ_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4214669 5'
8440	21132	34268	0.5	1.7E+00	AF245513.1	NT	Hippoglossus hippoglossus Interferon Inducible Mx protein (Mx) mRNA, complete cds
8525	21217		2.3	1.7E+00	BF308000.1	EST_HUMAN	601894255F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4140084 5'
8605	21297	34440	0.59	1.7E+00	X69063.1	NT	M.musculus Ank-1 mRNA for erythroid ankyrin
8605	21297	34441	0.59	1.7E+00	X69063.1	NT	M.musculus Ank-1 mRNA for erythroid ankyrin
9047	25123	34892	2.18	1.7E+00	Q60479	SWISSPROT	HOMEBOX PROTEIN DLX-3
9047	25123	34893	2.18	1.7E+00	Q60479	SWISSPROT	HOMEBOX PROTEIN DLX-3
9506	22159		1.15	1.7E+00	AF161380.1	NT	Homo sapiens HSPC262 mRNA, partial cds
10071	22719		0.48	1.7E+00	AW95381.1	EST_HUMAN	EST365751 IMAGE resequences, MAGC Homo sapiens cDNA
11596	24195	37514	2.57	1.7E+00	W22424.1	EST_HUMAN	6787 Human retina cDNA Tsp509-cleaved sublibrary Homo sapiens cDNA not directional
12231	24884	31074	1.9	1.7E+00	AI678443.1	EST_HUMAN	tu82d07.x1 NCJ_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2257549 3' similar to contains MSR1.1
12717	24990	30970	1.84	1.7E+00	AI198573.1	EST_HUMAN	MSR1 repetitive element ;
2027	14762	27491	18.51	1.6E+00	AF199339.1	NT	qf50b01.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1753417 3' similar to contains L1.11 L1 repetitive element ;
							Homo sapiens lens epithelium-derived growth factor gene, alternatively spliced, complete cds

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Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2036	14771	27500	3.75	1.6E+00	AF077374.1	NT	Homo sapiens small proline-rich protein (SPRR3) gene, exons 1, 2, and 3 and complete cds
2042	14776	27505	1.54	1.6E+00	Y11344.1	NT	Mus musculus ST6GalNAcII gene, exon 2
2282	15007		1.24	1.6E+00	X98373.1	NT	B.napus gene encoding endo-polygalacturonase
2961	15727	28377	1.61	1.6E+00	W58426.1	EST_HUMAN	zid501.r1 Soares_fetal_NbHH19W Homo sapiens cDNA clone IMAGE:341689 5' similar to
4011	16757		5.68	1.6E+00	BF570077.1	EST_HUMAN	gb:D29805 N-ACETYL LACTOSAMINE SYNTHASE (HUMAN);
4319	17058	29682	1.9	1.6E+00	AF155827.1	NT	602180095T1 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:4310591 3'
4319	17058	29683	1.9	1.6E+00	AF155827.1	NT	Homo sapiens proliferation-associated SNF2-like protein (SMARCA6) mRNA, complete cds
							Homo sapiens proliferation-associated SNF2-like protein (SMARCA6) mRNA, complete cds
4942	17669	30277	0.84	1.6E+00	AF075394.1	NT	Urotaethis chinensis cytochrome c oxidase subunit I (COI) gene, mitochondrial gene encoding mitochondrial protein, partial cds
4942	17669	30278	0.84	1.6E+00	AF075394.1	NT	Urotaethis chinensis cytochrome c oxidase subunit I (COI) gene, mitochondrial gene encoding mitochondrial protein, partial cds
5024	17745	30356	2.86	1.6E+00	Y11344.1	NT	Mus musculus ST6GalNAcII gene, exon 2
5024	17745	30357	2.86	1.6E+00	Y11344.1	NT	Mus musculus ST6GalNAcII gene, exon 2
5737	18528	31450	2.16	1.6E+00	L04808.1	NT	Brachydanio rerio MHC class II DA-beta-2*01 gene, 3' end
5823	18612	31543	0.79	1.6E+00	AF005631.1	NT	Homo sapiens transglutaminase type I (Tgase1) gene, promoter region
6378	19147	32146	0.69	1.6E+00	BF380703.1	EST_HUMAN	IL2-UT0073-060900-145-E02 UT0073 Homo sapiens cDNA
6810	19373	32387	1.06	1.6E+00	AW294881.1	EST_HUMAN	UIH-B12-ahr-b-04-0-U1.s1 NCI_CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2727511 3'
7145	19832	32901	2.73	1.6E+00	BE697267.1	EST_HUMAN	RCO-GT0415-200700-032-c10 GT0415 Homo sapiens cDNA
7928	20624		1.19	1.6E+00	Q46378	SWISSPROT	VIRULENCE FACTOR MVIN HOMOLOG
8277	20971	34112	3.28	1.6E+00	AJ297131.1	NT	Mus musculus SIL, MAP_17, GYP_a, SQL & GYP_b genes
8788	21490	34636	0.83	1.6E+00	11437222	NT	Homo sapiens hypothetical protein PRO0971 (PRO0971), mRNA
8798	21490	34637	0.83	1.6E+00	11437222	NT	Homo sapiens hypothetical protein PRO0971 (PRO0971), mRNA
8970	21660	34810	0.47	1.6E+00	BE388331.1	EST_HUMAN	601283925F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3605647 5'
9360	25121	33549	1.94	1.6E+00	X52046.1	NT	M.musculus COL3A1 gene for collagen alpha-I
9360	25121	33550	1.94	1.6E+00	X52046.1	NT	M.musculus COL3A1 gene for collagen alpha-I
9487	22140		0.66	1.6E+00	AF043466.1	NT	Thermotogaobacter ethanolicus D-xylose-binding protein (xylF) gene, complete cds
9834	22288	35480	1.32	1.6E+00	T41290.1	EST_HUMAN	ph6b6_19/1TV Outward Alu-primed hncDNA library Homo sapiens cDNA clone ph6b6_19/1TV
							Drosophila melanogaster signal transducing adaptor protein (S-TAM), serine threonine kinase IAI (IAL), and
10047	22895	35911	0.5	1.6E+00	AF121361.1	NT	zinc finger protein (DNZ1) genes, complete cds
10085	22733	35947	1.15	1.6E+00	AW835644.1	EST_HUMAN	QV4-LT0016-090200-100-d07 LT0016 Homo sapiens cDNA
10085	22733	35948	1.15	1.6E+00	AW835644.1	EST_HUMAN	QV4-LT0016-090200-100-d07 LT0016 Homo sapiens cDNA
10242	22890	36102	0.47	1.6E+00	AF037352.1	NT	Mus musculus T cell receptor gamma locus, TCR gamma 1 and gamma 3 gene clusters
10491	23137	36365	0.45	1.6E+00	AF162084.1	NT	Glugea pleococcosi beta-tubulin 2 (btub2) gene, partial cds

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Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10670	23361	36602	1.95	1.6E+00	P54817	SWISSPROT	CAPSID PROTEIN P40 [CONTAINS: ASSEMBLIN (PROTEASE) ; CAPSID ASSEMBLY PROTEIN]
10728	23416	36657	1.27	1.6E+00	AA216387.1	EST_HUMAN	nc16b02.s1 NCL_CGAP_P1 Homo sapiens cDNA clone IMAGE:1008267 similar to contains element MIER4 repetitive element
10747	18612	31543	5.27	1.6E+00	AF005631.1	NT	Homo sapiens transglutaminase type I (Tgase1) gene, promoter region
11705	24200	37626	3.46	1.6E+00	AF104313.1	NT	Homo sapiens unknown mRNA
31	12859	25476	5.31	1.5E+00	U53449.1	NT	Rattus norvegicus jun dimerization protein 2 (jdp-2) mRNA, complete cds
225	13037	25674	2.2	1.5E+00	AE02201.2	NT	Chlamydomonas reinhardtii AR39, section 32 of 94 of the complete genome
606	13384		2.03	1.5E+00		NT	Mus musculus a disintegrin and metalloproteinase domain (ADAM) 15 (metagldin) (Adam15), mRNA
2410	15131	27867	1.95	1.5E+00	AJ131402.1	NT	Potato virus A RNA complete genome, isolate U
2519	15235	27975	2	1.5E+00	6678350	NT	Mus musculus T-cell lymphoma invasion and metastasis 1 (Tiam1), mRNA
3135	15131	27867	1.85	1.5E+00	AJ131402.1	NT	Potato virus A RNA complete genome, isolate U
3368	16127	28785	0.72	1.5E+00	AE001945.1	NT	Deinococcus radiodurans R1 section 82 of 229 of the complete chromosome 1
5642	18437	31350	0.83	1.5E+00	AI655301.1	EST_HUMAN	ht2f10.x1 NCL_CGAP_G06 Homo sapiens cDNA clone IMAGE:2240587 3' similar to TR:000237 O00237 HKF-1 ;
5642	18437	31351	0.83	1.5E+00	AI655301.1	EST_HUMAN	ht2f10.x1 NCL_CGAP_G06 Homo sapiens cDNA clone IMAGE:2240587 3' similar to TR:000237 O00237 HKF-1 ;
6312	19083	32088	3.02	1.5E+00	R17878.1	EST_HUMAN	X010602.1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:31693 5'
7028	19720		1.37	1.5E+00	BE785356.1	EST_HUMAN	601478745F1 NIH_MGC 68 Homo sapiens cDNA clone IMAGE:3881555 5'
7050	19751	32814	23.98	1.5E+00	P47179	SWISSPROT	HYPOTHETICAL 118.4 KD PROTEIN IN BAT2-DAL5 INTERGENIC REGION PRECURSOR
7060	19751	32815	23.98	1.5E+00	P47179	SWISSPROT	HYPOTHETICAL 118.4 KD PROTEIN IN BAT2-DAL5 INTERGENIC REGION PRECURSOR
7245	19330	33006	0.61	1.5E+00	AA889259.1	EST_HUMAN	ak26f10.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1407115 3'
7493	20165	33257				EST_HUMAN	an07b11.s1 Stragene schizo brain S11 Homo sapiens cDNA clone IMAGE:1684893 3' similar to gb:S95936 SERO TRANSFERRIN PRECURSOR (HUMAN);
7727	20390		0.64	1.5E+00	AB039887.1	NT	Homo sapiens WDR4 gene for WD repeat protein, complete cds
8021	20716	33848	0.99	1.5E+00	BE867446.1	EST_HUMAN	601509586F1 NIH_MGC 71 Homo sapiens cDNA clone IMAGE:3911181 5'
8542	21234	34377	0.84	1.5E+00	K02138.1	NT	Mouse germline IgM chain gene, mu-delta region
8914	21605		0.48	1.5E+00	AB038516.1	NT	Homo sapiens hGP1b alpha gene for platelet glycoprotein Ib alpha, complete cds
9032	21722	34876	0.46	1.5E+00	BF217818.1	EST_HUMAN	601882682F1 NIH_MGC 57 Homo sapiens cDNA clone IMAGE:4095135 5'
9383	22045	35217	0.64	1.5E+00	R81928.1	EST_HUMAN	Y03h01.1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:147697 5'
9535	22188	35374	1.39	1.5E+00	AW376957.1	EST_HUMAN	Q13-CT0192-261099-008-d09 CT0192 Homo sapiens cDNA
9760	22411	35618	6.39	1.5E+00	BF376754.1	EST_HUMAN	RC0-TN0078-150900-034-g05 TN0078 Homo sapiens cDNA
9952	22600		1.77	1.5E+00	BF337944.1	EST_HUMAN	602035771F1 NCL_CGAP_Bri64 Homo sapiens cDNA clone IMAGE:4183865 5'
10096	22744	35958	1.66	1.5E+00	AA017689.1	EST_HUMAN	ze38g06.1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:381306 5'

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Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10096	22744	35959	1.86	1.5E+00	AA017689.1	EST_HUMAN	ze38g06.r1 Scores refine N2b4HR Homo sapiens cDNA clone IMAGE:361306 5'
11376	23982	37282	4.46	1.5E+00	AL134197.1	EST_HUMAN	DKFZp547P243_s1 547 (synonym: hfr1) Homo sapiens cDNA clone DKFZp547P243 3'
11530	24130		6.55	1.5E+00	X07380.1	NT	Maize mitochondrial RNA-Ser gene and RNA-Phe pseudogene
11629	24226	37549	2.1	1.5E+00	AI400798.1	EST_HUMAN	ig94d09.x1 NCI CGAP CLL1 Homo sapiens cDNA clone IMAGE:2116433 3'
11629	24226	37550	2.1	1.5E+00	AI400798.1	EST_HUMAN	ig94d09.x1 NCI CGAP CLL1 Homo sapiens cDNA clone IMAGE:2116433 3'
12222	25325	30713	1.44	1.5E+00	D63480.1	NT	Human mRNA for KIAA0146 gene, partial cds
12445	24815		3.38	1.5E+00	AL445065.1	NT	Thermoplasma acidophilum complete genome, segment 3/5
28	12856	25472	2.78	1.4E+00	7661685	NT	Homo sapiens DKFZP586M0122 protein (DKFZP586M0122), mRNA
28	12856	25473	2.76	1.4E+00	7661685	NT	Homo sapiens DKFZP586M0122 protein (DKFZP586M0122), mRNA
2333	15057		6.92	1.4E+00	U67922.1	NT	Ovis aries prion protein gene, complete cds
2675	15384	28125	2.21	1.4E+00	X74463.1	NT	Human papillomavirus type 7 genomic DNA
2776	15481	28221	2.61	1.4E+00	AF064564.2	NT	Fugu rubripes neurofibromatosis type 1 (NF1), A-kinase anchor protein (AKAP84), BAW protein (BAW), and WSB1 protein (WSB1) genes, complete cds
2776	15481	28222	2.61	1.4E+00	AF064564.2	NT	Fugu rubripes neurofibromatosis type 1 (NF1), A-kinase anchor protein (AKAP84), BAW protein (BAW), and WSB1 protein (WSB1) genes, complete cds
4545	17280		1.81	1.4E+00	BF681547.1	EST_HUMAN	602156687F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4297556 5'
5288	18083	30754	1.61	1.4E+00	AW054976.1	EST_HUMAN	w45g07.x1 NCI CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2510460 3'
5441	18240		5.57	1.4E+00	AB032983.1	NT	Homo sapiens mRNA for KIAA1157 protein, partial cds
6186	18963	31936	2.72	1.4E+00	Q13472	SWISSPROT	DNA TOPOISOMERASE III ALPHA
6202	25420		4.02	1.4E+00	AB020712.1	NT	Homo sapiens mRNA for KIAA0905 protein, complete cds
6318	19089	32074	2.67	1.4E+00	Q92777	SWISSPROT	SYNAPSIN II
6318	19089	32075	2.67	1.4E+00	Q92777	SWISSPROT	SYNAPSIN II
7186	19872	32946	2.07	1.4E+00	AJ133289.1	NT	Homo sapiens cavedin-1/-2 locus, Contig1, D7S522, genes CAV2 (exons 1, 2a, and 2b), CAV1 (exons 1 and 2)
7201	19887	32962	1.17	1.4E+00	AW467760.1	EST_HUMAN	he23f05.x1 NCI CGAP_CML1 Homo sapiens cDNA clone IMAGE:2919873 3' similar to contains Alu repetitive element
7258	19942	33018	0.75	1.4E+00	P55268	SWISSPROT	LAMININ BETA-2 CHAIN PRECURSOR (S-LAMININ)
7258	19942	33019	0.75	1.4E+00	P55268	SWISSPROT	LAMININ BETA-2 CHAIN PRECURSOR (S-LAMININ)
8233	20927		0.68	1.4E+00	P07983	SWISSPROT	GLUCOAMYLASE PRECURSOR (GLUCAN 1,4-ALPHA-GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOXYDROLASE)
8693	21385		4.47	1.4E+00	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region, segment 1/2
8991	21681	34829	1.73	1.4E+00	R20459.1	EST_HUMAN	y933f12.r1 Scores infant brain 1N1B Homo sapiens cDNA clone IMAGE:34345 5'
8097	21785	34951	4.65	1.4E+00	BE084667.1	EST_HUMAN	RC1-BT0313-301299-012-05 BT0313 Homo sapiens cDNA
9131	21819	34985	0.51	1.4E+00	AF134844.1	NT	Sceloporus undulatus ornithine transcarbamylase (OTC) mRNA, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10108	22756	35988	0.79	1.4E+00	BF675546.1	EST_HUMAN	602133135F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4288137 5'
10151	22798	36015	0.61	1.4E+00	BE146374.1	EST_HUMAN	IL5-HT0198-291099-008-C04 HT0198 Homo sapiens cDNA
10151	22799	36016	0.61	1.4E+00	BE146374.1	EST_HUMAN	IL5-HT0198-291099-008-C04 HT0198 Homo sapiens cDNA
10424	23070	36291	1.06	1.4E+00	D63441.1	NT	Pandorina colemaniae chloroplast rbcL gene for ribulose biphosphate carboxylase, partial cds
10424	23070	36292	1.06	1.4E+00	D63441.1	NT	Pandorina colemaniae chloroplast rbcL gene for ribulose biphosphate carboxylase, partial cds
11003	23875	36931	1.34	1.4E+00	AA195528.1	EST_HUMAN	z36609.r1 Soares_Nhi-MP_u_S1 Homo sapiens cDNA clone IMAGE:665612 5' similar to contains element
11188	23853	37139	6.16	1.4E+00	AB006882.1	NT	MER22 repetitive element ;
11381	23988	37288	4.42	1.4E+00	BE962107.2	EST_HUMAN	Homo sapiens APECED mRNA for AIRE-1, complete cds
11381	23988	37289	4.42	1.4E+00	BE962107.2	EST_HUMAN	601655184R1 NIH_MGC_85 Homo sapiens cDNA clone IMAGE:3845805 3'
11404	24053	37357	3.46	1.4E+00	U30790.1	NT	601655184R1 NIH_MGC_85 Homo sapiens cDNA clone IMAGE:3845805 3'
11404	24053	37358	3.46	1.4E+00	U30790.1	NT	Pneumocystis carinii f. sp. ratti guanine nucleotide binding protein alpha subunit (pcg1) gene, complete cds
12078	25256		1.48	1.4E+00	AL161500.2	NT	Pneumocystis carinii f. sp. ratti guanine nucleotide binding protein alpha subunit (pcg1) gene, complete cds
557	13339		1.81	1.3E+00	Z79840.1	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 12
882	13651	26320	3.42	1.3E+00	AJ271192.1	NT	M.mucedo gene encoding 4-Dihydroxyethyl-trispartate dehydrogenase
1107	13864		20.26	1.3E+00	Y19213.1	NT	Cantharellus sp. partial 25S rRNA gene, isolate Tibet
1274	14024	26682	13.71	1.3E+00	4507998	NT	Homo sapiens putative psihbA pseudogene for hair keratin, exons 2 to 7
1274	14024	26683	13.71	1.3E+00	4507998	NT	Homo sapiens zinc finger protein 157 (HZF22) (ZNF157) mRNA
1334	14083		1.26	1.3E+00	U61730.2	NT	Homo sapiens zinc finger protein 157 (HZF22) (ZNF157) mRNA
1605	14351		2.27	1.3E+00	AE002398.2	NT	Colix lactyme-jobi dihydriolipicolinate synthase (dapa) gene, complete cds
2239	14967		1	1.3E+00	AB030447.1	NT	Chlamydia muridarum, section 86 of 85 of the complete genome
2405	15128	27862	1.27	1.3E+00	P25391	SWISSPROT	Cyprinus carpio MRPb and MASPb genes for mannose-binding lectin-associated serine protease (MASP) and MASP-related protein, complete cds
2553	15268		1.75	1.3E+00	BE966735.2	EST_HUMAN	LAMININ ALPHA-1 CHAIN PRECURSOR (LAMININ A CHAIN)
2940	15705	28354	0.73	1.3E+00	6755621	NT	601661233R1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3915945 3'
3584	16339	28984	0.89	1.3E+00	AF016494.1	NT	Mus musculus alpha-spectrin 1, erythroid (Spna4), mRNA
5427	18226	30838	1.09	1.3E+00	P19732	NT	Fugu rubripes gamma-aminobutyric acid receptor beta subunit gene, partial cds; 55kd erythrocyte membrane protein (P55), synaptic vesicle-associated integral membrane protein (VAMP-1), procollagen C-proteinase enhancer protein (PCOLCE) genes, complete c>
5622	18418	31330	0.6	1.3E+00	M27138.1	NT	PHENOL HYDROXYLASE P3 PROTEIN (PHENOL 2-MONOXYGENASE P3 COMPONENT)
5863	18650	31590	0.81	1.3E+00	BF668325.1	EST_HUMAN	Human estradiol 17 beta-dehydrogenase gene, complete cds
5928	18712	31867	7.57	1.3E+00	AW362834.1	EST_HUMAN	602145264F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4309095 5'
							PMO-CT0289-291199-004-008 CT0289 Homo sapiens cDNA

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5928	18712	31688	7.57	1.3E+00	AW362834.1	EST_HUMAN	PMO-CT0289-291199-004-008 CT0289 Homo sapiens cDNA
6323	19093	32081	1.34	1.3E+00	M33496.1	NT	D.melanogaster no-on-transient A gene product, complete cds
6652	19414	32081	0.75	1.3E+00	Q00156	SWISSPROT	HYPOPHOSPHATASE 64 PROTEIN
6739	19573	32606	0.62	1.3E+00	M13918.2	NT	Homo sapiens fibronectin receptor alpha-subunit precursor (ITGA5) mRNA, partial cds
6854	19554	32584	1.17	1.3E+00	BE63819.1	EST_HUMAN	TCBAP1D0859 Pediatric pre-B cell acute lymphoblastic leukemia Baylar-HGSC project=TCBA Homo sapiens cDNA clone TCBAP0859
7000	19692	32743	0.81	1.3E+00	BE243571.1	EST_HUMAN	ACYLPHOSPHATASE, ORGAN-COMMON TYPE ISOZYMES A AND B (ACYLPHOSPHATE)
7358	20039	33117	1.01	1.3E+00	P24540	SWISSPROT	PHOSPHOHYDROLASE
8197	20891	34029	1.28	1.3E+00	AJ009912.1	NT	Sus scrofa plp gene
8346	21039	34176	2.78	1.3E+00	BE963379.2	EST_HUMAN	601657145R1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3866195 3'
8459	21151	34294	0.86	1.3E+00	BE974280.1	EST_HUMAN	601680250R2 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3950532 3'
8611	21303		1.78	1.3E+00	9810247	NT	Homo sapiens GL004 protein (GL004), mRNA
8889	21381	34625	0.79	1.3E+00	AJ927629.1	EST_HUMAN	wo85a07.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2462100 3'
9415	22093		5.24	1.3E+00	AF042084.1	NT	Homo sapiens heparan glucosaminyl N-deacetylase/N-sulfotransferase-2 gene, complete cds
9424	22102	35273	2.56	1.3E+00	X72019.1	NT	S.alba phr-1 mRNA for photolyase
9424	22102	35274	2.56	1.3E+00	X72019.1	NT	S.alba phr-1 mRNA for photolyase
9524	22177	35361	0.86	1.3E+00	AF059250.1	NT	Homo sapiens lipoygenase (ALOX12B) mRNA, complete cds
9569	22222	35407	1.56	1.3E+00	Q00754	SWISSPROT	LYSOSOMAL ALPHA-MANNOSIDASE PRECURSOR (MANNOSIDASE, ALPHA B) (LYSOSOMAL ACID
9651	22303	35498	1.14	1.3E+00	AJ927629.1	EST_HUMAN	wo85a07.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2462100 3'
9726	22377	35578	0.79	1.3E+00	AJ223962.1	NT	Lactococcus lactis cremoris NCDO-invt1 chromosomal inversion junction DNA
9726	22377	35579	0.79	1.3E+00	AJ223962.1	NT	Lactococcus lactis cremoris NCDO-invt1 chromosomal inversion junction DNA
9768	22417	35624	4.53	1.3E+00	BE963379.2	EST_HUMAN	601657145R1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3866195 3'
9826	22477		0.48	1.3E+00	AI559944.1	EST_HUMAN	lq77a12.x1 NCI_CGAP_UH1 Homo sapiens cDNA clone IMAGE:2214814 3' similar to gb:U14723
10050	22698	35913	0.46	1.3E+00	AF061251.1	NT	CLUSTERIN PRECURSOR (HUMAN);
10050	22698	35914	0.46	1.3E+00	AF061251.1	NT	Escherichia coli serotype O157:H7 O antigen gene cluster
10113	22761	35974	1.62	1.3E+00	AE004392.1	NT	Escherichia coli serotype O157:H7 O antigen gene cluster
10130	22778	35991	1.35	1.3E+00	M29953.1	NT	Vibrio cholerae chromosome II, section 49 of 83 of the complete chromosome
10483	23129		0.82	1.3E+00	AL163302.2	NT	Campylobacter jejuni kanamycin phosphotransferase (aphA-7) gene, complete cds
10511	23157	36383	0.45	1.3E+00	AI990846.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C102
10592	23286		4.6	1.3E+00	Q14117	SWISSPROT	ws32e10.x1 NCI_CGAP_GC8 Homo sapiens cDNA clone IMAGE:2498922 3' similar to SW:TRXB_HUMAN Q16881 THIOREDOXIN REDUCTASE
							DIHYDROPYRIMIDINASE (DHPASE) (HYDANTOINASE) (DHP)

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Single Exon Probes Expressed In Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10822	23505	36744	1.93	1.3E+00	P25289	SWISSPROT	MRNA 3'-END PROCESSING PROTEIN RNA15
10846	23528	36772	2.01	1.3E+00	Z18892.2	NT	Mus musculus desmulin gene
11307	23966		1.8	1.3E+00	AW274791.1	EST_HUMAN	xp09e03.x1 NCJ_CGAP_HIN9 Homo sapiens cDNA clone IMAGE:2739868 3'
11527	24127	37433	3.21	1.3E+00	D42042.1	NT	Human mRNA for KIAA0085 gene, partial cds
11624	24221	37544	3.16	1.3E+00	Z98682.1	NT	Bacillus subtilis genomic DNA 23.9kb fragment
12210	24675		2.64	1.3E+00	AF187873.1	NT	Cavia porcellus inwardly-rectifying potassium channel Kir2.2 (KCNJ12) gene, complete cds
12386	24780	31035	6.3	1.3E+00	BF348043.1	EST_HUMAN	802023185F1 NCJ_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4158452 5'
12489	25153		2.73	1.3E+00	P33464	SWISSPROT	E1 GLYCOPROTEIN PRECURSOR (MATRIX GLYCOPROTEIN) (MEMBRANE GLYCOPROTEIN)
12489	24848		2.15	1.3E+00	AF187035.1	NT	Sturmira lilium cytochrome b gene, complete cds; mitochondrial gene for mitochondrial product
635	13414	26050	11.05	1.2E+00	AA676246.1	EST_HUMAN	222408.st Soares_fetal_liver脾 INFLS_S1 Homo sapiens cDNA clone IMAGE:431535 3'
804	13576	26239	0.87	1.2E+00	P05228	SWISSPROT	HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PFHRP-III)
804	13576	26240	0.87	1.2E+00	P05228	SWISSPROT	HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PFHRP-III)
804	13576	26241	0.87	1.2E+00	P05228	SWISSPROT	HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PFHRP-III)
858	13627		1.35	1.2E+00	8824234	NT	Homo sapiens hypothetical protein PRO3077 (PRO3077), mRNA
1138	13893	26554	5.64	1.2E+00	AF080245.2	NT	Eleis oleifera sesquiterpene synthase mRNA, complete cds
1183	13935	26600	1.28	1.2E+00	AJ252242.1	NT	pea seed-borne mosaic virus complete genome
1183	13935	26601	1.28	1.2E+00	AJ252242.1	NT	pea seed-borne mosaic virus complete genome
2003	14739	27463	1.22	1.2E+00	AF140631.1	NT	Homo sapiens G-protein coupled receptor 14 (GPR14) gene, complete cds
3108	15873	28512	1.24	1.2E+00	AB020681.1	NT	Homo sapiens mRNA for KIAA0874 protein, partial cds
3163	15926	28573	5.98	1.2E+00	AL161563.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 63
3163	15926	28574	5.98	1.2E+00	AL161563.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 63
3280	16041		2.59	1.2E+00	P54910	SWISSPROT	CONJUGAL TRANSFER PROTEIN TRBE PRECURSOR
3699	16452	29091	6.69	1.2E+00	U79902.1	NT	Mus musculus subtilisin-like serine protease LPC (PC7) gene, exons 1 to 9, partial cds
3967	16716	29354	1.78	1.2E+00	BF373570.1	EST_HUMAN	MR0-FT0175-050900-203-g06_1 FT0175 Homo sapiens cDNA
4266	16110	28786	1.11	1.2E+00	AF188740.1	NT	Homo sapiens LHX3 gene, intron 2
4438	17174		1.57	1.2E+00	M87060.1	NT	Rattus rattus cardiac AEs gene, exons 1-23
4487	17222	29850	0.96	1.2E+00	AF161509.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 21
4523	17255	29892	1.89	1.2E+00	AF158495.1	NT	Homo sapiens post-synaptic density 95 (DLG4) gene, complete cds
4548	17283		6.43	1.2E+00	Y09200.1	NT	T. plinatum chloroplast rbcL gene, partial
5351	18154	30836	1.1	1.2E+00	U20780.1	NT	Human extracellular calcium-sensing receptor mRNA, complete cds
5487	18268	31156	1.91	1.2E+00	AW813276.1	EST_HUMAN	MR3-ST0191-140200-013-c05 ST0191 Homo sapiens cDNA
5784	18575	31504	0.83	1.2E+00	AF016052.1	NT	Homo sapiens zinc finger protein ZNF191 (ZNF191) gene, complete cds
6060	18840	31801	2.51	1.2E+00	X74885.1	NT	D.hydai ayt1 repeat cluster DNA, fragment D
6119	18897	31895	4.42	1.2E+00	BE003113.1	EST_HUMAN	QV4-BN0090-270400-190-a03 BN0090 Homo sapiens cDNA

Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6198	18974	31951	1.54	1.2E+00	X89084.1	NT	C. glutamicum pla gene and ackA gene
6198	18974	31952	1.54	1.2E+00	X89084.1	NT	C. glutamicum pla gene and ackA gene
6241	19016	31989	39.54	1.2E+00	AA759254.1	EST_HUMAN	ah84g12.s1 Scores: testis, NHT Homo sapiens cDNA clone 1322374 3'
6342	19112	32101	0.55	1.2E+00	N33295.1	EST_HUMAN	y98b12.s1 Scores: melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:273599 3' similar to gbIM87855 HUMALU472 Human carcinoma cell-derived Alu RNA transcript, (rRNA); gb.J04970 CARBOXYPEPTIDASE M PRECURSOR (HUMAN);
6408	19177	32175	0.68	1.2E+00	P17671	SWISSPROT	ECDSYONE-INDUCIBLE PROTEIN E75-A
6412	19180	32179	2.06	1.2E+00	AW813276.1	EST_HUMAN	MR3-ST0191-140200-013-c05 ST0191 Homo sapiens cDNA
6815	19476	32498	1.17	1.2E+00	AB029010.1	NT	Homo sapiens mRNA for KIAA1087 protein, partial cds
6829	19478	32512	3.11	1.2E+00	AJ002141.1	NT	Mus musculus DSSP gene
7153	19840		0.94	1.2E+00	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
7282	25109	33044	4.86	1.2E+00	AV734585.1	EST_HUMAN	AV734585 cda Homo sapiens cDNA clone cdaAFH03 5'
7650	20220	33323	2.49	1.2E+00	X74207.1	NT	L.lactis pyrD and pyrF genes
7603	20269	33376	0.56	1.2E+00	J05218.1	NT	Chicken muscarinic acetylcholine receptor (cm4 mAChR) gene, complete cds
7715	20379	33492	0.56	1.2E+00	BE787646.1	EST_HUMAN	601481761F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3884270 5'
8467	21159	34302	3.32	1.2E+00	AB033030.1	NT	Homo sapiens mRNA for KIAA1204 protein, partial cds
8561	21253	34391	0.68	1.2E+00	P38427	SWISSPROT	ALPHA-ALPHA-TREHALOSE-PHOSPHATE SYNTHASE [UDP-FORMING] 123 KD SUBUNIT (TREHALOSE-6-PHOSPHATE SYNTHASE) (UDP-GLUCOSE-GLUCOSEPHOSPHATE)
8775	21467		0.51	1.2E+00	7706271	NT	GLUCOSYLTRANSFERASE
8923	21614	34758	1.87	1.2E+00	AW377210.1	EST_HUMAN	Homo sapiens CGI-30 protein (LOC51611), mRNA
9138	21826	34951	0.5	1.2E+00	H48599.1	EST_HUMAN	MR2-CT0222-207099-001-e07 CT0222 Homo sapiens cDNA
9298	21966	35138	3.75	1.2E+00	Z32850.1	NT	y88a06.1 Scores: fetal liver spleen 1NLS Homo sapiens cDNA clone IMAGE:202066 5'
9505	22158	35339	1.81	1.2E+00	D11745.1	EST_HUMAN	R.communis gene for pyrophosphate-dependent phosphofructokinase beta subunit
9831	22482	35684	2.86	1.2E+00	X56832.1	NT	HUMHM01A01 Liver HepG2 cell line. Homo sapiens cDNA clone hm01a01
10224	22872		0.73	1.2E+00	AB009866.1	NT	H. sapiens ENO3 gene for muscle specific enolase
11318	24009	37314	3.78	1.2E+00	AW817817.1	EST_HUMAN	Homo sapiens Motho gene, exon 1
11357	24046		10.62	1.2E+00	BE160761.1	EST_HUMAN	PM0-ST0264-161199-001-d01 ST0264 Homo sapiens cDNA
11435	23202	36434	4.36	1.2E+00	U50147.1	EST_HUMAN	PM1-HT0422-160200-007-g10 HT0422 Homo sapiens cDNA
12178	25227	30817	17.06	1.2E+00	AL163203.2	NT	Rattus norvegicus synapse-associated protein 102 mRNA, complete cds
12199	24667		2.8	1.2E+00	AF001515.1	NT	Homo sapiens chromosome 21 segment HS21C003
451	13237	25876	1.53	1.1E+00	D96960.1	NT	Bacillus halodurans genomic DNA, section 9/14
1757	14499	27200	1.33	1.1E+00	AW995393.1	EST_HUMAN	Human mRNA for KIAA0227 gene, partial cds
1892	14629	27339	0.98	1.1E+00	AW575889.1	EST_HUMAN	QVO-BN0042-170300-163-g12 BN0042 Homo sapiens cDNA
							UI-HF-BR0p-ajk-f-02-0-JL.s1 NIH_MGC_52 Homo sapiens cDNA clone IMAGE:3074834 3'

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3324	16084	28734	6.48	1.1E+00	AL163213.2	NT	Homo sapiens chromosome 21 segment HS21C013
3324	16084	28735	6.48	1.1E+00	AL163213.2	NT	Homo sapiens chromosome 21 segment HS21C013
3480	16236	28892	1.11	1.1E+00	8922641	NT	Homo sapiens hypothetical protein FLJ10749 (FLJ10749), mRNA
3567	16322	28970	1.01	1.1E+00	AI808360.1	EST_HUMAN	wf54h11.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2359461 3' similar to
3707	16460	29098	1.05	1.1E+00	AE003886.1	NT	SW:P531_HUMAN Q12888 P53-BINDING PROTEIN 63BP1 ;
3707	16460	29099	1.05	1.1E+00	AE003886.1	NT	Xylella fastidiosa, section 32 of 229 of the complete genome
3798	16550		1.02	1.1E+00	X85374.1	NT	Xylella fastidiosa, section 32 of 229 of the complete genome
4190	16931		5.69	1.1E+00	5835331	NT	H. parahaeuolyticus hphIM(A), hphIM(C), hphIR and menB genes
4634	17369		0.81	1.1E+00	U34992.1	NT	R. unicomis complete mitochondrial genome
4934	17682	30272	3.45	1.1E+00	U18466.1	NT	Garchinus plumbeus Ig lambda light chain gene, complete cds
4935	17683	30273	1.05	1.1E+00	AJ271740.1	NT	African swine fever virus, complete genome
5129	17847	30464	1.07	1.1E+00	6680080	NT	Drosophila melanogaster D-Titin gene, exons 1-37
5224	18031	30657	1.39	1.1E+00	6978550	NT	Homo sapiens putative GR6 protein (GR6), mRNA
5526	18324	31225	15.75	1.1E+00	BE960184.1	EST_HUMAN	Rattus norvegicus Aquaporin 4 (Aqp4), mRNA
5545	18342	31250	1.2	1.1E+00	AI138582.1	EST_HUMAN	601652776R1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3825835 3'
6001	18782	31743	1.1	1.1E+00	11419739	NT	qd85c03.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1736260 3'
6181	18958	31932	0.62	1.1E+00	AF197861.1	NT	Homo sapiens solute carrier family 6 (neurotransmitter transporter), member 14 (SLC6A14), mRNA
6313	19084	32069	0.82	1.1E+00	R06037.1	EST_HUMAN	Macgregoria pulchra cytochrome b gene, complete cds; mitochondrial gene for mitochondrial product
6616	19379	32394	0.72	1.1E+00	AJ404004.1	NT	ye89e03.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:124924 5'
7155	19842	32956	0.58	1.1E+00	AF101091.1	NT	Mus musculus mRNA for ER protein 68 (EP68 gene)
7196	19882	32956	0.72	1.1E+00	X55981.1	NT	Homo sapiens collagen type XI alpha-1 (COL11A1) gene, exons 25 through 28
7389	20068	33146	2.18	1.1E+00	Z72338.1	NT	Maize mRNA for endase (2-phospho-D-glycerate hydrolase)
7389	20068	33147	2.18	1.1E+00	Z72338.1	NT	Herpes simplex virus type 1 (strain KOS) UL41 gene
7411	20088	33172	8.84	1.1E+00	AL161588.2	NT	Herpes simplex virus type 1 (strain KOS) UL41 gene
7480	25115	33247	0.8	1.1E+00	11967960	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 84
8032	20727	33960	3.01	1.1E+00	BF693986.1	EST_HUMAN	Mus musculus silent mating type information regulation 2, (S.cerevisiae, homolog)-like (Sir2), mRNA
8120	20814	33950	0.64	1.1E+00	AI478339.1	EST_HUMAN	602082582F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4246628 5'
8636	21328	34471	0.71	1.1E+00	AB003088.1	NT	im39h11.x1 NCJ_CGAP_KK11 Homo sapiens cDNA clone IMAGE:2160549 3'
8714	21408	34549	0.75	1.1E+00	S80750.1	NT	Acetabularia calliculus mitochondrial COX-like gene
							VH-anti-cytomegalovirus glycoprotein B antibody 4D4 heavy chain variable region [human, mRNA Partial, 375 nt]

Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8824	21518	34861	0.45	1.1E+00	AI079948.1	EST_HUMAN	oz34f05.x1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:1677249 3'
9337	20408		0.69	1.1E+00	BE384876.1	EST_HUMAN	601278279F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3617418 5'
9528	22181	35365	0.53	1.1E+00	AJ245772.1	NT	Mus musculus mRNA for stretch responsive muscle (X-chromosome) protein (Srmx gene)
9580	22233		1.2	1.1E+00	Y12227.1	NT	Arabidopsis thaliana DNA, 24 kb surrounding PFL locus
9672	22324	35520	1.14	1.1E+00	L76301.1	NT	Yersinia pseudotuberculosis psaE, psaF, adfresin (psaA), chaperone (psaB), and usher (psaC) genes, complete cds
9732	22383	35585	1.37	1.1E+00	AB023151.1	NT	Homo sapiens mRNA for KIAA0934 protein, partial cds
9837	22488	35690	4.59	1.1E+00	AL161515.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 27
9898	22548	35742	18.34	1.1E+00	6754021	NT	Mus musculus guanine nucleotide binding protein (G protein), gamma 3 subunit (Gng3), mRNA
10398	23044	36280	1.1	1.1E+00	P73769	SWISSPROT	DNA MISMATCH REPAIR PROTEIN MUTS
10504	23150	36375	0.73	1.1E+00	AI878921.1	EST_HUMAN	au51ct11.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2518292 5' similar to gb:D10522
10547	23243	36478	2.25	1.1E+00	11067384	NT	Human mRNA for 80K-L protein, complete cds. (HUMAN);
10806	23300		3.1	1.1E+00	AF068942.1	NT	Homo sapiens KIAA0626 gene product (KIAA0626), mRNA
11023	23695	36958	1.28	1.1E+00	11439596	NT	Klebsorridium fluitans cytochrome c oxidase subunit 2 (cox2) gene, mitochondrial gene encoding mitochondrial protein, partial cds
11026	23698	36961	1.58	1.1E+00	L16877.1	NT	Homo sapiens potassium inwardly-rectifying channel, subfamily J, member 11 (KCNJ11), mRNA
11042	17901		5.23	1.1E+00	8922973	NT	Homo sapiens cytochrome P4502C9 (CYP2C9) gene, 5' flank and exon 1
11048	23718	36988	3.68	1.1E+00	AF012862.1	NT	Homo sapiens hypothetical protein FLJ11280 (FLJ11280), mRNA
11048	23718	36989	3.68	1.1E+00	AF012862.1	NT	Petrosselinum crispum cytosolic glucose-6-phosphate dehydrogenase 1 (c68PDH1) mRNA, complete cds
11328	24019	37323	4.58	1.1E+00	AB09699.1	EST_HUMAN	Petrosselinum crispum cytosolic glucose-6-phosphate dehydrogenase 1 (c68PDH1) mRNA, complete cds
11561	24160	37470	1.63	1.1E+00	D99501.1	NT	w76e11.x1 Soares_NFL_T_OBC_S1 Homo sapiens cDNA clone IMAGE:2361548 3'
11561	24160	37471	1.63	1.1E+00	D99501.1	NT	Human PBI gene, complete cds
12153	24639		3.66	1.1E+00	P07866	SWISSPROT	Human PBI gene, complete cds
12250	24897	31078	1.93	1.1E+00	AF216696.1	NT	LOW TEMPERATURE ESSENTIAL PROTEIN
12378	25225		2.09	1.1E+00	AF234189.1	NT	Taenia solium immunogenic protein T576 mRNA, partial cds
12388	25200		1.44	1.1E+00	8393196	NT	Dicystotilum discoidium isopentenyl pyrophosphate isomerase (Dipi) mRNA, complete cds
97	12923		2.46	1.0E+00	U23808.1	NT	Rattus norvegicus C-reactive protein, member of the pentraxin family (Crip), mRNA
111	12932	25569	0.73	1.0E+00	D88425.1	NT	Xeropus laevis rhodopsin gene, complete cds
408	13194		2.25	1.0E+00	AB021884.1	NT	Gavia cobaya mRNA for serine/threonine kinase, complete cds
562	13344	25971	1.2	1.0E+00	AJ251690.1	NT	Marchantia polymorpha genes for 26S rRNA, 5S rRNA, 18S rRNA, 5.8S rRNA and 26S rRNA
662	13438	26079	4.38	1.0E+00	AL163218.2	NT	Girardia tigrina mRNA for homeodomain transcription factor (so gene)
						NT	Homo sapiens chromosome 21 segment HS21C018

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663	13439		0.95	1.0E+00	AF125984.1	NT	Aedes aegypti mucin-like protein MUC1 mRNA, complete cds
1365	15567		3.03	1.0E+00	X80416.1	NT	V. carteri Algal-CAM mRNA
1751	14493	27183	0.93	1.0E+00	AB006531.1	NT	Plautia stali intestine virus RNA for nonstructural
2489	15206	27947	1.18	1.0E+00	P48355	SWISSPROT	DNA GYRASE SUBUNIT B
2489	15206	27948	1.18	1.0E+00	P48355	SWISSPROT	DNA GYRASE SUBUNIT B
2878	15645	28287	3.82	1.0E+00	P24008	SWISSPROT	3-OXO-5-ALPHA-STEROID 4-DEHYDROGENASE 1 (STEROID 5-ALPHA-REDUCTASE 1) (SR TYPE 1)
2878	15645	28288	3.82	1.0E+00	P24008	SWISSPROT	3-OXO-5-ALPHA-STEROID 4-DEHYDROGENASE 1 (STEROID 5-ALPHA-REDUCTASE 1) (SR TYPE 1)
2967	15733		1.17	1.0E+00	O14226	SWISSPROT	HYPOTHETICAL 67.9 KD PROTEIN C8F12.08C IN CHROMOSOME 1
3194	15957	28609	1.24	1.0E+00	AA628453.1	EST_HUMAN	af26908.s1 Soares, total_tetus_Nb2HF8_gw Homo sapiens cDNA clone IMAGE:1032830 3' similar to
3585	12923		1.24	1.0E+00	U23806.1	NT	WP: C42D8.3 CE04204 : contains element MER22 MER22 repetitive element ;
3669	16422	29063	1.04	1.0E+00	AJ223816.1	NT	Xenopus laevis rhodopsin gene, complete cds
4050	16795	29424	0.76	1.0E+00	AF223391.1	NT	Agaricus bisporus mRNA for tyrosinase
4242	16983		0.79	1.0E+00	8922245	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
4954	17880		0.93	1.0E+00	D10852.1	NT	Homo sapiens hypothetical protein FLJ10139 (FLJ10139), mRNA
4975	17898	30306	0.74	1.0E+00	AF092505.1	NT	Rattus norvegicus mRNA for N-acetylglucosaminyltransferase III, complete cds
5200	18008	30629	3.53	1.0E+00	Z97022.1	NT	Mus musculus dipeptidyl aminopeptidase-like protein 6 (Dpp6) gene, partial cds; and proximal Rump white inversion breakpoint
5759	18551	31472	4.97	1.0E+00	AF248054.1	NT	Hordeum vulgare gene encoding cysteine proteinase
5759	18551	31473	4.97	1.0E+00	AF248054.1	NT	Bos taurus micromolar calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds
5887	18554	31595	1.53	1.0E+00	Z97341.2	NT	Bos taurus micromolar calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds
6024	18804	31765	4.7	1.0E+00	P04501	SWISSPROT	Arabidopsis thaliana DNA chromosome 4, ESSA1 FCA contig fragment No. 6
6030	18810	31770	1.49	1.0E+00	AW452782.1	EST_HUMAN	FIBER PROTEIN
6397	19166	32166	1.95	1.0E+00	U75902.1	NT	U1-H-B3-abx-d-09-Q-U1.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:308869 3'
6447	19215	32213	0.81	1.0E+00	AF104689.1	NT	Mus musculus subtilisin-like serine protease LPC (PCT) gene, exons 1 to 8, partial cds
6534	19300		1.06	1.0E+00	P46506	SWISSPROT	Homo sapiens cell cycle protein (P42G4) gene, exons 2 through 5
6679	19596	32634	1.33	1.0E+00	Y11204.1	NT	SRB-11 PROTEIN
							V. carteri gene encoding volvoxopsin

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7038	19730	32788	1.09	1.0E+00	S52770.1	NT	insulin-like growth factor-binding protein 4 [cattle, pulmonary artery endothelial cells, mRNA, 2028 nt]
7378	20058		9.29	1.0E+00	P20273	SWISSPROT	B-CELL RECEPTOR CD22 PRECURSOR (LEU-14) (B-LYMPHOCYTE CELL ADHESION MOLECULE) (BL-CAM)
7611	20277	33385	1.56	1.0E+00	AF192531.1	NT	Homo sapiens endothelin-converting enzyme 2 (ECE2) mRNA, complete cds
7626	20282	33401	5.26	1.0E+00	AA775181.1	EST_HUMAN	ac79608.s1 Stratiogene lung (#837210) Homo sapiens cDNA clone IMAGE:368791 3'
7861	20558	33681	1.36	1.0E+00	BE868267.1	EST_HUMAN	601443950F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3848005 5'
7861	20556	33682	1.36	1.0E+00	BE868267.1	EST_HUMAN	601443950F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3848005 5'
8041	17680		1.19	1.0E+00	D10852.1	NT	Rattus norvegicus mRNA for N-acetylglucosaminyltransferase III, complete cds
8248	20942	34079	2.02	1.0E+00	Q02207	SWISSPROT	PEROXISOMAL HYDRATASE-DEHYDROGENASE-EPIMERASE (HDE) (MULTIFUNCTIONAL BETA-OXIDATION PROTEIN) (MFP) [INCLUDES: 2-ENOYL-COA HYDRATASE; D-3-HYDROXYACYL COA DEHYDROGENASE]
8248	20942	34080	2.02	1.0E+00	Q02207	SWISSPROT	PEROXISOMAL HYDRATASE-DEHYDROGENASE-EPIMERASE (HDE) (MULTIFUNCTIONAL BETA-OXIDATION PROTEIN) (MFP) [INCLUDES: 2-ENOYL-COA HYDRATASE; D-3-HYDROXYACYL COA DEHYDROGENASE]
8376	21069		0.85	1.0E+00	P51784	SWISSPROT	UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 11 (UBIQUITIN THIOLESTERASE 11) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 11) (DEUBIQUITINATING ENZYME 11)
8408	21101	34237	0.5	1.0E+00	Q9Y5T5	SWISSPROT	UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 16 (UBIQUITIN THIOLESTERASE 16) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 16) (DEUBIQUITINATING ENZYME 16) (UBIQUITIN PROCESSING PROTEASE UBP-M)
8408	21101	34238	0.5	1.0E+00	Q9Y5T5	SWISSPROT	UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 16 (UBIQUITIN THIOLESTERASE 16) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 16) (DEUBIQUITINATING ENZYME 16) (UBIQUITIN PROCESSING PROTEASE UBP-M)
8436	25122		2.34	1.0E+00	BE147331.1	EST_HUMAN	RC1-HT0229-181099-011-e06 HT0229 Homo sapiens cDNA
8476	21168	34312	0.88	1.0E+00	U42720.2	NT	Simian immunodeficiency virus Gag protein (gag) gene, complete cds; Pol protein (pol) gene, partial cds; and Vif protein (vif), Vpr protein (vpr), Tat protein (tat), Rev protein (rev), Vpu protein (vpu), Env protein (env), and Nef protein (nef) genes, >
8625	21317	34459	1.27	1.0E+00	M38427.1	NT	Human immunodeficiency virus type 1 (HIV-1), isolate SF33,
9171	21841	35008	2.43	1.0E+00	BE907592.1	EST_HUMAN	601497581F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3898421 5'
9381	22043	35215	1.69	1.0E+00	6753429	NT	Mus musculus chloride channel activated 1 (Clca1), mRNA
9381	22043	35216	1.69	1.0E+00	6753429	NT	Mus musculus chloride channel activated 1 (Clca1), mRNA
9510	22163	35345	1.83	1.0E+00	AV689554.1	EST_HUMAN	AV689554 GKC Homo sapiens cDNA clone GKCCYA11 5'
9518	22169	35351	1.43	1.0E+00	U44952.1	NT	Xenopus laevis zona pellucida C glycoprotein precursor (XZPC) mRNA, complete cds
9516	22169	35352	1.43	1.0E+00	U44952.1	NT	Xenopus laevis zona pellucida C glycoprotein precursor (XZPC) mRNA, complete cds

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9753	22404	35609	0.49	1.0E+00	X15498.1	NT	Human Coronavirus gene for membrane protein
9753	22404	35610	0.49	1.0E+00	X15498.1	NT	Human Coronavirus gene for membrane protein
10012	22660	35875	0.71	1.0E+00	5174582	NT	Homo sapiens MHC binding factor, beta (MHCBBF) mRNA
10012	22660	35876	0.71	1.0E+00	5174582	NT	Homo sapiens MHC binding factor, beta (MHCBBF) mRNA
10104	22752	35966	0.81	1.0E+00	A1077920.1	EST_HUMAN	oy15d07.s1 Soares_senescent_fibroblasts NBHSF Homo sapiens cDNA clone IMAGE:1665901 3'
10225	22873	36085	4.36	1.0E+00	AV758825.1	EST_HUMAN	AV758825 BM Homo sapiens cDNA clone BMFAWC04 5'
10375	23021	36237	16.16	1.0E+00	AA004982.1	EST_HUMAN	zh94a02.r1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:428906 5'
10375	23021	36238	16.16	1.0E+00	AA004982.1	EST_HUMAN	zh94a02.r1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:428906 5'
10407	23053	36270	1.1	1.0E+00	L11910.1	NT	Human retinoblastoma susceptibility gene exons 1-27, complete cds
10893	23573	36823	4.57	1.0E+00	S90825.1	NT	PBR1=proline-rich protein (intron 3) [human, Genomic, 888 nt]
11025	23697	36960	1.49	1.0E+00	AA701494.1	EST_HUMAN	z163b11.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:435453 3' similar to contains Alu repetitive element; contains element MER38 repetitive element;
11522	24122		1.59	1.0E+00	L47613.1	NT	Picea glauca EMB13 mRNA
11744	18008	30629	1.55	1.0E+00	Z97022.1	NT	Hordeum vulgare gene encoding cysteine protease
11838	24422	37763	12.29	1.0E+00	Q60019	SWISSPROT	NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 8 (NADH DEHYDROGENASE 1, CHAIN 8) (NDH-1, CHAIN 8)
11868	24452	37764	1.38	1.0E+00	9626187	NT	Human adenovirus type 5, complete genome
12049	24568		3.01	1.0E+00	P15306	SWISSPROT	THROMBOMODULIN PRECURSOR (FETOMODULIN) (TM)
12370	24772		2.32	1.0E+00	AW976184.1	EST_HUMAN	EST388293 MAGC resequences, MAGN Homo sapiens cDNA
2643	15353	28097	1.19	9.9E-01	AL163302.2	NT	Homo sapiens chromosome 21 segment HS21C102
3591	16345		0.97	9.9E-01	AF174585.1	NT	Apple mosaic virus RNA 2 putative polymerase gene, complete cds
5547	18344	31253	10.09	9.9E-01	P49657	SWISSPROT	SERINE/THREONINE PROTEIN KINASE MINIBRAIN
5779	18570	31498	0.93	9.9E-01	Q09632	SWISSPROT	PROBABLE OXIDOREDUCTASE ZK1290.5 IN CHROMOSOME II
9160	21830		1.37	9.9E-01	U65667.1	NT	Lycopodium esculentum putative Mt1 copy 1 nematode-resistance gene
9455	22005		2.18	9.9E-01	Q28842	SWISSPROT	B2 BRADYKININ RECEPTOR (BK-2 RECEPTOR)
10514	23308	36547	2.37	9.9E-01	AJ005029.1	NT	Danio rerio mRNA for Eph-like receptor tyrosine kinase rtk8
11592	24191	37508	2.3	9.9E-01	Y11972.1	NT	B. aphidicola 16S rDNA (host T. suberi)
11592	24191	37509	2.3	9.9E-01	Y11972.1	NT	B. aphidicola 16S rDNA (host T. suberi)
510	13294	25926	1.14	9.8E-01	P22567	SWISSPROT	AMINO-ACID ACETYLTRANSFERASE (N-ACETYL-GLUTAMATE SYNTHASE) (AGS) (NAGS)
2295	15020		1.21	9.8E-01	AJ003108.1	NT	Callitrix jacchus UBE1 gene derived retroposon on the Y chromosome
2804	15509		1.01	9.8E-01	AF174644.1	NT	Xenopus laevis rac GTPase mRNA, complete cds
3781	18533	29171	0.92	9.8E-01	O67551	SWISSPROT	PROBABLE ENDONUCLEASE IV (ENDONUCLEASE IV)
7099	18788	32852	4.67	9.8E-01	AJ302158.1	NT	Enterobacteriaceae sp. JM983 partial groES gene for GroES-like protein and partial groEL gene for GroEL-like protein, isolate JM983

Single Exon Probes Expressed in Brain

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7099	19788	32853	4.67	9.8E-01	AJ302158.1	NT	Enterobacteriaceae sp. JM983 partial groES gene for GroES-like protein and partial groEL gene for GroEL-like protein, isolate JM983
7545	20215	33316	1.15	9.8E-01	BF034018.1	EST_HUMAN	601456337F1 NIH_MGC_96 Homo sapiens cDNA clone IMAGE:3860049 5'
7545	20215	33317	1.15	9.8E-01	BF034018.1	EST_HUMAN	601456337F1 NIH_MGC_96 Homo sapiens cDNA clone IMAGE:3860049 5'
8619	21311	34453	0.91	9.8E-01	P38652	SWISSPROT	PHOSPHOGLUCOMUTASE (GLUCOSE PHOSPHOMUTASE) (PGM)
10336	22983		1.13	9.8E-01	AA825855.1	EST_HUMAN	6d55404.st NCI_CGAP_GCBT Homo sapiens cDNA clone IMAGE:1371847 3'
10916	23596	36842	2.29	9.8E-01	BE258705.1	EST_HUMAN	601110258F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3350750 5'
10916	23596	36843	2.29	9.8E-01	BE258705.1	EST_HUMAN	601110258F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3350750 5'
11764	24355	37688	1.57	9.8E-01	AI680876.1	EST_HUMAN	b42c10.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2272242 3'
12256	24702		1.56	9.8E-01	U52111.2	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRT), CDM protein (CDM), adrenoleukodystrophy protein >
7058	19749	32812	2.28	9.7E-01	U26716.1	NT	Drosophila melanogaster sodium channel protein (para) gene, exons 9, 10, 11, 12 and optional segments b, c, d and e, partial cds
8401	21094	34230	1.68	9.7E-01	AF149112.1	NT	Triticum aestivum stripe rust resistance protein Yr10 (Yr10) gene, complete cds
8407	21100	34236	1.3	9.7E-01	M90544.1	NT	Salmonella typhimurium adenine-methyltransferase (moe) and restriction endonuclease (res)
11123	23792		3.64	9.7E-01	BF511209.1	EST_HUMAN	U1-H-B14-act-e-07-Q-U1.st NCI_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3085140 3'
4425	17161	29791	1.5	9.6E-01	AW799874.1	EST_HUMAN	PM2-UM0053-240300-005-112 UM0053 Homo sapiens cDNA
5667	18462	31376	3.77	9.6E-01	Z70556.1	NT	Parvovirus B19 DNA, patient C, genome position 2448-2994
5667	18462	31377	3.77	9.6E-01	Z70556.1	NT	Parvovirus B19 DNA, patient C, genome position 2448-2994
6848	19410	32424	0.61	9.6E-01	Z97341.2	NT	Arabidopsis thaliana DNA chloroplast 4, ESSA I FCA contig fragment No. 6
8291	20985		2.33	9.6E-01	X95275.1	NT	P. falciparum complete gene map of plastid-like DNA (IR-A)
8750	21442	34589	0.59	9.6E-01	L81138.1	NT	Rattus norvegicus (strain R21) Rps2r gene, complete cds
11503	24104	37416	3.47	9.6E-01	AV752805.1	EST_HUMAN	AV752605 NPD Homo sapiens cDNA clone NPDBAG06 5'
11503	24104	37417	3.47	9.6E-01	AV752805.1	EST_HUMAN	AV752605 NPD Homo sapiens cDNA clone NPDBAG06 5'
11952	24505		1.92	9.6E-01	11421722	NT	Homo sapiens centrosomal protein 2 (CEP2), mRNA
12558	25301	30710	2.18	9.6E-01	U91423.1	NT	Sphyrna tiburo NADH dehydrogenase subunit 2 (NADH2) gene, mitochondrial gene encoding mitochondrial protein, partial cds
2480	15198	27938	1.05	9.5E-01	7705591	NT	Homo sapiens CGI-125 protein (LOC51003), mRNA
2673	15382	28122	0.97	9.5E-01	Q02934	SWISSPROT	ENDOGLUCANASE I PRECURSOR (EGI) (ENDO-1,4-BETA-GLUCANASE) (CELLULOSE I)
3762	16514	29150	2.04	9.5E-01	BE902340.1	EST_HUMAN	601675639F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3958473 5'
3762	16514	29151	2.04	9.5E-01	BE902340.1	EST_HUMAN	601675639F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3958473 5'
8899	21590	34730	0.89	9.5E-01	AI190182.1	EST_HUMAN	qd57d07.x1 Soares testis NHT Homo sapiens cDNA clone IMAGE:1733581 3'
9003	21693	34843	1.05	9.5E-01	AW861102.1	EST_HUMAN	RC1-CT0295-241199-011-b02 CT0295 Homo sapiens cDNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11209	23872	37159	1.68	9.5E-01	BF218771.1	EST_HUMAN	601885163F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4103630 5'
11429	23196	36427	2.42	9.5E-01	AW293799.1	EST_HUMAN	UI-H-B12-ahp-f03-0-UI.s1 NCL CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2727677 3'
11795	24385	37718	1.55	9.5E-01	T87204.1	EST_HUMAN	ya63d04.s1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:66631 3'
3196	15959		3.33	9.4E-01	AF165990.1	NT	Bartonella claridgeiae RNA polymerase beta subunit (rpoB) gene, partial cds
3212	15975		2.08	9.4E-01	AF080595.1	NT	Plimipheila brachycarpa zinc finger protein (ZFP1) mRNA, complete cds
8764	21456	34606	0.67	9.4E-01	M90724.1	NT	Human Fc-gamma-receptor1A (FCGR2A) gene, exon 4
12202	24670		1.92	9.4E-01	BE781251.1	EST_HUMAN	601466703F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3869929 5'
12557	25219		1.79	9.4E-01	11419857	NT	Homo sapiens epidermal growth factor receptor (avian erythroblastic leukemia viral (v-erb-b) oncogene homolog) (EGFR), mRNA
1726	14488		1.05	9.3E-01	AF242382.1	NT	Homo sapiens phytenoyl-CoA hydroxylase (PHYH) gene, exon 5
2640	15351	28095	1.36	9.3E-01	BE071172.1	EST_HUMAN	RC5-BT0503-271199-011-B01 BT0503 Homo sapiens cDNA
4015	16761	29388	0.88	9.3E-01	M20219.1	NT	Bovine papillomavirus type 2, complete genome
4015	16761	29389	0.88	9.3E-01	M20219.1	NT	Bovine papillomavirus type 2, complete genome
5505	18303	31204	1.56	9.3E-01	AF213884.1	NT	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cds
5592	18388	31298	3.99	9.3E-01	L36189.1	NT	Spodoptera frugiperda methyleneletrahydrofolate dehydrogenase mRNA, complete cds
7966	20661	33785	1.85	9.3E-01	AA847040.1	EST_HUMAN	oe09b03.s1 NCL CGAP_Ov2 Homo sapiens cDNA clone IMAGE:1385357
8713	21405		1.04	9.3E-01	AF061981.1	NT	Xenopus laevis CCH zinc finger protein C3H-2 (C3H-2) mRNA, complete cds
8835	21527	34673	0.95	9.3E-01	AL161534.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 34
12681	24970		3.12	9.3E-01	AF271207.1	NT	Aedes triseriatus putative large subunit ribosomal protein rpl34 mRNA, complete cds
12802	25049		1.48	9.3E-01	U82871.2	NT	Homo sapiens chromosome Xq28 melanoma antigen family A2a (MAGEA2A), melanoma antigen family A12 (MAGEA12), melanoma antigen family A2b (MAGEA2B), melanoma antigen family A3 (MAGEA3), caltractin (CALT), NAD(P)H dehydrogenase-like protein (NSDHL), and LI>
3233	15995	28648	2.93	9.2E-01	BE822702.1	EST_HUMAN	601441338T1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3916184 3'
4822	17553		0.97	9.2E-01	BF128973.1	EST_HUMAN	601817814F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4041363 5'
5831	18426		1.15	9.2E-01	7106410	NT	Mus musculus solute carrier family 30 (zinc transporter), member 4 (Slc30a4), mRNA
5898	18683	31631	7.36	9.2E-01	BF037586.1	EST_HUMAN	601461153F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3964661 5'
6337	19302	32306	0.81	9.2E-01	M64703.1	NT	N. crassa valyl-tRNA synthetase (cyl-20/un-3) gene
9560	22213	35399	0.92	9.2E-01	AL161565.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 65
9648	22300	39496	1.07	9.2E-01	6871677	NT	Mus musculus carbonic anhydrase 4 (Car4), mRNA
10165	22813	36031	3.16	9.2E-01	11430963	NT	Homo sapiens lysosomal apyrase-like protein 1 (LALP1), mRNA
10315	22982	36178	1.9	9.2E-01	BF593251.1	EST_HUMAN	7c58e06.x1 NCL CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3578219 3' similar to SW.NU6M_TRYBB
10543	23239	36473	1.63	9.2E-01	BE563811.1	EST_HUMAN	P04540 NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 5 ;
							601334943F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3688714 5'

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Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11722	24318	37039	1.79	9.2E-01	BF132402.1	EST_HUMAN	601820312F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4052018 5'
1621	14368	27057	1.98	9.1E-01	T96675.1	EST_HUMAN	yes2f01.s1 Soares fetal liver spleen 1NLS Homo sapiens cDNA clone IMAGE:121369 3' similar to contains Alu repetitive element
2120	14851		2.76	9.1E-01	8923058	NT	Homo sapiens hypothetical protein FLJ20048 (FLJ20048), mRNA
3200	15963	28614	1.15	9.1E-01	T26418.1	EST_HUMAN	AB200G8R Infant brain, LLNL array of Dr. M. Soares 1NIB Homo sapiens cDNA clone LLAB200G8 5'
3200	15963	28615	1.15	9.1E-01	T26418.1	EST_HUMAN	AB200G8R Infant brain, LLNL array of Dr. M. Soares 1NIB Homo sapiens cDNA clone LLAB200G8 5'
6075	18854	31821	1.28	9.1E-01	L36033.1	NT	Human pre-B cell stimulating factor homologue (SDF1b) mRNA, complete cds
6413	19181	32180	3.53	9.1E-01	Q61704	SWISSPROT	INTER-ALPHA-TRYPsin INHIBITOR HEAVY CHAIN H3 PRECURSOR (ITI HEAVY CHAIN H3)
7475	20148	33241	17.62	9.1E-01	AA086623.1	EST_HUMAN	0571g08.s1 NCJ CGAP GCB1 Homo sapiens cDNA clone IMAGE:1336882 3'
7637	20302	33410	2.34	9.1E-01	U72995.1	NT	Rattus norvegicus Rab3 GDP/GTP exchange protein mRNA, complete cds
10075	22723	35940	0.45	9.1E-01	P38432	SWISSPROT	P80-COLLIN
12291	25284		27.98	9.1E-01	AF050113.1	NT	Homo sapiens uncoupling protein-3 (UCP3) gene, complete cds
4346	17085	29714	2.08	9.0E-01	AF099810.1	NT	Homo sapiens neurexin III-alpha gene, partial cds
7291	19974	33052	0.72	9.0E-01	L42547.1	NT	Danio rerio LIM class homeodomain protein (lim5) mRNA, complete cds
7321	20004		1.18	9.0E-01	D38621.1	NT	Xenopus laevis gene for aldolase, complete cds
9249	21928	35100	0.49	9.0E-01	AF086781.1	NT	Danio rerio semaphorin Z1a mRNA, complete cds
5610	18408	31318	2.68	8.9E-01	AF026198.1	NT	Fugu rubripes neural cell adhesion molecule L1 homolog (L1-CAM) gene, complete cds; putative protein 1 (PUT1) gene, partial cds; mitosis-specific chromosome segregation protein SMC1 homolog (SMC1) gene, complete cds; and calcium channel alpha-1 subunit
6154	18931		1.38	8.9E-01	X00986.1	NT	Rabbit MHC fragment RLA-DF DNA
8325	21018	34154	0.71	8.9E-01	AF259697.1	NT	Oithona nana cytochrome-c oxidase subunit I (cox) gene, partial cds; mitochondrial gene for mitochondrial product
11787	24377	37707	2.51	8.9E-01	AE003944.1	NT	Xylella fastidiosa, section 90 of 229 of the complete genome
12138	24627		2.86	8.9E-01	AE002196.2	NT	Chlamydia pneumoniae AR39, section 21 of 94 of the complete genome
12762	25343		2.51	8.9E-01	AF150836.1	EST_HUMAN	qb64d08.x1 Soares fetal heart NBH119W Homo sapiens cDNA clone IMAGE:1704879 3'
4505	17240	29873	3.82	8.8E-01	O26350	SWISSPROT	PUTATIVE F420-DEPENDENT NADP REDUCTASE
5289	18094	30755	0.87	8.8E-01	AF310817.1	NT	Pseudorabies virus Ea glycoprotein M gene, complete cds
10131	22779	35992	0.83	8.8E-01	7656978	NT	Homo sapiens cell death-inducing DFFA-like effector B (CIDEb), mRNA
11018	23690	36353	4.96	8.8E-01	Z28337.1	NT	M.aeruginosa (HUB 5-2-4) DNA from plasmid PMA1
11988	25382		1.8	8.7E-01	D90911.1	NT	Synochocystis sp. PCC6803 complete genome, 13/27, 1576593-1719643
452	13238	25877	1.54	8.7E-01	AF106953.2	NT	Homo sapiens SOS1 (SOS1) gene, partial cds
2401	15122	27859	1.07	8.7E-01	5901893	NT	Homo sapiens AT-binding transcription factor 1 (ATBFT1), mRNA

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2877	15644	28286	5.05	8.7E-01	AA595863.1	EST_HUMAN	m05f1.1.s1 NCL CGAP_P14.1 Homo sapiens cDNA clone IMAGE:1076877
4946	17673		3.17	8.7E-01	AF121970.1	NT	Pseudomonas aeruginosa topoisomerase (top), putative transcriptional regulatory protein OhbR (ohbR), ortho-halobenzoate 1,2-dioxygenase beta-ISP protein OhbA (ohbA), OhbC (ohbC), ortho-halobenzoate 1,2-dioxygenase alpha-ISP protein OhbB (ohbB), and put-
5102	17820		0.97	8.7E-01	AJ288085.1	NT	Homo sapiens partial LGALS9 gene for galectin-9, exon 3
7939	20634	33761	0.62	8.7E-01	AW897335.1	EST_HUMAN	RC4-NN0057-120500-013-c07 NN0057 Homo sapiens cDNA
8828	21520	34665	0.69	8.7E-01	AJ239436.1	EST_HUMAN	qh38608.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1848786 3'
8828	21520	34666	0.69	8.7E-01	AJ239458.1	EST_HUMAN	qh38608.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1848786 3'
9638	22280	35483	1.57	8.7E-01	AE004963.1	NT	Pseudomonas aeruginosa PAO1, section 524 of 629 of the complete genome
10202	22850	36065	0.61	8.7E-01	BF570189.1	EST_HUMAN	602185541T1 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:4309906 3'
10202	22850	36066	0.61	8.7E-01	BF570189.1	EST_HUMAN	602185541T1 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:4309906 3'
10735	23422	36665	5.25	8.7E-01	BF363970.1	EST_HUMAN	QV0-NN1021-100800-337-c03 NN1021 Homo sapiens cDNA
11739	24332	37657	5.47	8.7E-01	BF107694.1	EST_HUMAN	601823884R1 NIH_MGC_79 Homo sapiens cDNA clone IMAGE:4043564 3'
11739	24332	37658	5.47	8.7E-01	BF107694.1	EST_HUMAN	601823884R1 NIH_MGC_79 Homo sapiens cDNA clone IMAGE:4043564 3'
462	13247		1.75	8.6E-01	X17012.1	NT	Rat GFII gene for insulin-like growth factor II
838	13608	26279	3.45	8.6E-01	W69089.1	EST_HUMAN	zd44e03.r1 Soares_Fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:343516 5'
2268	14994	27793	0.96	8.6E-01	4503210	NT	Homo sapiens cytochrome P450, subfamily XXVIIA (steroid 27-hydroxylase, cerebrotendinous xanthomatosis), polypeptide 1 (CYP27A1b) mRNA
3608	16361	29003	0.85	8.6E-01	AL161565.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 65
3782	16334	29172	1.55	8.6E-01	U49724.1	NT	Drosophila melanogaster melanin (Dmerlin) mRNA, complete cds
5808	18597	31524	10.86	8.6E-01	X60547.1	NT	Chicken lipoprotein lipase gene
5808	18597	31525	10.86	8.6E-01	X60547.1	NT	Chicken lipoprotein lipase gene
6609	19372	32365	2.06	8.6E-01	AF143732.1	NT	Grus canadensis recombination activating protein 1 (RAG-1) gene, partial cds
6609	19372	32366	2.06	8.6E-01	AF143732.1	NT	Grus canadensis recombination activating protein 1 (RAG-1) gene, partial cds
7427	20104		0.78	8.6E-01	AE000591.1	NT	Helicobacter pylori 26695 section 69 of 134 of the complete genome
7628	20523		1.12	8.6E-01	AP001518.1	NT	Bacillus halodurans genomic DNA, section 12/14
7941	20636	33763	0.55	8.6E-01	AF077837.1	NT	Drosophila melanogaster collapsin response mediator protein (CRMP) mRNA, complete cds
9585	22238		0.48	8.6E-01	AE000979.1	NT	Archaeoglobus fulgidus section 128 of 172 of the complete genome
12518	26144		1.35	8.6E-01	AL112162.1	NT	Borhyia cinerea strain T4 cDNA library under conditions of nitrogen deprivation
6626	19388	32401	0.95	8.5E-01	AF165214.1	NT	Bacteriophage D3, complete genome
7425	20102	33189	2.51	8.5E-01	BE542612.1	EST_HUMAN	601067107F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3453505 5'
8317	21010	34148	0.78	8.5E-01	P06601	SWISSPROT	SEGMENTATION PROTEIN PAIRED
8402	21095	34231	0.67	8.5E-01	AJ243213.1	NT	Homo sapiens partial 5-HT4 receptor gene, exons 2 to 5

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Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10248	22898	36105	1.17	8.5E-01	AB006798.1	NT	Cyanidium caldarium gene for SigC, complete cds
10248	22898	36106	1.17	8.5E-01	AB006799.1	NT	Cyanidium caldarium gene for SigC, complete cds
12278	25298		2.24	8.5E-01	11418543	NT	Homo sapiens human immunodeficiency virus type 1 enhancer-binding protein 1 (HIVP1), mRNA
4702	17438	30067	0.73	8.4E-01	AF083976.2	NT	Fowl adenovirus 8, complete genome
5406	25068	30910	2.28	8.4E-01	L78726.1	NT	Human fibroblast growth factor receptor 3 (FGFR3) gene, intron 7
5406	25068	30911	2.28	8.4E-01	L78726.1	NT	Human fibroblast growth factor receptor 3 (FGFR3) gene, intron 7
7708	20372	33485	0.63	8.4E-01	AF051142.1	NT	Maestra brassicae pheromone binding protein 2 precursor (PBP2) mRNA, complete cds
9858	22508		2.88	8.4E-01	AJ248287.1	NT	Pyrococcus abyssi complete genome, segment 5/6
724	13498	26151	2.8	8.3E-01	U93437.1	NT	Thermus thermophilus cytochrome c-552 (cycA) and CycB (cycB) genes, complete cds
3091	16866	28497	2.99	8.3E-01	AL161806.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 18
3790	16542	29177	0.79	8.3E-01	AB010879.1	NT	Nicotiana tabacum mRNA for chloroplast ribosomal protein L10, complete cds
3993	16741	29375	3.35	8.3E-01	Y19177.1	NT	Streptomyces antibioticus polyketide biosynthetic gene cluster
5187	17995	30511	2.41	8.3E-01	AL161540.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 40
9588	22221		4.51	8.3E-01	AJ791952.1	EST_HUMAN	nr01f12.y5 NCI CGAP_C08 Homo sapiens cDNA clone IMAGE:1078495 5' similar to contains THR11 THR repetitive element
10010	22658	35872	1.27	8.3E-01	AF098070.1	NT	Drosophila melanogaster Lis1 homolog mRNA, complete cds
10118	22786	35978	3.46	8.3E-01	AF108133.1	NT	Mus musculus neuro-d4 gene, exons 3 through 12 and partial cds
10572	23267	36505	3.35	8.3E-01	AE000903.1	NT	Methanobacterium thermoautotrophicum from bases 1270510 to 1283409 (section 109 of 148) of the complete genome
10560	23284		2.03	8.3E-01	7212472	NT	Phytophthora infestans mitochondrion, complete genome
11274	23935	37227	2	8.3E-01	AF020503.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHIT) gene, exon 5
2045	14778	27506	2.3	8.2E-01	AB000489.1	NT	Rattus norvegicus mRNA for RPHO-1, complete cds
2083	14815		1.31	8.2E-01	AF145589.1	NT	Mus musculus trophinin (Tnn) gene, complete cds
2686	15395		1.08	8.2E-01	AW376990.1	EST_HUMAN	IL3-C10219-161199-031-C08 C10219 Homo sapiens cDNA
6876	19593	32631	0.75	8.2E-01	AJ010142.1	NT	Amanita muscaria mRNA for SC1125 protein
6797	19541	32569	3.49	8.2E-01	AW378433.1	EST_HUMAN	GM4-HT0243-081199-037-e01 HT0243 Homo sapiens cDNA
7169	25106	32926	4.74	8.2E-01	Z12126.1	NT	S.cerevisiae MET1, LEU4, and POL1 genes encoding MET14 protein, alpha-isopropylmalate (alpha-IPM) synthetase (partial), and DNA polymerase alpha (partial)
8343	21036	34173	0.59	8.2E-01	BE283145.1	EST_HUMAN	601144885F2 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3160412 5'
9924	22572	35770	0.65	8.2E-01	AB014530.1	NT	Homo sapiens thiodoxin-related protein mRNA, complete cds
8959	22607	35812	1.37	8.2E-01	AF052659.1	NT	Homo sapiens thiodoxin-related protein mRNA, complete cds
10123	22771	35985	0.59	8.2E-01	AF223888.1	NT	Oncorhynchus tshawytscha isolate T-20 somatolactin precursor gene, exon 1
10123	22771	35988	0.59	8.2E-01	AF223888.1	NT	Oncorhynchus tshawytscha isolate T-20 somatolactin precursor gene, exon 1

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10283	22831	36145	3.65	8.2E-01	Q9J170	SWISSPROT	MCKUSICK-KAUFMAN/BARDET-BIEDL SYNDROMES PUTATIVE CHAPERONIN
10283	22831	36146	3.65	8.2E-01	Q9J170	SWISSPROT	MCKUSICK-KAUFMAN/BARDET-BIEDL SYNDROMES PUTATIVE CHAPERONIN
11641	24238	37562	4.65	8.2E-01	L10127.1	NT	Molluscum contagiosum virus type 1 ORF1 and ORF2 DNA
11735	24328	37652	6.38	8.2E-01	P10383	SWISSPROT	OVARIAN TUMOR LOCUS PROTEIN
11740	24333	37659	6.02	8.2E-01	H87398.1	EST_HUMAN	yw14d02.1 Soares placent 866weeks 2NbHP809W Homo sapiens cDNA clone IMAGE:252195 5'
12288	24723	31054	2.37	8.2E-01	AJ001261.1	NT	similar to gb:M36072 60S RIBOSOMAL PROTEIN L7A (HUMAN);
2762	15467		1.08	8.1E-01	AF191839.1	NT	Mus musculus TANK binding kinase TBK1 (Tbk1) mRNA, complete cds
3451	16207	28857	3.08	8.1E-01	AF055066.1	NT	Mus musculus MHC class 1 region
3451	16207	28858	3.08	8.1E-01	AF055066.1	NT	Homo sapiens MHC class 1 region
4863	17592		0.74	8.1E-01	AF202634.1	NT	Homo sapiens MHC class 1 region
6223	18997	31973	0.84	8.1E-01	U16790.1	NT	Drosophila melanogaster NalK-A TPase beta subunit isoform 4 (Jybelaz) mRNA, complete cds
6526	19282	32295	2.66	8.1E-01	Q13491	SWISSPROT	Mus musculus putative collagen alpha-2(XI) chain (COL11A2) gene, partial cds
6526	19292	32296	2.66	8.1E-01	Q13491	SWISSPROT	NEURONAL MEMBRANE GLYCOPROTEIN M8-B
7229	19914	32987	0.78	8.1E-01	AB007877.1	NT	NEURONAL MEMBRANE GLYCOPROTEIN M8-B
7412	20089	33173	0.65	8.1E-01	O47477	SWISSPROT	Homo sapiens KIA0417 mRNA, complete cds
							CYTCHROME B
7811	20506	33628	0.75	8.1E-01	AF022713.2	NT	Drosophila melanogaster putative inorganic phosphate cotransporter (Picot) gene, partial cds; putative sodium channel (Nach) and putative amylase-related protein (Amyrel) genes, complete cds; and putative serine-enriched protein (gprs) gene, partial cds
7811	20506	33629	0.75	8.1E-01	AF022713.2	NT	Drosophila melanogaster putative inorganic phosphate cotransporter (Picot) gene, partial cds; putative sodium channel (Nach) and putative amylase-related protein (Amyrel) genes, complete cds; and putative serine-enriched protein (gprs) gene, partial cds
8507	21199	34344	0.93	8.1E-01	AP001517.1	NT	Bacillus halodurans genomic DNA, section 11/14
8507	21199	34345	0.93	8.1E-01	AP001517.1	NT	Bacillus halodurans genomic DNA, section 11/14
8688	21360	34507	1.08	8.1E-01	AW242647.1	EST_HUMAN	xn01h03.x1 NCI CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2692489 3' similar to SW:LYAR_MOUSE Q08288 CELL GROWTH REGULATING NUCLEOLAR PROTEIN ; contains MER22.b1 PTR5.repetitive element;
10025	22673	35888	0.7	8.1E-01	P06425	SWISSPROT	PROBABILE E4 PROTEIN
10311	22958	36174	0.5	8.1E-01	NB4541.1	EST_HUMAN	KK9872F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone KK9872 5' similar to
11484	24067	37374	2.63	8.1E-01	BE938558.1	EST_HUMAN	EST(CLONE C-0PE11)
11484	24067	37375	2.63	8.1E-01	BE938558.1	EST_HUMAN	RCO-TN0080-220800-025-d10 TN0080 Homo sapiens cDNA
12022	24550	31110	1.57	8.1E-01	AE001711.1	NT	RCO-TN0080-220800-025-d10 TN0080 Homo sapiens cDNA
172	12985		3.49	8.0E-01	AJ271510.1	NT	Thermoplasma maritima section 23 of 136 of the complete genome
							Staphylococcus aureus partial pla gene for phosphate acetyltransferase allele 15

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
282	13089	25730	13.81	8.0E-01	AJ132772.1	NT	Bos taurus tub and rif genes
1595	14341	27031	1.12	8.0E-01	8394087	NT	Rattus norvegicus protease (prosome, macropain) 28 subunit, alpha (Psmc1), mRNA
2029	14784		1.91	8.0E-01	BF530962.1	EST_HUMAN	602072473F1 NCI_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4215091 5'
3075	15841	28484	1.2	8.0E-01	AF127897.1	NT	Saimiri boliviensis olfactory receptor (SBO27) gene, partial cds
3307	16087	28716	1.35	8.0E-01	AB008193.1	NT	Mus musculus gene for olfactory receptor (SBO27) gene, partial cds
3690	16443		1.52	8.0E-01	AL162758.2	NT	Neisseria meningitidis serogroup A strain Z2491 complete genome, segment 7/7
4496	17232	28862	6.05	8.0E-01	X83739.2	NT	G.gallus mRNA for nicotinic acetylcholine receptor (nAChR) beta 3 subunit
7899	20584		2.25	8.0E-01	AW901489.1	EST_HUMAN	RCO-NN1012-270300-021-h06 NN1012 Homo sapiens cDNA
8423	21116	34254	0.98	8.0E-01	Y11095.1	NT	Rice stripe virus RNA 3
10876	23556	36803	2.78	8.0E-01	Q92793	SWISSPROT	CREB-BINDING PROTEIN
441	13227	25870	1.16	7.9E-01	D11476.1	NT	Lyttorina dispar nuclear polyhedrosis virus gene for DNA polymerase, complete cds
698	13473		1.14	7.9E-01	AE002130.1	NT	Ureaplasma urealyticum section 31 of 59 of the complete genome
1600	14348		22.89	7.9E-01	AB040885.1	NT	Homo sapiens mRNA for KIAA1452 protein, partial cds
1652	14398		1.2	7.9E-01	U32739.1	NT	Haemophilus influenzae Rd section 54 of 163 of the complete genome
2259	14888	27726	5.86	7.9E-01	AB004816.1	NT	Oryctolagus cuniculus mRNA for mitsugumin29, complete cds
2260	14987	27727	2.4	7.9E-01	AF130459.1	NT	Danio rerio Trp4-associated protein Tap1A (tap1A) mRNA, complete cds
3508	16282	28916	3.01	7.9E-01	AF228664.1	NT	Gallus gallus SOX8 transcription factor (SOX8) mRNA, complete cds
4288	17008		0.85	7.9E-01	BE263612.1	EST_HUMAN	601192033F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3635785 5'
4572	17307	29935	1.13	7.9E-01	6753745	NT	Mus musculus embigin (Emb), mRNA
4572	17307	29938	1.13	7.9E-01	6753745	NT	Mus musculus embigin (Emb), mRNA
6252	19026	32000	0.67	7.9E-01	D38145.1	NT	Human mRNA for prostacyclin synthase, complete cds
8008	20703	33631	2.79	7.9E-01	X90996.1	NT	P. salivum GR gene
9447	22124	35304	4.04	7.9E-01	U01912.1	NT	Giardia lamblia variant-specific surface protein G3M-B (vspG3M-B) mRNA, partial cds
9949	22597	35801	4.47	7.9E-01	P19719	SWISSPROT	SMALL HYDROPHOBIC PROTEIN
9991	22639	35849	0.91	7.9E-01	AV700860.1	EST_HUMAN	AV700860 GKC Homo sapiens cDNA clone GKCDRE12 3'
10408	23054	36271	1.94	7.9E-01	AB000631.1	NT	Streptococcus mutans DNA for sigma 42 protein, dTDP-4-keto-L-rhamnose reductase, complete cds
10516	23162	36389	0.52	7.9E-01	P15305	SWISSPROT	DYNEIN HEAVY CHAIN (DYHC)
10929	23609		2.74	7.9E-01	7662471	NT	Homo sapiens KIAA1072 protein (KIAA1072), mRNA
11173	23840	37123	2.02	7.9E-01	P19022	SWISSPROT	NEURAL-CADHERIN PRECURSOR (N-CADHERIN)
896	13625		2.24	7.8E-01	Z43785.1	EST_HUMAN	HSC-KH041 normalized infant brain cDNA Homo sapiens cDNA clone c-1kh04
2273	14999	27737	7.47	7.8E-01	AW959567.1	EST_HUMAN	EST371637 MAGC resequences, MAGC Homo sapiens cDNA
4653	17387	30020	0.73	7.8E-01	U87305.1	NT	Rattus norvegicus transmembrane receptor Unc5H1 mRNA, complete cds
5978	18760	31724	2.28	7.8E-01	AF115896.1	NT	Sphenodon punctatus alpha enolase mRNA, partial cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6124	18902	31871		7.8E-01	P05231	SWISSPROT	INTERLEUKIN-6 PRECURSOR (IL-6) (B-CELL STIMULATORY FACTOR 2) (BSF-2) (INTERFERON BETA-2) (HYBRIDOMA GROWTH FACTOR)
6371	19140	32138	0.88	7.8E-01	AL445066.1	NT	Thermoplasma acidophilum complete genome; segment 4/5
8389	21082	34216	1.02	7.8E-01	BF108927.1	EST_HUMAN	7154405 x1 Soares NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3525178 3'
9133	21821	34987	1.3	7.8E-01	Y10159.1	NT	D discoideum racGAP gene
9231	21910	35083	0.51	7.8E-01	4826873	NT	Homo sapiens nucleoporin 214kD (CAN) (NUP214), mRNA
10024	22872		0.97	7.8E-01	Q25452	SWISSPROT	MUSCLE CALCIUM CHANNEL ALPHA-1 SUBUNIT (MDL-ALPHA1)
12271	25275		2.5	7.8E-01	L29280.1	NT	Arabidopsis thaliana 1-amino-1-cyclopropanecarboxylate synthase (ACS5) gene, complete cds
139	12954	25596	7.61	7.7E-01	AF184345.1	NT	Lyopersicon hirsutum ADP-glucose pyrophosphorylase large subunit (AGP-L1) mRNA, complete cds
709	13483						Mus musculus major histocompatibility locus class II region: major histocompatibility protein class II alpha chain (Iaalpha) and major histocompatibility protein class II beta chain (Ib beta) genes, complete cds;
2717	15424	28163	2.26	7.7E-01	AF050157.1	NT	butyrophilin-like (NG9), butyrophilin-lp>
			2.21	7.7E-01	O33915	SWISSPROT	CITRATE SYNTHASE
3351	16111		0.84	7.7E-01	8383408	NT	Homo sapiens UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 7 (GalNAc-T7) (GALNAC-T7), mRNA
3586	16340	28085	3.98	7.7E-01	AF118085.1	NT	Homo sapiens PRO1975 mRNA, complete cds
4365	17103	29738	3.38	7.7E-01	AF199488.1	NT	Coturnix coturnix japonica sub-species japonica beta-actin mRNA, partial cds
4365	17103	29739	3.38	7.7E-01	AF199488.1	NT	Coturnix coturnix japonica sub-species japonica beta-actin mRNA, partial cds
5473	18272	31165	1.45	7.7E-01	P16553	SWISSPROT	RAFFINOSE INVERTASE (INVERTASE)
5473	18272	31168	1.45	7.7E-01	P16553	SWISSPROT	RAFFINOSE INVERTASE (INVERTASE)
5866	18663	31594	0.85	7.7E-01	R08600.1	EST_HUMAN	Y24802.81 Soares fetal liver spleen 1NLS Homo sapiens cDNA clone IMAGE:127755 3'
9744	22395	35600	0.51	7.7E-01	AB021134.1	NT	Daphnia magna hemoglobin gene cluster (dhb3, dhb1 and dhb2 genes), complete cds
12161	24644		4.55	7.7E-01	11497621	NT	Archaeoglobus fulgidus, complete genome
6008	18789	31751	4.88	7.6E-01	AF059510.1	NT	Arabidopsis thaliana 3-methylcrotonyl-CoA carboxylase non-biotinylated subunit (MCCB) mRNA, complete cds
6008	18789	31752	4.88	7.6E-01	AF059510.1	NT	Arabidopsis thaliana 3-methylcrotonyl-CoA carboxylase non-biotinylated subunit (MCCB) mRNA, complete cds
6425	19193	32189	0.81	7.6E-01	P37938	SWISSPROT	MATING-TYPE PROTEIN A-ALPHA 24
6751	17920	30555	0.94	7.6E-01	AI253399.1	EST_HUMAN	ac14b12.x1 Stanley Frontal NS pool 2 Homo sapiens cDNA clone IMAGE:2030879
6751	17920	30585	0.94	7.6E-01	AI253399.1	EST_HUMAN	ac14b12.x1 Stanley Frontal NS pool 2 Homo sapiens cDNA clone IMAGE:2030879
8951	19433	32449	0.88	7.6E-01	U72487.1	NT	Rattus norvegicus calcium-independent alpha-latrotoxin receptor mRNA, complete cds

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7964	20659	33784	1.38	7.6E-01	AF146793.2	NT	Mus musculus neuromedin U precursor (Nmu) gene, partial cds; iPhLP (Tphlp) gene, partial cds; CLOCK (Clock) gene, complete cds; PFT27 (Pft27) gene, complete cds; and H5AR (H5ar) gene, complete cds
8026	20721	33852	1.88	7.6E-01	6857752	NT	Mus musculus adyillin (Adyil-pending). mRNA
8026	20721	33853	1.88	7.6E-01	6857752	NT	Mus musculus adyillin (Adyil-pending). mRNA
8866	21557	34703	0.74	7.6E-01	6783577	NT	Mus musculus cytochrome P450, 2b9, phenobarbital inducible, type a (Cyp2b9), mRNA
9179	21849	35015	5.03	7.6E-01	P30372	SWISSPROT	MUSGARINIC ACETYLCHOLINE RECEPTOR M2
9179	21849	35016	5.03	7.6E-01	P30372	SWISSPROT	MUSGARINIC ACETYLCHOLINE RECEPTOR M2
11330	24021	37325	2.68	7.6E-01	X86347.1	NT	H. aspersa mRNA for neurofilament NIF70
11330	24021	37326	2.68	7.6E-01	X86347.1	NT	H. aspersa mRNA for neurofilament NIF70
11711	24306		3.64	7.6E-01	AL161592.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 88
11831	24489		3.73	7.6E-01	AB020702.1	NT	Homo sapiens mRNA for KIAA0895 protein, partial cds
500	13284		1.44	7.5E-01	AL163301.2	NT	Homo sapiens chromosome 21 segment HS21C101
570	13351	25979	1.23	7.5E-01	AF020503.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHIT) gene, exon 5
3354	16114	28769	0.95	7.5E-01	C14203.1	EST_HUMAN	C14203 Clontech human aorta polyA+ mRNA (#6572) Homo sapiens cDNA clone GEN-037E11 5'
7421	20098	33186	1.01	7.5E-01	AF052730.1	NT	Drosophila melanogaster tyrosine kinase receptor protein (eph) mRNA, complete cds
11177	23844	37130	1.5	7.5E-01	AB047819.1	NT	Homo sapiens GCN5/GCN1 gene for chorion-specific transcription factor GCN5, complete cds
12228	24682		4.8	7.5E-01	AF163151.2	NT	Homo sapiens dentin sialophosphoprotein precursor (DSPP) gene, complete cds
12742	25008	30975	1.46	7.5E-01	AE000823.1	NT	Methanobacterium thermoautotrophicum from bases 317350 to 328792 (section 29 of 148) of the complete genome
1108	13865	28522	1.78	7.4E-01	AI598146.1	EST_HUMAN	in14p09.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2167577 3' similar to contains Alu repetitive element; contains element MIR repetitive element
2342	15065	27802	0.96	7.4E-01	AB011106.1	NT	Homo sapiens mRNA for KIAA0534 protein, partial cds
4276	17015	29842	4.73	7.4E-01	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
7743	20439	33562	1.23	7.4E-01	AL161551.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 51
7743	20439	33563	1.23	7.4E-01	AL161551.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 51
8531	21223	34365	0.83	7.4E-01	BF346286.1	EST_HUMAN	602018456F1 NCI_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4154340 5'
8613	21305		0.76	7.4E-01	U87960.1	NT	Rattus norvegicus leukocyte common antigen receptor (LAR) gene, trans-spliced alternative untranslated exon
8994	21684	34634	6.95	7.4E-01	BE747503.1	EST_HUMAN	601573026F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3834174 5'
9054	21743	34901	1.14	7.4E-01	AA187986.1	EST_HUMAN	zp67h01.s1 Stragene endothelial cell 937223 Homo sapiens cDNA clone IMAGE:625287 3' similar to SW:TCPO_MOUSE P42932 T-COMPLEX PROTEIN 1, THETA SUBUNIT;
10302	22849	36164	0.76	7.4E-01	11424933	NT	Homo sapiens NY-REN-45 antigen (LOC51133), mRNA

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11665	24260	37582	1.65	7.4E-01	AB021490.2	NT	Oryzias latipes gene for membrane guanylyl cyclase OIGC1, complete cds
11665	24260	37583	1.65	7.4E-01	AB021490.2	NT	Oryzias latipes gene for membrane guanylyl cyclase OIGC1, complete cds
11800	24467		3.62	7.4E-01	6763217	NT	Mus musculus complement component 1 inhibitor (C1nh), mRNA
12008	24542		1.78	7.4E-01	AI472841.1	EST_HUMAN	ta13h01.x1 NCI_CGAP_Lym5 Homo sapiens cDNA clone IMAGE:2049885 3'
2698	15765	28413	0.8	7.3E-01	P09710	SWISSPROT	HYPOTHETICAL PROTEIN HKLF1 (RL1) (TRL1)
4575	17310	29838	0.7	7.3E-01	AE001166.1	NT	Borrelia burgdorferi (section 52 of 70) of the complete genome
4652	17386	30019	4.37	7.3E-01	AF225421.1	NT	Homo sapiens HT017 mRNA, complete cds
5040	17759	30373	1.01	7.3E-01	O43103	SWISSPROT	FERRICHRONE SIDEROPHORE PEPTIDE SYNTHETASE
6511	19278	32276	5.92	7.3E-01	L35772.1	NT	Mus musculus antigen (CD72) gene
6511	19278	32277	5.92	7.3E-01	L35772.1	NT	Mus musculus antigen (CD72) gene
6994	25103	32735	0.87	7.3E-01	AJ011418.1	NT	Lycopodium obscurum mRNA for ubiquitin activating enzyme
7359	20040	33118	0.66	7.3E-01	Z14133.1	NT	D.melanogaster Chc mRNA for clathrin heavy chain
7445	20121	33210	7.84	7.3E-01	M26511.1	NT	V.alginolyticus sucrose (scrB) gene, complete cds
7445	20121	33211	7.84	7.3E-01	M26511.1	NT	V.alginolyticus sucrose (scrB) gene, complete cds
11407	24056	37361	3.83	7.3E-01	AA878019.1	EST_HUMAN	z25b08.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:431799 3'
11407	24056	37362	3.83	7.3E-01	AA878019.1	EST_HUMAN	z25b08.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:431799 3'
812	13583		3.89	7.2E-01	L29281.1	NT	Rattus norvegicus initiation factor-2 kinase (eIF-2a) mRNA, complete cds
1950	14685	27398	2.32	7.2E-01	X79140.1	NT	N.tabacum NeIF-4A13 mRNA
2463	15181	27920	1.27	7.2E-01	AB009605.1	NT	Gallus gallus gene for melanocortin 2-receptor, complete cds
3063	15829	28473	1.38	7.2E-01	AF198100.1	NT	Fowlpox virus, complete genome
3445	16201	28851					
3601	16364	28894	2.56	7.2E-01	AF065608.1	NT	Giardia intestinalis variant-specific surface protein (vsp417-6) gene, vsp417-6(A-1 allele, complete cds
4040	16785		1.06	7.2E-01	AB002307.1	NT	Human mRNA for KIAA0309 gene, partial cds
4718	17450	30083	0.7	7.2E-01	AF108093.1	NT	Homo sapiens IA-2 gene, intron 18
5075	17794	30410	2.65	7.2E-01	D90314.1	NT	L.mesenteroides gene for sucrose phosphorylase (EC 2.4.1.7)
7112	19800	32864	0.74	7.2E-01	P33066	SWISSPROT	NUCLEOSIDE TRIPHOSPHATASE I (NUCLEOSIDE TRIPHOSPHATE PHOSPHOHYDROLASE I) (NPH I)
8353	21046	34183	0.88	7.2E-01	U69633.1	NT	Solanum tuberosum cold-stress inducible protein (C17) gene, complete cds
8862	21553		1.11	7.2E-01	AF236061.1	NT	Oryctolagus cuniculus RING-finger binding protein mRNA, partial cds
10239	22887	36100	0.46	7.2E-01	AV743773.1	EST_HUMAN	AV743773 CB Homo sapiens cDNA clone CBMAFD06 5'
10639	23330	36568	2.33	7.2E-01	BF670061.1	EST_HUMAN	802118381F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4275381 5'
11104	23774	37049	4.02	7.2E-01	U62623.1	NT	Rattus norvegicus cytochrome mRNA, complete cds
							Dbs=Dbt guanine nucleotide exchange factor homolog [mice, 32D murine hemopoietic cell line, mRNA, 3923 nt]

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12422	24798		2.9	7.2E-01	AP000063.1	NT	Aeropyrum pernix genomic DNA, section 6/7
676	13451	26094	12.73	7.1E-01	D21070.1	NT	Rana catesbeiana mRNA for bullfrog skeletal muscle calcium release channel (ryanodine receptor) alpha
3059	15825	28470	11.76	7.1E-01	AJ270777.1	NT	Isoform (RyR1), complete cds
4184	16925	29555	3.18	7.1E-01	7305360	NT	Homo sapiens partial TCF-4 gene for T-cell transcription factor-4, exons 15-16
4184	16925	29556	3.18	7.1E-01	7305360	NT	Mus musculus ctgogelin (Otog), mRNA
5858	18845	31585	1.63	7.1E-01	BF681034.1	EST_HUMAN	Mus musculus ctgogelin (Otog), mRNA
5858	18845	31588	1.63	7.1E-01	BF681034.1	EST_HUMAN	602155438F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4296344 5'
6850	19550	32580	7.68	7.1E-01	U98232.1	NT	602155438F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4296344 5'
8091	20785	33918	0.56	7.1E-01	H64244.1	EST_HUMAN	Drosophila melanogaster 6-pyruvoyl-tetrahydropterin synthase (pr) gene, complete cds
8635	21327	34469	0.93	7.1E-01	BE074185.1	EST_HUMAN	y989d09.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:202861 3'
8635	21327	34470	0.93	7.1E-01	BE074185.1	EST_HUMAN	RC1-BT0567-301299-011-d09 BT0567 Homo sapiens cDNA
9755	22408	35613	1.43	7.1E-01	BE904405.1	EST_HUMAN	RC1-BT0567-301299-011-d09 BT0567 Homo sapiens cDNA
10309	22958	36172	1.22	7.1E-01	M12961.1	NT	601496330F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3898495 5'
12211	25205		2.21	7.1E-01	AA421492.1	EST_HUMAN	Human T-cell receptor gamma-chain J2 gene
1207	13958	26924	0.99	7.0E-01	AB014514.1	NT	zid06h11.s1 Soares testis NHT Homo sapiens cDNA clone IMAGE:731109 3'
1207	13958	26925	0.99	7.0E-01	AB014514.1	NT	Homo sapiens mRNA for KIAA0614 protein, partial cds
							Homo sapiens mRNA for KIAA0614 protein, partial cds
2450	15189	27907	1.13	7.0E-01	N62412.1	EST_HUMAN	z73e07.s1 Soares multiple sclerosis 2NbHMSP Homo sapiens cDNA clone IMAGE:288708 3' similar to contains Alu repetitive element
							z73e07.s1 Soares multiple sclerosis 2NbHMSP Homo sapiens cDNA clone IMAGE:288708 3' similar to contains Alu repetitive element
2450	15189	27908	1.13	7.0E-01	N62412.1	EST_HUMAN	z73e07.s1 Soares multiple sclerosis 2NbHMSP Homo sapiens cDNA clone IMAGE:288708 3' similar to contains Alu repetitive element
4998	17719		1.78	7.0E-01	AL163301.2	NT	Homo sapiens chromosome 21 segment HS21C101
5862	18849		1.11	7.0E-01	AB021316.1	NT	Arabidopsis thaliana mRNA for chlorophyll b synthase, complete cds
8276	20870		11.78	7.0E-01	AE000253.1	NT	Escherichia coli K-12 MG1655 section 143 of 400 of the complete genome
9216	21895	35084	0.57	7.0E-01	U53888.1	NT	Clostridium acetobutylicum mannitol-specific phosphotransferase system (PTS) system, mliA, mliR, mliF, and mliD genes, complete cds
9216	21895	35085	0.57	7.0E-01	U53888.1	NT	Clostridium acetobutylicum mannitol-specific phosphotransferase system (PTS) system, mliA, mliR, mliF, and mliD genes, complete cds
10526	23172	36400	0.49	7.0E-01	U34682.1	NT	Danio rerio complement factor B mRNA, complete cds
11064	23734	37008	1.94	7.0E-01	AV763842.1	EST_HUMAN	AV763842 MDS Homo sapiens cDNA clone MDSCHD4 5'
11064	23734	37007	1.94	7.0E-01	AV763842.1	EST_HUMAN	AV763842 MDS Homo sapiens cDNA clone MDSCHD4 5'
949	13715	26380	11.02	6.9E-01	U68674.1	NT	Candida albicans squalene epoxidase (CAERG1) gene, complete cds and translational regulator gene, partial cds

Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
949	13715	26381	11.02	6.9E-01	U69674.1	NT	Candida albicans squalene epoxidase (CAERG1) gene, complete cds and translational regulator gene, partial cds
1287	14037	26708	2.74	6.9E-01	AA593530.1	EST_HUMAN	h228a09 s1 NCJ_CGAP_Gast1 Homo sapiens cDNA clone IMAGE:1085176 3'
3213	15976	28627	1.97	6.9E-01	AE002271.2	NT	Chlamydia muridarum, section 3 of 85 of the complete genome
5894	18488	31409	0.91	6.9E-01	AB035682.1	NT	Branchiostoma belcheri BNA3 mRNA for notochord actin, complete cds
5900	18885	31633	0.82	6.9E-01	Y18278.1	NT	Drosophila melanogaster mRNA for A-kinase anchor protein DAKAP550, partial
6277	19050	32027	1.36	6.9E-01	BE296188.1	EST_HUMAN	601177333F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3532328 5'
7697	20360	33474	0.85	6.9E-01	AF248863.1	NT	Strongylocentrotus purpuratus myosin V, complete cds
7879	20574	33700	2.96	6.9E-01	AL161573.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 69
7879	20574	33701	2.96	6.9E-01	AL161573.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 69
9069	21768		0.79	6.9E-01	AF118046.1	NT	Entamoeba dispar cation transporting ATPase (atpase) gene, partial cds
9594	22247	35431	0.59	6.9E-01	AF206319.1	NT	Musa acuminata pectate lyase 1 (PL1) mRNA, complete cds
9594	22247	35432	0.59	6.9E-01	AF206319.1	NT	Musa acuminata pectate lyase 1 (PL1) mRNA, complete cds
11223	23886	37172	2.38	6.9E-01	D89013.1	NT	Homo sapiens DAN gene, complete cds
11223	23886	37173	2.38	6.9E-01	D89013.1	NT	Homo sapiens DAN gene, complete cds
11878	25197		3.01	6.9E-01	Q99958	SWISSPROT	FORKHEAD BOX PROTEIN C2 (FORKHEAD-RELATED PROTEIN FKHL14) (MESENCHYME FORK HEAD PROTEIN 1) (MFH-1 PROTEIN) (TRANSCRIPTION FACTOR FKHL14)
937	13704	26369	1.05	6.8E-01	AF017784.1	NT	Giardia intestinalis carbamate kinase gene, complete cds
2680	15389		0.99	6.8E-01	D90917.1	NT	Synechocystis sp. PCC6803 complete genome, 27/27, 3418852-3573470
2832	14356	27045	1.49	6.8E-01	AA854475.1	EST_HUMAN	aj75a05.s1 Soares, parathyroid, tumor N6HPA Homo sapiens cDNA clone IMAGE:1402258 3' similar to
4533	17268	29901	1.45	6.8E-01	J00762.1	NT	gbX56411_maf1 ALCOHOL DEHYDROGENASE CLASS II PI CHAIN (HUMAN);
9538	22191	35375	1.45	6.8E-01	AB037766.1	NT	Rat(hooded) prolactin gene : exon iii and flanks
11027	23699	36962	1.92	6.8E-01	AJ276675.1	NT	Homo sapiens mRNA for KIAA1345 protein, partial cds
11027	23699	36963	1.92	6.8E-01	AJ276675.1	NT	Stagonospora avenae bgl1 gene for beta-glucosidase, exons 1-4
11058	23728	37000	2.4	6.8E-01	AF039393.1	NT	Stagonospora avenae bgl1 gene for beta-glucosidase, exons 1-4
11058	23728	37001	2.4	6.8E-01	AF039393.1	NT	Mus musculus zinc finger protein (Peg3) mRNA, complete cds
				6.8E-01	AF039393.1	NT	Mus musculus zinc finger protein (Peg3) mRNA, complete cds
11607	24205	37527	1.36	6.8E-01	AF110520.1	NT	Mus musculus major histocompatibility complex region NG27, NG28, RPS28, NADH oxidoreductase, NG29, KIFC1, Fas-binding protein, BING1, tapasin, RaGDS-like, KE2, BING4, beta 1,3-galactosyl transferase, and RPS18 genes, complete cds; Sacm21 gene, partial>
11607	24205	37528	1.36	6.8E-01	AF110520.1	NT	Mus musculus major histocompatibility complex region NG27, NG28, RPS28, NADH oxidoreductase, NG29, KIFC1, Fas-binding protein, BING1, tapasin, RaGDS-like, KE2, BING4, beta 1,3-galactosyl transferase, and RPS18 genes, complete cds; Sacm21 gene, partial>

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Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
291	13097	25739	44.11	6.7E-01	AF213884.1	NT	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cds
330	13131	25766	21.34	6.7E-01	AF213884.1	NT	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cds
2143	14873	27606	1.73	6.7E-01	AA451884.1	EST_HUMAN	zx12g12.s1 Soares_tetns_Nb2HF8_5w Homo sapiens cDNA clone IMAGE:786310 3' similar to contains element TAR1 repetitive element
2163	15587	27628	2.51	6.7E-01	AF186073.1	NT	Drosophila melanogaster Mst85C gene, complete cds; NMDMC isoform (Nmdnc) gene, complete cds, alternatively spliced; and transcription factor (Relish) gene, complete cds, alternatively spliced
2994	15760	28408	3.41	6.7E-01	6678590	NT	Mus musculus Wiskott-Aldrich syndrome protein (Wasp), mRNA
4419	17155	29786	0.79	6.7E-01	X74421.1	NT	S. tuberosum mRNA for glucose-6-phosphate dehydrogenase
5422	18221	30932	0.94	6.7E-01	J04836.1	NT	M. barkeri ATPase alpha and beta subunit (atpA and atpB) genes, complete cds
5422	18221	30933	0.94	6.7E-01	J04836.1	NT	M. barkeri ATPase alpha and beta subunit (atpA and atpB) genes, complete cds
6231	19005	31981	1.18	6.7E-01	9635035	NT	Gallid herpesvirus 2, complete genome
6231	19005	31982	1.18	6.7E-01	9635035	NT	Gallid herpesvirus 2, complete genome
7215	19900		4.34	6.7E-01	AE004606.1	NT	Pseudomonas aeruginosa PA01, section 167 of 529 of the complete genome
7240	19925	33000	0.92	6.7E-01	AE001486.1	NT	Helicobacter pylori, strain J99 section 47 of 132 of the complete genome
10044	22692		0.68	6.7E-01	M34046.1	NT	Human placental protein 14 (PP14) gene, complete cds
10873	23553	38800	2.07	6.7E-01	BF354649.1	EST_HUMAN	CM3-HT0769-010600-197-c03 HT0769 Homo sapiens cDNA
11436	23203	36435	3.59	6.7E-01	O14357	SWISSPROT	N-ACETYLGLUCOSAMINYL-PHOSPHATIDYL-INOSITOL BIOSYNTHETIC PROTEIN GPI1
11659	24255	37578	1.66	6.7E-01	AA342521.1	EST_HUMAN	EST48065 Fetal spleen Homo sapiens cDNA 3' end
2505	15222	27964	1.29	6.6E-01	AF075240.1	NT	Homo sapiens SLIT1 protein (SLIT2) mRNA, partial cds
2704	15411	28148	1.44	6.6E-01	AF198339.1	NT	Homo sapiens lens epithelium-derived growth factor gene, alternatively spliced, complete cds
3650	16403	29043	4.57	6.6E-01	Y07689.1	NT	C. albicans random DNA marker, 282bp
4089	16832						
5125	17843	30461	0.85	6.6E-01	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
6240	19014	31988	1.13	6.6E-01	AL161572.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 68
7585	20253	33359	4.29	6.6E-01	6680577	NT	Mus musculus kinesin light chain 2 (Klc2), mRNA
8464	21156	34299	3.76	6.6E-01	AV660506.1	EST_HUMAN	AV660506 GLC Homo sapiens cDNA clone GLCGLD04 3'
9564	22217		0.52	6.6E-01	AV704700.1	EST_HUMAN	AV704700 ADB Homo sapiens cDNA clone ADBCAF11 5'
12470	24836	31033	2	6.6E-01	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
610	13388	26019	1.48	6.6E-01	AE004382.1	NT	Vibrio cholerae chromosome II, section 39 of 93 of the complete chromosome
			18.23	6.5E-01	M75140.1	NT	H. vulgaris Na,K-ATPase alpha subunit mRNA, complete cds

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
610	13388	26020	18.23	6.5E-01	M75140.1	NT	H. vulgaris Na,K-ATPase alpha subunit mRNA, complete cds
3426	16183	28833	4.25	6.5E-01	AB041225.1	NT	Mus musculus gene for Tob2, complete cds
4249	16990	29615	4.23	6.5E-01	AJ272265.1	NT	Homo sapiens SPP2 gene for secreted phosphoprotein 24 precursor, exons 1-8
4277	17016	29643	0.78	6.5E-01	AL161539.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 39
5003	17726	30329	2.6	6.5E-01	U28921.1	NT	Phaseolus vulgaris ATPase gamma subunit mRNA, nuclear gene encoding mitochondrial protein, partial cds
5357	25067	30843	1.77	6.5E-01	P19480	SWISSPROT	TRANSCRIPTION REGULATORY PROTEIN SNF5 (SWISNF COMPLEX COMPONENT SNF5)
5627	18424	31337	0.62	6.5E-01	AL163249.2	NT	Homo sapiens chromosome 21 segment HS21C049
5625	19387	32400	1.5	6.5E-01	D88348.1	NT	Chicken mRNA for 115-kDa melanosomal matrix protein, complete cds
7566	20236	33340	0.84	6.5E-01	A1799882.1	EST_HUMAN	wc46a02.x1 NCI_CGAP_P128 Homo sapiens cDNA clone IMAGE:2321642 3'
9737	22398		0.8	6.5E-01	T78904.1	EST_HUMAN	yc21b04.s1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:108847 3'
10233	22881	36094	1.96	6.5E-01	AF119676.1	NT	Mus musculus small GTP-binding protein RAB25 (Rab25) gene, complete cds
10529	23228	36460	2.68	6.5E-01	H87583.1	EST_HUMAN	hw1706.r1 Soares placenta_8to9weeks_2NbhP806W Homo sapiens cDNA clone IMAGE:252515 5'
10585	23280	36518	3.5	6.5E-01	AA601287.1	EST_HUMAN	no15c07.s1 NCI_CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1100748 3'
10690	23381		3.93	6.5E-01	AU138078.1	EST_HUMAN	AU138078 PLACE1 Homo sapiens cDNA clone PLACE1007810 5'
11599	24198	37518	2.42	6.5E-01	AF014115.1	NT	Plasmodium berghei cytochrome c oxidase subunit III, cytochrome c oxidase subunit I, and cytochrome b genes, mitochondrial genes encoding mitochondrial proteins, complete cds
12267	24710		2.07	6.5E-01	BE465050.1	EST_HUMAN	hw74a10.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3179130 3'
12504	25146		1.81	6.5E-01	Z74145.1	NT	S. cerevisiae chromosome IV reading frame ORF YDL097c
245	13054	25694	8.05	6.4E-01	U48948.1	NT	Drosophila melanogaster 8kd dynein light chain mRNA, complete cds
2593	15307	28043	1.16	6.4E-01	AF161184.1	NT	Pseudomonas fluorescens tryptophan halogenase (pna) gene, complete cds
3449	16205	28855	2.16	6.4E-01	U48854.2	NT	Mus musculus dystroglycan 1 (DAG1) gene, exons 1 and 2 and complete cds
3842	16593	29230	1.06	6.4E-01	AB048827.1	NT	Homo sapiens mRNA for KIAA1607 protein, partial cds
8510	21202	34347	1.82	6.4E-01	A5001247.1	NT	Treponema pallidum section 83 of 87 of the complete genome
9989	22637	35848	8.8	6.4E-01	U92828.1	NT	Homo sapiens ataxia telangiectasia (ATM) gene, complete cds
10004	22652	35864	1.22	6.4E-01	BF670405.1	EST_HUMAN	60216028F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4291126 5'
12882	24777		5.99	6.4E-01	AV759212.1	EST_HUMAN	AV759212 MDS Homo sapiens cDNA clone MDSGCG09 5'
425	13211	25658	4.58	6.3E-01	P05228	SWISSPROT	HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PFHRP-III)
522	13308	25938	2.25	6.3E-01	U32689.1	NT	Haemophilus influenzae Rd section 4 of 163 of the complete genome
2159	14889	27623	2.02	6.3E-01	U81136.1	NT	Shigella flexneri multi-antigenic resistance locus
2583	15297	28035	3.51	6.3E-01	U75331.1	NT	Gallus gallus bone morphogenetic protein 1 (BMP1) mRNA, partial cds
2583	15297	28036	3.51	6.3E-01	U75331.1	NT	Gallus gallus bone morphogenetic protein 1 (BMP1) mRNA, partial cds

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Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5873	18755	31716	0.94	6.3E-01	BE093906.1	EST_HUMAN	PMO-BT0757-010500-002-a05 BT0757 Homo sapiens cDNA
6504	19269	32271	0.84	6.3E-01	L27798.1	NT	Streptococcus dysgalactiae (mag) gene, complete cds
6504	19289	32272	0.84	6.3E-01	L27798.1	NT	Streptococcus dysgalactiae (mag) gene, complete cds
8419	21112		3.44	6.3E-01	BE902044.1	EST_HUMAN	601676889F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3959351 5'
8784	21478	34624	0.95	6.3E-01	BE2927.1	NT	glycoprotein IIIa (Alu 1 and 3 fusion junction) [human, Genomic Mutant, 300 nt]
9120	21808	34975	0.8	6.3E-01	BF216984.1	EST_HUMAN	601884050F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4102588 5'
9320	21987	35159	2.45	6.3E-01	9627621	NT	Varidla virus, complete genome
9320	21987	35160	2.45	6.3E-01	9627621	NT	Varidla virus, complete genome
9838	22489		0.67	6.3E-01	AE002329.2	NT	Chlamydia muridarum, section 59 of 85 of the complete genome
10326	22973	36193	1.47	6.3E-01	Z73003.1	NT	S.cerevisiae chromosome VII reading frame ORF YGR218w
10427	23073	36294	1.19	6.3E-01	AE000313.1	NT	Escherichia coli K-12 MG1655 section 203 of 400 of the complete genome
10456	23102		0.45	6.3E-01	AW795395.1	EST_HUMAN	PMO-UM0018-130500-003-g12 UM0018 Homo sapiens cDNA
10993	23667	36924	2.21	6.3E-01	AA877715.1	EST_HUMAN	nr09h06.s1 NCI_CGAP_Co10 Homo sapiens cDNA clone IMAGE:1161371 3' similar to TR:002916 O02916
11308	23967	37288	9.25	6.3E-01	AI904160.1	EST_HUMAN	HLARK. ;
11402	24051	37355	1.66	6.3E-01	P47003	SWISSPROT	CM-BT043-090289-046 BT043 Homo sapiens cDNA
11581	24180	37495	1.84	6.3E-01	P36073	SWISSPROT	HYPOTHETICAL 13.7 KD PROTEIN IN INO1-IDS2 INTERGENIC REGION
11988	25355	30607	4.37	6.3E-01	9910293	NT	HYPOTHETICAL 15.3 KD PROTEIN IN VMA12-APN1 INTERGENIC REGION
12078	25887		1.45	6.3E-01	AF105227.1	NT	Mus musculus keratin complex 2, gene 6g (Krt2-6g), mRNA
12283	25272		2.93	6.3E-01	X83528.1	NT	Mus musculus 3'-phosphoadenosine 5'-phosphosulfate synthetase (PAPSS) mRNA, complete cds
5780	18571	31499	2.31	6.2E-01	Q10135	SWISSPROT	C. limicola pscD gene
7394	20073		3.44	6.2E-01	AF022253.1	NT	HYPOTHETICAL 142.5 KD PROTEIN C29E2.02 IN CHROMOSOME 1
7443	25114	33209	1.33	6.2E-01	AL021127.2	NT	Mus musculus calcium-sensing receptor related protein 4 (Casr-rs4) mRNA, partial cds
8200	20894	34031	4.52	6.2E-01	H72255.1	EST_HUMAN	Mus musculus chromosome X contigA; putative Magea9 gene, Caltractin, NAD(P) steroid dehydrogenase end Zinc finger protein 185
8755	21447	34595	0.52	6.2E-01	AF034411.1	NT	ys01608.s1 Soares fetal liver spleen tNfLS Homo sapiens cDNA clone IMAGE:213542 3'
9349	20420	33540	1.55	6.2E-01	BE562887.1	EST_HUMAN	Lycopodium esculentum cytosolic Cu,Zn superoxide dismutase (Sod) gene, partial cds; and dehydroquinone dehydratase/shikimate:NAD(P) oxidoreductase gene, complete cds
9410	22072		2.55	6.2E-01	M24461.1	NT	601336148F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3690010 5'
9978	22628	35834	6.2	6.2E-01	AL161511.2	NT	Human pulmonary surfactant-associated protein SP-B (SFTPB) mRNA, complete cds
10121	22769	35982	0.5	6.2E-01	11420793	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 23
10121	22769	35983	0.5	6.2E-01	11420793	NT	Homo sapiens potassium voltage-gated channel, Shab-related subfamily, member 1 (KCNB1), mRNA
10121	22769	35983	0.5	6.2E-01	11420793	NT	Homo sapiens potassium voltage-gated channel, Shab-related subfamily, member 1 (KCNB1), mRNA

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10434	23080	36305	5.2	6.2E-01	P27410	SWISSPROT	NON-STRUCTURAL POLYPROTEIN [CONTAINS: RNA-DIRECTED RNA POLYMERASE; THIOL PROTEASE P3C; HELICASE (2C LIKE PROTEIN); COAT PROTEIN]
10434	23080	36308	5.2	6.2E-01	P27410	SWISSPROT	NON-STRUCTURAL POLYPROTEIN [CONTAINS: RNA-DIRECTED RNA POLYMERASE; THIOL PROTEASE P3C; HELICASE (2C LIKE PROTEIN); COAT PROTEIN]
2393	15114		4.38	6.1E-01	6678076	NT	Mus musculus secreted acidic cysteine rich glycoprotein (Sparc), mRNA
5449	18248	31137	1.15	6.1E-01	M5940.1	NT	Caenorhabditis elegans N2 CcMyoD (hlt-1) alternatively spliced genes, complete cds
6770	19514	32540	4.02	6.1E-01	M64733.1	NT	Rat TRPM-2 gene, complete cds
6770	19514	32541	4.02	6.1E-01	M64733.1	NT	Rat TRPM-2 gene, complete cds
6920	19666	32702	0.94	6.1E-01	AW105663.1	EST_HUMAN	xd50h03.x1 NCL_CGAP_OV23 Homo sapiens cDNA clone IMAGE:2597237 3' similar to gb:X12671_rna1 HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1 (HUMAN);
7005	19697	32751	0.72	6.1E-01	Q63769	SWISSPROT	SUSHI REPEAT-CONTAINING PROTEIN SRPX PRECURSOR (DRS PROTEIN) (DOWN-REGULATED BY V-SRC)
8132	20826	33862	3.27	6.1E-01	AF033535.1	NT	Arabidopsis thaliana putative zinc transporter (ZIP1) mRNA, complete cds
8694	21386	34528	1.08	6.1E-01	11431065	NT	Homo sapiens mitogen-activated protein kinase kinase kinase 4 (MAP4K4), mRNA
8694	21386	34529	1.09	6.1E-01	11431065	NT	Homo sapiens mitogen-activated protein kinase kinase kinase 4 (MAP4K4), mRNA
9315	21982	35153	18.74	6.1E-01	AF236117.1	NT	Homo sapiens G-protein coupled receptor EDG-7 mRNA, complete cds
9315	21982	35154	18.74	6.1E-01	AF236117.1	NT	Homo sapiens G-protein coupled receptor EDG-7 mRNA, complete cds
9742	22363	35597	0.93	6.1E-01	AE004452.1	NT	Pseudomonas aeruginosa PA01, section 13 of 529 of the complete genome
9946	22594	35797	1.06	6.1E-01	AF119117.1	NT	Homo sapiens dopamine transporter (SLC6A3) gene, complete cds
11738	24331	37655	2.57	6.1E-01	S83182.1	NT	hyaluronan-binding protein-hepatocyte growth factor activator homolog [human, plasma, mRNA, 2408 nt]
11738	24331	37656	2.57	6.1E-01	S83182.1	NT	hyaluronan-binding protein-hepatocyte growth factor activator homolog [human, plasma, mRNA, 2408 nt]
12074	25159	30899	2.28	6.1E-01	AB041350.1	NT	Mus musculus Ccl4a5 mRNA for type IV collagen alpha 5 chain, complete cds
12694	24977		1.57	6.1E-01	X95287.1	NT	M.mazei orfA, orfB, and orfC of archaeal ABC-transporter system
482	13267	25903	1.24	6.0E-01	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
548	13331		3.09	6.0E-01	5902899	NT	Homo sapiens adaptor-related protein complex 3, mu 2 subunit (CLA20), mRNA
1341	14089	26765	1.91	6.0E-01	AF065253.1	NT	Human respiratory syncytial virus strain CH63-63b attachment protein (G) gene, complete cds
3795	16547	29180	0.92	6.0E-01	AJ233396.1	NT	Viral hemorrhagic septicemia virus N, P, M, G, Nv, L genes, French strain 07-71
4165	16905		1.09	6.0E-01	AF058895.1	NT	Homo sapiens Notch3 (NOTCH3) gene, exons 26, 27, and 28
5199	18007	30628	2	6.0E-01	P20298	SWISSPROT	D(2) DOPAMINE RECEPTOR
5353	18156	30839	2.86	6.0E-01	AW139713.1	EST_HUMAN	UI-H-B11-aeb-a-10-0-U1.s1 NCL_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2718618 3'
6445	19213	32210	2.78	6.0E-01	U98813.1	NT	Musca domestica insecticide-susceptible strain voltage-sensitive sodium channel mRNA, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6563	19328	32335	0.68	6.0E-01	Q04912	SWISSPROT	MACROPHAGE-STIMULATING PROTEIN RECEPTOR PRECURSOR (MSP RECEPTOR) (P185-RON) (CDW136) (CD136 ANTIGEN)
7254	19938	33013	6.99	6.0E-01	AJ277661.1	NT	Homo sapiens partial LMO1 gene for LIM domain only 1 protein, exon 1
8023	20718	33850	4.39	6.0E-01	P02835	SWISSPROT	SEGMENTATION PROTEIN FUSHI TARAZU
8023	20718	33851	4.39	6.0E-01	P02835	SWISSPROT	SEGMENTATION PROTEIN FUSHI TARAZU
9723	22374	35574	1.61	6.0E-01	AB008193.1	NT	Homo sapiens genes for leukotriene B4 receptor BLT2, leukotriene B4 receptor BLT1, complete cds
10173	22821		1.46	6.0E-01	Q01497	SWISSPROT	PEROXISOMAL MEMBRANE PROTEIN PER9 (PEROXIN-3)
10990	23684	36921	1.49	6.0E-01	AJ131892.1	NT	Gallus gallus mRNA for Hyperion protein, 419 kD isoform
10990	23684	36922	1.49	6.0E-01	AJ131892.1	NT	Gallus gallus mRNA for Hyperion protein, 419 kD isoform
11540	24140	37449	3.77	6.0E-01	AI420623.1	EST_HUMAN	008107.x1 NCL CGAP_P128 Homo sapiens cDNA clone IMAGE:2095621 3'
12354	24758	31060	2.25	6.0E-01	11421663	NT	Homo sapiens nuclear factor (erythroid-derived 2)-like 3 (NFE2L3), mRNA
12455	24824		2.8	6.0E-01	AA706087.1	EST_HUMAN	299605.s1 Soares_fetal_liver_spleen.1NFLS.S1 Homo sapiens cDNA clone IMAGE:462776 3'
12639	25208	30815	3.04	6.0E-01	9055303	NT	Mus musculus cGMP-inhibited phosphodiesterase (Pde3a), mRNA
12684	25142		2.06	6.0E-01	BE157617.1	EST_HUMAN	RC1-H10375-030300-015-c03 HT0375 Homo sapiens cDNA
980	13745	26407	1.36	5.9E-01	U32701.1	NT	Haemophilus influenzae Rd section, 16 of 163 of the complete genome
3284	16028	28675	2.29	5.9E-01	AL163267.2	NT	Homo sapiens chromosome 21 segment HS21C067
3284	16028	28676	2.29	5.9E-01	AL163267.2	NT	Homo sapiens chromosome 21 segment HS21C067
4196	16937		4.21	5.9E-01	AF162756.1	NT	Rattus norvegicus cerenxin 2 mRNA, partial cds
6373	19142	32139	1.55	5.9E-01	AF065440.2	NT	Homo sapiens low density lipoprotein receptor-related protein II (LRP2) gene, exon 1 and partial cds
7166	19853	32922	1.32	5.9E-01	AB023486.1	NT	Homo sapiens gene for histamine H2 receptor, promoter region and complete cds
7296	18978		0.61	5.9E-01	X88801.1	NT	G.gallus gene for skeletal alpha-actinin, exon EF2
7898	20593	33725	0.48	5.9E-01	D90911.1	NT	Synchaocystis sp. PC08803 complete genome, 13/27, 1576593-1719643
8536	21228	34370	0.48	5.9E-01	D12922.1	NT	Legionella pneumophila gene for iron superoxide dismutase, complete cds
9443	22120	35299	0.82	5.9E-01	AF063204.2	NT	Chlamydia trachomatis strain KUW/31/Cx major outer membrane protein (omp1) gene, complete cds
9813	22464		0.74	5.9E-01	P06483	SWISSPROT	E6 PROTEIN
10098	22736	35951	1.15	5.9E-01	P55284	SWISSPROT	VASCULAR ENDOTHELIAL-CADHERIN PRECURSOR (VE-CADHERIN) (CADHERIN-5)
10569	23264	36502	2.5	5.9E-01	Q9X013	SWISSPROT	THYMIDYLATE KINASE (DTMP KINASE)
10578	23271	36507	1.72	5.9E-01	AF197944.1	NT	Xenopus laevis receptor protein tyrosine phosphatase delta (XPT-P-D) mRNA, complete cds
10881	23561	36908	2.91	5.9E-01	AW937175.1	EST_HUMAN	PM1-DT0041-180100-002-n03 DT0041 Homo sapiens cDNA
11149	23816	37099	1.95	5.9E-01	AF064626.1	NT	Mus spretus strain SPRET/EJ CD48 antigen (C448) gene, partial cds
11458	24062	37368	1.56	5.9E-01	P47135	SWISSPROT	JSN1 PROTEIN

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11458	24062	37369	1.56	5.9E-01	P47135	SWISSPROT	JSN1 PROTEIN
12021	24549	31109	2	5.9E-01	L42320.1	NT	Oryctolagus cuniculus alpha 1 anti-trypsin (alpha 1 AT) gene, promoter region
12252	24698		4.35	5.9E-01	AB017705.1	NT	Aspergillus oryzae pyrG gene for oradine-5'-phosphate decarboxylase, complete cds
12465	24832		5.72	5.9E-01	P34926	SWISSPROT	MICROTUBULE-ASSOCIATED PROTEIN 1A [CONTAINS: MAP1 LIGHT CHAIN LC2]
1902	14639	27348	1.36	5.8E-01	P40472	SWISSPROT	SIM1 PROTEIN
2569	15283	28021	1.01	5.8E-01	7305230	NT	Mus musculus low density lipoprotein B (Ldlb), mRNA
4478	17213	29838	4.37	5.8E-01	AB009077.1	NT	Vigna radiata mRNA for proton pyrophosphatase, complete cds
5280	18095		0.82	5.8E-01	AE002152.1	NT	Ureaplasma urealyticum section 53 of 59 of the complete genome
5444	18243	31131	0.62	5.8E-01	Q10699	SWISSPROT	POTENTIAL 5'-3' EXONUCLEASE
6091	18869	31835	1.09	5.8E-01	D78659.1	EST_HUMAN	HUM500E06B Human placenta polyA+ (TFujliwara) Homo sapiens cDNA clone GEN-500E06 5'
6220	18994	31970	0.66	5.8E-01	D50601.1	NT	Shigella sonnei DNA for 26 ORFs, complete cds
6715	19630		2.48	5.8E-01	S65061.1	NT	cyclic AMP-regulated phosphoprotein [rats, mRNA, 1030 nt]
7787	20482		2.61	5.8E-01	H41571.1	EST_HUMAN	yn91b03.s1 Soares adult brain N2b5HB55Y Homo sapiens cDNA clone IMAGE:175757 3' similar to
7885	20680	33805	0.64	5.8E-01	A1280051.1	EST_HUMAN	gb:S78187 M-PHASE INDUCER PHOSPHATASE 2 (HUMAN);
7985	20680	33806	0.64	5.8E-01	A1280051.1	EST_HUMAN	qh85d10.x1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1853779 3'
8090	20784	33914	3.41	5.8E-01	P14328	SWISSPROT	SPORE COAT PROTEIN SP96
8090	20784	33915	3.41	5.8E-01	P14328	SWISSPROT	SPORE COAT PROTEIN SP96
8789	21481	34628	8.97	5.8E-01	AJ270774.1	NT	Homo sapiens partial TCF-4 gene for T-cell transcription factor-4, exons 8-11
8871	21562	34707	0.99	5.8E-01	Q27368	SWISSPROT	TRANSCRIPTION FACTOR E2F
8872	21563	34708	0.51	5.8E-01	Q20471	SWISSPROT	PUTATIVE CASEIN KINASE 1F46F2.2 IN CHROMOSOME X
9496	22149		0.81	5.8E-01	BF031606.1	EST_HUMAN	601557774F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3827298 5'
10911	23591	36837	7.56	5.8E-01	AJ243213.1	NT	Homo sapiens partial 5-HT4 receptor gene, exons 2 to 5
10962	23638		3.97	5.8E-01	BF700092.1	EST_HUMAN	602127577F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4284403 5'
11089	23759		1.99	5.8E-01	BF700092.1	EST_HUMAN	602127577F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4284403 5'
1480	14227	26912	1.12	5.7E-01	P06727	SWISSPROT	APOLIPROTEIN A-IV PRECURSOR (APO-AIV)
1480	14227	26913	1.12	5.7E-01	P06727	SWISSPROT	APOLIPROTEIN A-IV PRECURSOR (APO-AIV)
3038	15804		0.89	5.7E-01	6755253	NT	Mus musculus plasmacytoma variant translocation 1 (Pvt1), mRNA
3217	15980	28631	1.62	5.7E-01	Q9WTJ2	SWISSPROT	PUTATIVE TRANSCRIPTION FACTOR OVO-LIKE 1 (MOVO1) (MOVO1A)
3495	16251		2.82	5.7E-01	AB033503.1	NT	Populus euramericana peacs-2 mRNA for 1-aminocyclopropane-1-carboxylate synthase, complete cds
6262	18036	32011	5.13	5.7E-01	BF035413.1	EST_HUMAN	601454962F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3858590 5'
6611	19374	32388	0.81	5.7E-01	AA194201.1	EST_HUMAN	z38c06.r1 Soares NHMPu_S1 Homo sapiens cDNA clone IMAGE:685674 5'
6763	17932	30568	1.33	5.7E-01	AL111440.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation

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Single Exon Probes Expressed in Brain

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7664	20328	33438	2.14	5.7E-01	P00373	SWISSPROT	PYRROLINE-5-CARBOXYLATE REDUCTASE (P5CR) (P5C REDUCTASE)
7870	20565		0.5	5.7E-01	AJ251835.1	NT	Mus musculus Kcnq1, Lirp05, Mash2, Tapa-1, Tesc4 and Tesc6 genes, alternative transcripts
8279	20973		0.47	5.7E-01	AI065061.1	EST_HUMAN	HA0895 Human fetal liver cDNA library Homo sapiens cDNA
9699	22350	35544	1.19	5.7E-01	AL161532.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 32
9699	22350	35545	1.19	5.7E-01	AL161532.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 32
10475	23121	36351	0.72	5.7E-01	BF540962.1	EST_HUMAN	MR3-HT0738-180700-003-e02 HT0736 Homo sapiens cDNA
11983	24524		1.52	5.7E-01	BE715051.1	EST_HUMAN	602067712F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4066810 5'
12658	24958		3.01	5.7E-01	BE959722.2	EST_HUMAN	601654814R1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:3839783 3'
3357	16117	28772	1.3	5.6E-01	AB018283.2	NT	Homo sapiens mRNA for KIAA0740 protein, partial cds
3357	16117	28773	1.3	5.6E-01	AB018283.2	NT	Homo sapiens mRNA for KIAA0740 protein, partial cds
3863	16613	29252	0.97	5.6E-01	AL161501.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 13
4215	16956	29578	0.74	5.6E-01	D83135.1	NT	Chicken TBP gene, exon8, complete cds
8702	21394	34541	4.01	5.6E-01	AV684703.1	EST_HUMAN	AV684703 GKC Homo sapiens cDNA clone GKCF5F05 5'
8702	21394	34542	4.01	5.6E-01	AV684703.1	EST_HUMAN	AV684703 GKC Homo sapiens cDNA clone GKCF5F05 5'
9275	22029	35199	1.08	5.6E-01	AB038782.1	NT	Homo sapiens MUC3A gene for intestinal mucin, partial cds
11884	24457		2.57	5.6E-01	BE888280.1	EST_HUMAN	601514007F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3915457 5'
11997	24535	37272	1.63	5.6E-01	AA493335.1	EST_HUMAN	hg75g10.s1 NCL_CGAP_P16 Homo sapiens cDNA clone IMAGE:940674 similar to contains element PTR7 repetitive element:
12352	16613	29252	1.69	5.6E-01	AL161501.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 13
12379	24778		2.7	5.6E-01	P50505	SWISSPROT	HIGH AFFINITY POTASSIUM TRANSPORTER
12773	25027		4.26	5.6E-01	BF73829.1	EST_HUMAN	60213029F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4271334 5'
1189	13941	28606	0.85	5.5E-01	8393912	NT	Rattus norvegicus Propionyl Coenzyme A carboxylase, beta polypeptide (Pccb), mRNA
2705	15412	28149	6.93	5.5E-01	P03341	SWISSPROT	GAG POLYPEPTIDE [CONTAINS: INNER COAT PROTEIN P12; CORE PROTEIN P15; CORE SHELL PROTEIN P30; NUCLEOPROTEIN P10]
2705	15412	28149	6.93	5.5E-01	P03341	SWISSPROT	GAG POLYPEPTIDE [CONTAINS: INNER COAT PROTEIN P12; CORE PROTEIN P15; CORE SHELL PROTEIN P30; NUCLEOPROTEIN P10]
2919	15885	28330	1	5.5E-01	5902085	NT	Homo sapiens superkiller viralicidic activity 2 (S. cerevisiae homolog)-like (SKIV2L), mRNA
3062	15828		1.55	5.5E-01	H46219.1	EST_HUMAN	yo18a10.s1 Soares adult brain N2b5fHB55Y Homo sapiens cDNA clone IMAGE:178266 3'
3228	15991	28644	4.22	5.5E-01	AF227240.1	NT	Rabbit oral papillomavirus, complete genome
3678	16431	29073	1.7	5.5E-01	P48785	SWISSPROT	FOS-RELATED ANTIGEN-1
5082	17801	30419	1.79	5.5E-01	U69037.1	NT	Bos taurus MHC class II beta-chain BoLA-DIB1 gene, partial cds
7187	19873		0.65	5.5E-01	AB015593.1	NT	Carassius auratus gene for gonadotropin II beta subunit, complete cds
8348	21041	34178	1.04	5.5E-01	A791766.1	EST_HUMAN	or82c01.y5 NCL_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1602336 5'
9667	22319		0.7	5.5E-01	U98415.1	NT	Grimean-Congo hemorrhagic fever virus strain SPU 415/85 nucleoprotein gene, complete cds

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10276	22624	36136	0.96	5.5E-01	T05047.1	EST_HUMAN	EST02835 Fetal brain, Stragene (cat#336206) Homo sapiens cDNA clone HFBQ35
11087	23757	37033	1.86	5.5E-01	BF129507.1	EST_HUMAN	601811077R1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4054003 3'
140	12955	25597	4.91	5.4E-01	7657266	NT	Homo sapiens KIAA0929 protein Mx2 interacting nuclear target (MINT) homolog (KIAA0929), mRNA
140	12955	25598	4.91	5.4E-01	7657266	NT	Homo sapiens KIAA0929 protein Mx2 interacting nuclear target (MINT) homolog (KIAA0929), mRNA
571	13352	25980	1.16	5.4E-01	AF232006.1	NT	Pseudomonas syringae pv. tomato strain DC3000 AvrE (avrE), HrpW (hrpW), and GsIA (gsIA) genes, complete cds; and unknown genes
571	13352	25981	1.16	5.4E-01	AF232006.1	NT	Pseudomonas syringae pv. tomato strain DC3000 AvrE (avrE), HrpW (hrpW), and GsIA (gsIA) genes, complete cds; and unknown genes
1248	13997	26684	3.41	5.4E-01	AW896087.1	EST_HUMAN	QV4-NN0040-070400-160-c04 NN0040 Homo sapiens cDNA
2096	14830		3.43	5.4E-01	AE002247.2	NT	Chlamydomonas reinhardtii AR339, section 74 of 94 of the complete genome
2252	14980	27719	1.81	5.4E-01	AJ276882.1	NT	Drosophila melanogaster mRNA for 15,15' beta carotene dioxygenase (beta-diox gene)
5086	17785	30402	0.92	5.4E-01	M74439.1	NT	Rattus rattus UDP glucuronosyltransferase gene, complete cds
5571	18368	31278	0.74	5.4E-01	AW842327.1	EST_HUMAN	PM2-CN0030-030200-003-c10 CN0030 Homo sapiens cDNA
6098	18876	31845	0.83	5.4E-01	AB025017.1	NT	Rattus norvegicus gene for TIS11, complete cds
6928	19664	32710	0.87	5.4E-01	BE86892.2	EST_HUMAN	601660276R1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3906090 3'
7235	19920	32993	0.81	5.4E-01	Z21619.1	NT	S.cerevisiae RIB3 gene encoding DBP synthase
7235	19920	32994	0.81	5.4E-01	Z21619.1	NT	S.cerevisiae RIB3 gene encoding DBP synthase
7237	19922	32997	1.48	5.4E-01	Q64428	SWISSPROT	MITOCHONDRIAL TRIFUNCTIONAL ENZYME ALPHA SUBUNIT PRECURSOR (TP-ALPHA)
9890	22540		2.09	5.4E-01	BF572536.1	EST_HUMAN	[INCLUDES: LONG-CHAIN ENOYL-COA HYDRATASE; LONG CHAIN 3-HYDROXYACYL-COA DEHYDROGENASE]
11015	23687	36948	2.87	5.4E-01	P36838	SWISSPROT	602076545F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4243690 5'
11621	24218	37541	3.08	5.4E-01	Q60675	SWISSPROT	NITRATE REDUCTASE [NADPH] (NR)
11621	24218	37542	3.08	5.4E-01	Q60675	SWISSPROT	LAMININ ALPHA-2 CHAIN PRECURSOR (LAMININ M CHAIN) (MEROSIN HEAVY CHAIN)
11944	24489		3.5	5.4E-01	A1858398.1	EST_HUMAN	LAMININ ALPHA-2 CHAIN PRECURSOR (LAMININ M CHAIN) (MEROSIN HEAVY CHAIN)
503	13297	25921	1.54	5.3E-01	AF019413.1	NT	w37g04.x1 NCI_CGAP_U11 Homo sapiens cDNA clone IMAGE:2427126 3' similar to gb:M13452 LAMIN A (HUMAN);
2136	14866	27596	1.01	5.3E-01	AF113919.1	NT	Homo sapiens HLA class III region containing tenascin X (tenascin-X) gene, partial cds; cytochrome P450 21-hydroxylase (CYP21B), complement component C4 (C4B) G11, helicase (SK12W), RD, complement factor B (Bf), and complement component C2 (C2) genes, >
2136	14866	27597	1.01	5.3E-01	AF113919.1	NT	Brassica oleracea var. capitata phospholipase D2 (PLD2) gene, complete cds
2786	15491	28230	6.83	5.3E-01	4506328	NT	Brassica oleracea var. capitata phospholipase D2 (PLD2) gene, complete cds
							Homo sapiens protein tyrosine phosphatase, receptor-type, zeta polypeptide 1 (PTPRZ1) mRNA

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Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2786	15491	28231	0.83	5.3E-01	4506328	NT	Homo sapiens protein tyrosine phosphatase, receptor-type, zeta polypeptide 1 (PTPRZ1) mRNA
3237	15999	28649	2.74	5.3E-01	AF087658.1	NT	Homo sapiens secreted C-type lectin precursor (LSTCL) gene, complete cds
4187	16928		1.58	5.3E-01	U39887.1	NT	Mycoplasma genitalium section 9 of 51 of the complete genome
5371	18172	30860	1.96	5.3E-01	AB20921.1	EST_HUMAN	zu42h12.y5 Soares ovary tumor NBH0T Homo sapiens cDNA clone IMAGE:740711 5'
5371	18172	30861	1.96	5.3E-01	AB20921.1	EST_HUMAN	zu42h12.y5 Soares ovary tumor NBH0T Homo sapiens cDNA clone IMAGE:740711 5'
5466	18265	31156	0.84	5.3E-01	AA193672.1	EST_HUMAN	zu42g09.r1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:668112 5'
5466	18265	31157	0.84	5.3E-01	AA193672.1	EST_HUMAN	zu42g09.r1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:668112 5'
5559	18358	31266	1.82	5.3E-01	BE645820.1	EST_HUMAN	7e73c12.x1 NCL_CGAP_P128 Homo sapiens cDNA clone IMAGE:3288118 3' similar to gb:J02783
5559	18358	31267	1.82	5.3E-01	BE645820.1	EST_HUMAN	7e73c12.x1 NCL_CGAP_P128 Homo sapiens cDNA clone IMAGE:3288118 3' similar to gb:J02783
8802	21494		1.8	5.3E-01	L01950.2	NT	PROTEIN DISULFIDE ISOMERASE PRECURSOR (HUMAN); Roridula gorgonias ribulose 1,5-bisphosphate carboxylase (rbcl) gene, partial cds; chloroplast gene for chloroplast product
8854	21545	34692	0.81	5.3E-01	BF433956.1	EST_HUMAN	7q71c12.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE: 3' similar to contains element MER28
8854	21545	34693	0.81	5.3E-01	BF433956.1	EST_HUMAN	7q71c12.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE: 3' similar to contains element MER29
10111	22759	35971	0.62	5.3E-01	AI954210.1	EST_HUMAN	wx94b02.x1 NCL_CGAP_Mel15 Homo sapiens cDNA clone IMAGE:2551275 3' similar to
11550	24149	37460	7.3	5.3E-01	BE568291.1	EST_HUMAN	SW_COXA_HUMAN P20674 CYTOCHROME C OXIDASE POLYPEPTIDE VA PRECURSOR ; 601339867F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3682168 5'
11789	24379	37709	1.72	5.3E-01	Q05793	SWISSPROT	BASEMENT MEMBRANE-SPECIFIC HEPARAN SULFATE PROTEOGLYCAN CORE PROTEIN PRECURSOR (HSPG) (PERLECAN) (PLC)
11877	25208		4.03	5.3E-01	AA918053.1	EST_HUMAN	og30e05.s1 NCL_CGAP_Br7 Homo sapiens cDNA clone IMAGE:1441376 3' similar to gb:J02611
797	13569	26229	18.35	5.2E-01	L20770.1	NT	APOLIPOPROTEIN D PRECURSOR (HUMAN); Drosophila melanogaster helix-loop-helix mRNA, complete cds
1141	13896	26557	8.29	5.2E-01	Q9WV30	SWISSPROT	NUCLEAR FACTOR OF ACTIVATED T CELLS 5 (T CELL TRANSCRIPTION FACTOR NFAT5) (NF-AT5)
1169	13923	26585	1.77	5.2E-01	AF224492.1	NT	(REL DOMAIN-CONTAINING TRANSCRIPTION FACTOR NFAT5)
1879	14616		2.35	5.2E-01	AL163285.2	NT	Homo sapiens phospholipid scramblase 1 gene, complete cds
2142	14872	27605	2.55	5.2E-01	AB018283.2	NT	Homo sapiens chromosome 21 segment HS21C085
3117	15882	28521	1.23	5.2E-01	U65942.1	NT	Homo sapiens mRNA for KIAA0740 protein, partial cds
3231	15994		1	5.2E-01	D73443.1	NT	Chlamydomonas abortus strain S26/3 POMP91A and POMP90A precursor, genes, complete cds
3400	16158		1.58	5.2E-01	AL116780.1	NT	Azotobacter vinelandii tcd gene for isocitrate dehydrogenase, complete cds
3437	16193	28843	2.27	5.2E-01	AA984165.1	EST_HUMAN	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation am77g05.s1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:1616504 3'

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3623	16376		0.76	5.2E-01	AF020269.1	NT	Medicago sativa chloroplast malate dehydrogenase precursor (p1mdh) mRNA, nuclear gene encoding
4568	17303	29930	0.82	5.2E-01	6752947	NT	chloroplast protein, complete cds
4953	17679		1.02	5.2E-01	7106444	NT	Mus musculus acetylcholine receptor beta (Acrb), mRNA
5567	18364	31272	0.87	5.2E-01	AA284261.1	EST_HUMAN	Mus musculus vanilloid receptor-like protein 1 (Vrl1), mRNA
9630	25126	35474	0.75	5.2E-01	X02218.1	NT	zc4409.77 Scores_senescent_fibroblasts_NbHSF Homo sapiens cDNA clone IMAGE:325169 3'
9630	25126	35475	0.75	5.2E-01	X02218.1	NT	Chicken duplicated genes for histone H2A, H4 and a histone H3 gene
9630	25126	35475	0.75	5.2E-01	X02218.1	NT	Chicken duplicated genes for histone H2A, H4 and a histone H3 gene
9832	22483	35685	0.48	5.2E-01	AA194518.1	EST_HUMAN	zq05b09.r1 Stragene muscle 937209 Homo sapiens cDNA clone IMAGE:628783 5'
9926	22574	35772	1.35	5.2E-01	AF143962.2	NT	Homo sapiens PELOTA (PELOTA) gene, complete cds
12744	25010		7	5.2E-01	P18516	SWISSPROT	RETINOIC ACID RECEPTOR GAMMA (RAR-GAMMA) (RETINOIC ACID RECEPTOR DELTA) (RAR-DELTA)
603	13381	26013	1.84	5.1E-01	M58509.1	NT	Human adrenodoxin reductase gene, exons 3 to 12
633	13412	26047	4.49	5.1E-01	AJ233944.1	NT	Polyangium vitellinum (strain PI vt1) 16S rRNA gene
633	13412	26048	4.49	5.1E-01	AJ233944.1	NT	Polyangium vitellinum (strain PI vt1) 16S rRNA gene
1648	14394		1.09	5.1E-01	X87885.1	NT	R.norvegicus mRNA for mammalian fusca protein
2017	14752		1.29	5.1E-01	BF680395.1	EST_HUMAN	602139319F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4298117 5'
4057	16802	29433	3.86	5.1E-01	AB58495.1	EST_HUMAN	w39b12.x1 NCI_CGAP_U11 Homo sapiens cDNA clone IMAGE:2427263 3'
4164	16904	29533	2.81	5.1E-01	P06380	SWISSPROT	TRANSCRIPTION-REPAIR COUPLING FACTOR (TRCF)
5103	17821	30438	1.01	5.1E-01	U72653.1	NT	Human alpha 1a adrenergic receptor (alpha1a) gene, 5' flanking region
6128	18006	31874	0.67	5.1E-01	BE541098.1	EST_HUMAN	601063606F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3450000 5'
6183	18960		0.93	5.1E-01	AV712326.1	EST_HUMAN	AV712326 DCA Homo sapiens cDNA clone DCAAF07 5'
6818	19479	32502	1.69	5.1E-01	R80373.1	EST_HUMAN	y94a09.s1 Scores placenta Nb2HP Homo sapiens cDNA clone IMAGE:146872 3'
8470	21162	34304	0.83	5.1E-01	AW806881.1	EST_HUMAN	QV4-ST0023-160400-172-a01 ST0023 Homo sapiens cDNA
8470	21162	34305	0.83	5.1E-01	AW806881.1	EST_HUMAN	QV4-ST0023-160400-172-a01 ST0023 Homo sapiens cDNA
9583	22236	35420	4.33	5.1E-01	J05412.1	NT	Human regenerating protein (reg) gene, complete cds
9587	22240	35424	3.14	5.1E-01	W22302.1	EST_HUMAN	65B1 Human retina cDNA Tsp509I-cleaved sublibrary Homo sapiens cDNA not directional
10060	22708	35928	0.89	5.1E-01	M94579.1	NT	Human carboxyl ester lipase (CEL) gene, complete cds
12086	25137		4.26	5.1E-01	BF030207.1	EST_HUMAN	601556863F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3826767 5'
12326	24745		3.55	5.1E-01	BF439982.1	EST_HUMAN	hac51f10.x1 NCI_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:3406218 3' similar to contains element
2130	14861	27590	1.24	5.0E-01	4865552	NT	TAR1 repetitive element
2130	14861	27591	1.24	5.0E-01	4865552	NT	Homo sapiens postmeiotic segregation increased 2-like 9 (PMS2L9), mRNA
							Homo sapiens postmeiotic segregation increased 2-like 9 (PMS2L9), mRNA

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Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2140	14870	27601	3.19	5.0E-01	AF008210.1	NT	Buchnera aphidicola genomic fragment containing (chaperone Hsp60) groEL, DNA biosynthesis initiating protein (dnaA), ATP operon (atpCDGAHFEB), and putative chromosome replication protein (gidA) genes, complete cds; and termination factor Rho (rho) gene>
2140	14870	27602	3.19	5.0E-01	AF008210.1	NT	Buchnera aphidicola genomic fragment containing (chaperone Hsp60) groEL, DNA biosynthesis initiating protein (dnaA), ATP operon (atpCDGAHFEB), and putative chromosome replication protein (gidA) genes, complete cds; and termination factor Rho (rho) gene>
3811	16583	29198	1.13	5.0E-01	L39483.1	NT	Rattus norvegicus jagged protein mRNA, complete cds
3854	16604	29241	2.75	5.0E-01	AB033010.1	NT	Homo sapiens mRNA for KIAA1184 protein, partial cds
6547	19312	33334	0.65	5.0E-01	BF576199.1	EST_HUMAN	602132842F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4271939 5'
7562	20232	33336	0.75	5.0E-01	AL161549.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 49
7562	20232	33336	0.75	5.0E-01	AL161549.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 49
8428	21121	34399	1.92	5.0E-01	M92304.1	NT	Xenopus laevis smooth muscle beta-tropomyosin mRNA, complete cds
8589	21261	34399	0.71	5.0E-01	BF107848.1	EST_HUMAN	601823860R1 NIH_MGC_79 Homo sapiens cDNA clone IMAGE:4043485 3'
9358	20429	33547	2.74	5.0E-01	BF317121.1	EST_HUMAN	601903871F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4136632 5'
9525	22178	35362	1.36	5.0E-01	P35573	SWISSPROT	GLYCOTEN DEBRANCHING ENZYME (GLYCOTEN DEBRANCHER) [INCLUDES: 4-ALPHA-GLUCANOTRANSFERASE (OLIGO-1,4-1,4-GLUCANTRANSFERASE); AMYLO-1,6-GLUCOSIDASE (DEXTRIN 6-ALPHA-D-GLUCOSIDASE)]
9525	22178	35363	1.36	5.0E-01	P35573	SWISSPROT	GLYCOTEN DEBRANCHING ENZYME (GLYCOTEN DEBRANCHER) [INCLUDES: 4-ALPHA-GLUCANOTRANSFERASE (OLIGO-1,4-1,4-GLUCANTRANSFERASE); AMYLO-1,6-GLUCOSIDASE (DEXTRIN 6-ALPHA-D-GLUCOSIDASE)]
10280	22938		1.12	5.0E-01	BE869218.1	EST_HUMAN	601445024F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3849436 5'
12026	24554		4	5.0E-01	AF028215.1	NT	Mus musculus MRC OX-2 antigen homolog gene, exons 2-5, and complete cds
12715	24989		1.86	5.0E-01	AL163302.2	NT	Homo sapiens chromosome 21 segment HS21C102
12726	24997		4.39	5.0E-01	O13961	SWISSPROT	NUCLEAR ENVELOPE PROTEIN CUT11
772	13544	26205	2.43	4.9E-01	BF571462.1	EST_HUMAN	602076649F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4243860 5'
1656	14402	27090	1.54	4.9E-01	AJ243955.1	NT	Xenopus laevis mRNA for c-Jun protein, 1978 BP
1999	14638	27345	1.15	4.9E-01	LJ40869.1	NT	Cavia porcellus pulmonary surfactant protein A (SP-a) mRNA, complete cds
5321	18124	30763	0.89	4.9E-01	Q81554	SWISSPROT	FIBRILLIN 1 PRECURSOR
5946	18728	31686	3.05	4.9E-01	AF020931.1	NT	Homo sapiens diacylglycerol kinase 3 (DAGK3) gene, exon 10
5946	18728	31687	3.05	4.9E-01	AF020931.1	NT	Homo sapiens diacylglycerol kinase 3 (DAGK3) gene, exon 10
7352	20033	33111	1.61	4.9E-01	AB040051.1	NT	Oryza sativa subsp. japonica mtF-G mRNA for mitochondrial elongation factor G, complete cds
7605	20271	33378	0.84	4.9E-01	Q10606	SWISSPROT	PUTATIVE UNDECAPRENYL-PHOSPHATE ALPHA-N-ACETYL-GLUCOSAMINYLTRANSFERASE
7605	20271	33379	0.84	4.9E-01	Q10606	SWISSPROT	PUTATIVE UNDECAPRENYL-PHOSPHATE ALPHA-N-ACETYL-GLUCOSAMINYLTRANSFERASE
8988	21579		1.45	4.9E-01	BF209791.1	EST_HUMAN	601874064F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4102503 5'

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Single Exon Probes Expressed in Brain

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9086	21775	34939	0.99	4.9E-01	AW339905.1	EST_HUMAN	hc90c02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2807266 3' similar to TR:O95714 O95714 HERC2 ;
9196	25431		1.96	4.9E-01	10946863	NT	Mus musculus unc13 homolog (C. elegans) 1 (Unc13h1), mRNA
10216	22864	36076	0.84	4.9E-01	AF053980.1	NT	Mus musculus adenyl cyclase 1 (Adcy1) cDNA, partial cds
10419	23085	36286	0.77	4.9E-01	X90000.1	NT	H. sapiens DNA for BCL7A gene and BCL7A/IGH locus fusion
11925	24486		1.72	4.9E-01	AF176912.1	NT	Homo sapiens neurotrophin-1/B-cell stimulating factor-3 gene, complete cds
12709	25392		6.73	4.9E-01	AA613562.1	EST_HUMAN	nq22e11.s1 NCI_CGAP_Cot0 Homo sapiens cDNA clone IMAGE:1144652 3'
4298	17037		0.77	4.8E-01	4504850	NT	Homo sapiens potassium channel, subfamily K, member 5 (TASK-2) (KCNK5) mRNA, and translated products
5420	18219	30930	10.78	4.8E-01	J02987.1	NT	Saccharomyces cerevisiae sporulation protein (SPO11) gene required for meiotic recombination, complete cds
6578	19342	32356	0.78	4.8E-01	U92882.1	NT	Mus musculus slow skeletal muscle troponin T (Tnnt1) gene, complete cds
6589	19352		3.76	4.8E-01	AA659878.1	EST_HUMAN	nu8f09.s1 NCI_CGAP_Alv1 Homo sapiens cDNA clone IMAGE:1217513
7216	18901		1.99	4.8E-01	5031650	NT	Homo sapiens chromosome 21 segment HS21C009
7565	20235	33339	0.78	4.8E-01	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
7661	20325	33434	4.05	4.8E-01	AL161492.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 4
7661	20325	33435	4.05	4.8E-01	AL161492.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 4
7805	20500	33621	1.2	4.8E-01	AI820744.1	EST_HUMAN	y17710.y5 Soares breast 2NBHst Homo sapiens cDNA clone IMAGE:154795 5' similar to contains element MER6 repetitive element ;
9144	21875		0.92	4.8E-01	BE155148.1	EST_HUMAN	PM1-HT0350-201299-004-b04 HT0350 Homo sapiens cDNA
10629	23322		1.88	4.8E-01	X83502.1	NT	S. cerevisiae ORFs from chromosome X
12217	25165		3.04	4.8E-01	AF227565.1	NT	Trypanosoma cruzi transposon VIP II SIRE repeat region
12795	25216		1.68	4.8E-01	AJ132984.1	NT	Chlamydomonas reinhardtii cop gene, exons 1-8
6422	19190	32186	8.41	4.7E-01	BF217173.1	EST_HUMAN	601883880F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4086387 5'
6941	19423	32438	0.94	4.7E-01	AI204374.1	EST_HUMAN	q72809.x1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1755544 3'
7764	20460	33584	0.63	4.7E-01	T11414.1	EST_HUMAN	hbc811 Human pancreatic islet Homo sapiens cDNA clone hbc811 5'end
7764	20460	33585	0.63	4.7E-01	T11414.1	EST_HUMAN	hbc811 Human pancreatic islet Homo sapiens cDNA clone hbc811 5'end
8974	21664	34816	0.52	4.7E-01	6981501	NT	Rattus norvegicus Spermine binding protein (Sbp), mRNA
10751	23436		6.11	4.7E-01	AF102673.1	NT	Influenza A virus isolate hk57697 hemagglutinin (HA) gene, partial cds
11022	23694	36957	2.2	4.7E-01	U41069.1	NT	Human collagen alpha2(XI) (COL11A2) gene, exons 6 through 16, and partial cds
11252	23814	37206	1.61	4.7E-01	BF529658.1	EST_HUMAN	602043880F1 NCI_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4181303 5'
11349	24039	37342	1.7	4.7E-01	AW889448.1	EST_HUMAN	RC6-NT0029-240400-011-E08 NT0029 Homo sapiens cDNA
12116	24609		1.52	4.7E-01	BE887763.1	EST_HUMAN	601511333F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3912488 5'
12237	24689		1.51	4.7E-01	AW341561.1	EST_HUMAN	hd11c08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2809198 3'

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12813	25055		1.63	4.7E-01	AP000007.1	NT	<i>Pyrococcus horikoshii</i> OT3 genomic DNA, 1485001-1739505 nt position (777)
12817	25300		1.38	4.7E-01	6679502	NT	<i>Mus musculus</i> proteasome (prosome, macropain) 26S subunit, ATPase 3 (Psmc3), mRNA
3726	16479	29116	1.57	4.9E-01	BF693300.1	EST_HUMAN	602081103F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4245481 5'
3728	16479	29117	1.57	4.9E-01	BF693300.1	EST_HUMAN	602081103F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4245481 5'
5333	18136	30795	1	4.9E-01	BF313593.1	EST_HUMAN	601900234F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4129472 5'
5333	18136	30796	1	4.9E-01	BF313593.1	EST_HUMAN	601900234F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4129472 5'
5385	18185	30875	3.11	4.9E-01	Q90643	SWISSPROT	INTERFERON REGULATORY FACTOR 3 (IRF-3)
5385	18185	30876	3.11	4.9E-01	Q90643	SWISSPROT	INTERFERON REGULATORY FACTOR 3 (IRF-3)
5459	18288	31148	1.84	4.9E-01	BE734781.1	EST_HUMAN	601568756F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3843637 5'
5472	18271	31163	2.17	4.9E-01	A1247679.1	EST_HUMAN	qhs9h02.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1849011 3' similar to TR:O15338 O15338 BUTYROPHILIN.;
5472	18271	31164	2.17	4.9E-01	A1247679.1	EST_HUMAN	qhs9h02.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1849011 3' similar to TR:O15338 O15338 BUTYROPHILIN.;
5480	18279	31175	1.8	4.9E-01	P20050	SWISSPROT	MEIOSIS SPECIFIC PROTEIN HOP-1
5560	18387		0.96	4.9E-01	AF212124.1	NT	<i>Anolis schwartzi</i> cytochrome b gene, partial cds; mitochondrial gene for mitochondrial product
5845	18440		0.77	4.9E-01	BE817247.1	EST_HUMAN	PMO-BN0260-120800-001-F07 BN0260 Homo sapiens cDNA
5809	18588	31526	0.59	4.9E-01	D28215.1	NT	Unidentified soil bacteria 16S rRNA gene encoding 16S ribosomal RNA
6163	18940	31911	1.21	4.9E-01	AE000894.1	NT	<i>Methanobacterium thermoautotrophicum</i> from bases 1166751 to 1176238 (section 100 of 148) of the complete genome
6669	19586	32620	3.2	4.9E-01	U62332.1	NT	<i>Emicella nidulans</i> NEMPA (nempA) gene, mitochondrial gene encoding putative mitochondrial protein, complete cds
6669	19586	32621	3.2	4.9E-01	U62332.1	NT	<i>Emicella nidulans</i> NEMPA (nempA) gene, mitochondrial gene encoding putative mitochondrial protein, complete cds
7131	25105	32884	0.57	4.9E-01	L07320.1	NT	<i>Murine cytomegalovirus</i> s1 protein gene, complete cds
7629	20295	33403	0.91	4.9E-01	AA493577.1	EST_HUMAN	nh04h05.s1 NCI_QCAP_Thy1 Homo sapiens cDNA clone IMAGE:943353 similar to contains Alu repetitive element/contains element L1 repetitive element;
7658	20322		0.59	4.9E-01	Q90069	SWISSPROT	GENOME POLYPROTEIN [CONTAINS: N-TERMINAL PROTEIN (P1); HELPER COMPONENT PROTEINASE (HC-PRO); PROTEIN P3; 6 KD PROTEIN 1 (6K1); CYTOPLASMIC INCLUSION PROTEIN (CI); 6 KD PROTEIN 2 (6K2); GENOME-LINKED PROTEIN (VP6); NUCLEAR INCLUSION PROTEIN A (NI-A) (NI)]
8219	20913	34049	10.11	4.9E-01	BF697399.1	EST_HUMAN	602130953F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4287828 5'
9201	21870	35035	1.11	4.9E-01	P55202	SWISSPROT	ATRIAL NATRIURETIC PEPTIDE RECEPTOR B PRECURSOR (ANP-B) (ANPRB) (GC-B) (GUANYLATE CYCLASE)

Table 4
Single Exon Probes Expressed In Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source.	Top Hit Descriptor
9201	21870	35036	1.11	4.6E-01	P65202	SWISSPROT	ATRIAL NATRIURETIC PEPTIDE RECEPTOR B PRECURSOR (ANP-B) (ANPRB) (GC-B) (GUANYLATE CYCLASE)
9876	22528	35720	1.84	4.6E-01	A191563.4.1	EST_HUMAN	wg73e12.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2370768 3'
9878	22528	35721	1.84	4.6E-01	A191563.4.1	EST_HUMAN	wg73e12.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2370768 3'
10912	23692		2.3	4.6E-01	P68163	SWISSPROT	PUTATIVE VITELLOGENIN RECEPTOR PRECURSOR (VL)
10922	23602	36850	10.22	4.6E-01	BE185449.1	EST_HUMAN	IL5-HT0730-100500-075-g05 HT0730 Homo sapiens cDNA
10922	23602	36851	10.22	4.6E-01	BE185449.1	EST_HUMAN	IL5-HT0730-100500-075-g05 HT0730 Homo sapiens cDNA
11450	23217	38449	5.32	4.6E-01	AF019369.1	NT	Human thiopurine methyltransferase (TPMT) gene, exon 10 and complete cds
11450	23217	38450	5.32	4.6E-01	AF019369.1	NT	Human thiopurine methyltransferase (TPMT) gene, exon 10 and complete cds
12163	24645		1.77	4.6E-01	D53316.1	EST_HUMAN	HUM105F03B Clontech human fetal brain poly(A+ mRNA (#6535) Homo sapiens cDNA clone GEN-105F03
1904	14641	27350	1.43	4.5E-01	AE001931.1	NT	Delnocius radiodurans R1 section 68 of 229 of the complete chromosome 1
1904	14641	27351	1.43	4.5E-01	AE001931.1	NT	Delnocius radiodurans R1 section 68 of 229 of the complete chromosome 1
2873	15640	28284	4.5	4.5E-01	AA677098.1	EST_HUMAN	zf5d02.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:454179 3'
3312	16072	28722	4.58	4.5E-01	Q05793	SWISSPROT	BASEMENT MEMBRANE-SPECIFIC HEPARAN SULFATE PROTEOGLYCAN CORE PROTEIN
3372	16131	28787	1.07	4.5E-01	AF126378.1	NT	PRECURSOR (HSPG) (PERLECAN) (PLC)
4007	16753		0.95	4.5E-01	Q28247	SWISSPROT	Mus musculus DNA polymerase epsilon catalytic subunit (Pole) gene, exons 2 through 12
4055	16800	29431	0.88	4.5E-01	A1708908.1	EST_HUMAN	COLLAGEN ALPHA 5(IV) CHAIN
4155	17887		4.25	4.5E-01	AW873495.1	EST_HUMAN	as95e09.x1 Barstead aorta HPLRB6 Homo sapiens cDNA clone IMAGE:2353480 3'
4890	17617	30236	1.1	4.5E-01	BE963445.2	EST_HUMAN	ho80g02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:3041810 3'
5461	18260	31151	1.49	4.5E-01	AW608814.1	EST_HUMAN	601657225R1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3866023 3'
6510	19275		1.45	4.5E-01	Q00956	SWISSPROT	QV2-PT0012-140100-031-c09 PT0012 Homo sapiens cDNA
7312	19986	33073	1.27	4.5E-01	M37036.1	NT	COAT PROTEIN
7609	20180	33273	2.54	4.5E-01	A1858849.1	EST_HUMAN	Rat nuclear proteins B23.1 and B23.2
7621	20287	33396	0.95	4.5E-01	P50070	SWISSPROT	w132e02.x1 NCL_OGAP_U11 Homo sapiens cDNA clone IMAGE:2426618 3' similar to TR:Q92923 Q92923
8206	20900		0.86	4.5E-01	M32861.1	NT	SWISNF COMPLEX 170 KDA SUBUNIT ;
8302	20996	34134	3.5	4.5E-01	A1648596.1	EST_HUMAN	DNA PRIMASE
							D.melanogaster Shaw2 protein mRNA, complete cds
							tz56gt1.x1 NCL_OGAP_Oy35 Homo sapiens cDNA clone IMAGE:2282644 3'
8457	21149	34282	0.83	4.5E-01	Q52728	SWISSPROT	POLY-BETA-HYDROXYBUTYRATE POLYMERASE (POLY(3-HYDROXYBUTYRATE) POLYMERASE) (PHB POLYMERASE) (PHB SYNTHASE) (POLY(3-HYDROXYALKANOATE) POLYMERASE) (PHA POLYMERASE) (PHA SYNTHASE) (POLYHYDROXYALKANOIC ACID SYNTHASE)
8680	21372		2.34	4.5E-01	11444786	NT	Homo sapiens hypothetical protein DKFZp47G183 (DKFZp47G183), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8897	21588	34728	0.86	4.5E-01	AE000218.1	NT	Escherichia coli K-12 MG1655 section 108 of 400 of the complete genome
9840	22491		1.02	4.5E-01	9630816	NT	Bombayx mori nuclear polyhedrosis virus, complete genome
10392	23038	36254	24.62	4.5E-01	M86006.1	EST_HUMAN	EST02531 Fetal brain, Stratiene (cat#936206) Homo sapiens cDNA clone HFBCY17
10392	23038	36255	24.62	4.5E-01	M86006.1	EST_HUMAN	EST02531 Fetal brain, Stratiene (cat#936206) Homo sapiens cDNA clone HFBCY17
10772	23455	36599	2.15	4.5E-01	AW591271.1	EST_HUMAN	xo14h01.x1 NCL CGAP_UK3 Homo sapiens cDNA clone IMAGE:2703985 3' similar to SW:INT6_MOUSE
11217	23880		1.52	4.5E-01	AV719382.1	EST_HUMAN	AV719382 GLC Homo sapiens cDNA clone GLCCE12 5'
11895	25384		3.52	4.5E-01	BE871461.1	EST_HUMAN	601449201F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3852961 5'
12540	24880		1.58	4.5E-01	BF337531.1	EST_HUMAN	602035275F1 NCL CGAP_Brn84 Homo sapiens cDNA clone IMAGE:4783290 5'
12611	24918		3.37	4.5E-01	11422099	NT	Homo sapiens testis-specific kinase 2 (TESK2), mRNA
2388	15109	27847	3.39	4.4E-01	P49765	SWISSPROT	VASCULAR ENDOTHELIAL GROWTH FACTOR B PRECURSOR (VEGF-B) (VEGF RELATED FACTOR)
3310	16070	28719	1.29	4.4E-01	AF088790.1	NT	Rattus norvegicus SynGAP-b mRNA, complete cds
3310	16070	28720	1.29	4.4E-01	AF088790.1	NT	Rattus norvegicus SynGAP-b mRNA, complete cds
3313	16073	28723	2.92	4.4E-01	BF056726.1	EST_HUMAN	7f91d02.y1 NCL CGAP_Br16 Homo sapiens cDNA clone IMAGE:3393795 5'
4209	16950		1.88	4.4E-01	BE378707.1	EST_HUMAN	601237139F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3608393 5'
5334	18137	30797	1.2	4.4E-01	P04929	SWISSPROT	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR
5334	18137	30798	1.2	4.4E-01	P04929	SWISSPROT	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR
5602	18397	31309	1.59	4.4E-01	S65019.1	NT	mucin [rats, Sprague-Dawley, sulfur-dioxide-treated tracheal epithelium, mRNA Partial, 390 nt]
5619	18415	31328	2	4.4E-01	AV720408.1	EST_HUMAN	AV720408 GLC Homo sapiens cDNA clone GLCCSC12 5'
5864	18651	31591	1.46	4.4E-01	AI198413.1	EST_HUMAN	q62h11.x1 NCL CGAP_Brn25 Homo sapiens cDNA clone IMAGE:1861125 3' similar to TR:Q29168 Q29168
5864	18651	31592	1.46	4.4E-01	AI198413.1	EST_HUMAN	q62h11.x1 NCL CGAP_Brn25 Homo sapiens cDNA clone IMAGE:1861125 3' similar to TR:Q29168 Q29168
6146	18923	31894	1.78	4.4E-01	AW080795.1	EST_HUMAN	UNKNOWN PROTEIN ;
6236	19010		1.42	4.4E-01	AA776132.1	EST_HUMAN	xc27e08.x1 NCL CGAP_Cot18 Homo sapiens cDNA clone IMAGE:2585510 3' similar to TR:O95154 O95154
7297	19980	33056	1.04	4.4E-01	AE000571.1	EST_HUMAN	AFLATOXIN B1-ALDEHYDE REDUCTASE ;
7723	25119		0.6	4.4E-01	AE001188.1	NT	ae85d11.s1 Stratiene schizo brain S11 Homo sapiens cDNA clone IMAGE:970965 3' similar to gb:M16038
7740	20436		9.71	4.4E-01	Z11676.1	NT	TYROSINE-PROTEIN KINASE LYN (HUMAN);
8661	21353	34500	0.84	4.4E-01	AA056427.1	EST_HUMAN	Helicobacter pylori 26695 section 49 of 134 of the complete genome
9049	21738	34896	0.7	4.4E-01	AF112540.1	NT	Treponema pallidum section 4 of 87 of the complete genome
							S. tuberosum mRNA for induced stolon tip protein (partial)
							z169a03.s1 Stratiene colon (#837204) Homo sapiens cDNA clone IMAGE:509836 3'
							HIV-1 isolate 0810746 from USA, envelope glycoprotein (env) gene, partial cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9082	21771	34934	0.57	4.4E-01	AW612578.1	EST_HUMAN	h105c08.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2854222 3' similar to
9190	21860	35025	1.24	4.4E-01	O62836	SWISSPROT	SW:MSH6_HUMAN P52701 DNA MISMATCH REPAIR PROTEIN MSH6 ;
9862	22512	35709	2.19	4.4E-01	AI28850.1	EST_HUMAN	ZINC FINGER X-CHROMOSOMAL PROTEIN
9863	22513		1.88	4.4E-01	P28922	SWISSPROT	q38909.x1 NCL_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1910921 3'
9897	22645	35857	4.31	4.4E-01	P35590	SWISSPROT	GLYCOPROTEIN B PRECURSOR (GLYCOPROTEIN 14)
10273	22921	36132	1.33	4.4E-01	S76404.1	NT	TYROSINE-PROTEIN KINASE RECEPTOR TIE-1 PRECURSOR
10273	22921	36133	1.33	4.4E-01	S76404.1	NT	beta-HKA=H,K-ATPase beta-subunit [rats, Genomic, 8983 nt, segment 2 of 2]
12148	24635	31095	3.44	4.4E-01		NT	beta-HKA=H,K-ATPase beta-subunit [rats, Genomic, 8983 nt, segment 2 of 2]
12579	24903	31000	3.35	4.4E-01	6677874	NT	Mus musculus sodium channel, type X, alpha polypeptide (Scn10a), mRNA
12683	24971		1.81	4.4E-01	9627742	NT	Autographa californica nucleopolyhedrovirus, complete genome
12766	25152		1.43	4.4E-01	P54725	SWISSPROT	UV EXCISION REPAIR PROTEIN PROTEIN RAD23 HOMOLOG A (HHR23A)
402	13187	25835	2.17	4.4E-01	AW363338.1	EST_HUMAN	RC2-C70320-281199-012-c07 CT0320 Homo sapiens cDNA
402	13187	25836	2.17	4.3E-01	AF155218.1	NT	Callithrix jacchus MW/LW opsin gene, upstream flanking region
2875	15642		1.64	4.3E-01	AF155218.1	NT	Callithrix jacchus MW/LW opsin gene, upstream flanking region
3056	15822	28466	0.75	4.3E-01	AW935269.1	EST_HUMAN	CM2-D70003-070200-077-c01 DT0003 Homo sapiens cDNA
4131	18873	29501	1.29	4.3E-01	J00306.1	NT	MRO-BN0070-270300-008-g04 BN0070 Homo sapiens cDNA
4374	13187	25835	1.18	4.3E-01	AF155218.1	NT	Human somatostatin 1 gene and flanks
4374	13187	25836	1.18	4.3E-01	AF155218.1	NT	Callithrix jacchus MW/LW opsin gene, upstream flanking region
4902	17629		1.19	4.3E-01	AL161502.2	NT	Callithrix jacchus MW/LW opsin gene, upstream flanking region
5280	18085	30742	0.8	4.3E-01	P48634	SWISSPROT	Callithrix jacchus MW/LW opsin gene, upstream flanking region
5280	18085	30743	0.8	4.3E-01	P48634	SWISSPROT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 14
5798	18589	31515	1.59	4.3E-01	BE181655.1	EST_HUMAN	LARGE PROLINE-RICH PROTEIN BAT2 (HLA-B-ASSOCIATED TRANSCRIPT 2)
5817	18606	31534	2.02	4.3E-01	AF179825.1	NT	LARGE PROLINE-RICH PROTEIN BAT2 (HLA-B-ASSOCIATED TRANSCRIPT 2)
6608	19371	32384	4.78	4.3E-01	AJ001678.1	NT	QV1-HT0638-070500-191-d08 HT0638 Homo sapiens cDNA
6689	19606	32646	0.6	4.3E-01	AF075629.1	NT	Salmlr sclerous difactory receptor (SSC186) gene, partial cds
6767	19511		0.91	4.3E-01	O33367	SWISSPROT	Coturnix coturnix japonica lfrG gene
7328	20011		1.88	4.3E-01	BF348001.1	EST_HUMAN	Equus caballus microsatellite LEX027
7498	20188	33260	0.61	4.3E-01	U51002.1	NT	DNA GYRASE SUBUNIT B
8326	21019		2.72	4.3E-01	U97040.1	NT	602023134F1 NCL_CGAP_Brm67 Homo sapiens cDNA clone IMAGE:4158296 5'
9154	21885	35053	0.96	4.3E-01	Y14604.1	NT	Mus musculus Dlx-2 gene, complete cds
9626	22279	35468	2.18	4.3E-01	AW630048.1	EST_HUMAN	Methanococcus voltae flagella-related protein C-1 (flaC-flaI) genes, complete cds
9626	22279	35469	2.18	4.3E-01	AW630048.1	EST_HUMAN	Erwinia amylovora rcsV gene
							hh74e10.y1 NCL_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2868554 5'
							hh74e10.y1 NCL_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2868554 5'

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Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLASTE Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10128	22776	35960	0.84	4.3E-01	AW170559.1	EST_HUMAN	xt63e05.x1 Soares_NHCC cervical_tumor Homo sapiens cDNA clone IMAGE:2698400 3' similar to
10409	23055	36272	0.5	4.3E-01	H66292.1	EST_HUMAN	TR:O00189 O00189 MU-ADAPTIN-RELATED PROTEIN 2 ;
10849	19606	32646	2.45	4.3E-01	AF075629.1	NT	y45605.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:208209 3'
11166	23833	37113	1.29	4.3E-01	AW993658.1	EST_HUMAN	Equus caballus microsatellite LEX027
11168	23833	37114	1.29	4.3E-01	AW993658.1	EST_HUMAN	RC3-BN0034-290200-013-c12 BN0034 Homo sapiens cDNA
11745	24336	37662	1.84	4.3E-01	AI874332.1	EST_HUMAN	RC3-BN0034-290200-013-c12 BN0034 Homo sapiens cDNA
12770	25025		2.18	4.3E-01	AJ003022.1	NT	ts64d04.x1 NCI_CGAP_Ov35 Homo sapiens cDNA clone IMAGE:2283351 3'
1337	15566	28761	1.54	4.2E-01	Q39102	SWISSPROT	Streptomyces coelicolor wihH gene
1941	14676		1.23	4.2E-01	AA761653.1	EST_HUMAN	CELL DIVISION PROTEIN FTSH HOMOLOG PRECURSOR
3596	18349	28990	4.4	4.2E-01	AE003947.1	NT	n24a09.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1286696 3'
3628	18381	29021	1.41	4.2E-01	AI280338.1	EST_HUMAN	Xyella fastidiosae, section 93 of 229 of the complete genome
3698	17886		0.85	4.2E-01	NI81203.1	EST_HUMAN	ql94b01.x1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:1879945 3'
3984	19713	29352	0.97	4.2E-01	Q04886	SWISSPROT	788IE1 fetal brain cDNA Homo sapiens cDNA clone 788IE1-K similar to R07879, Z40498
4649	17383	30015	4.88	4.2E-01	AA594093.1	EST_HUMAN	SOX-9 PROTEIN
4731	17463	30100	3.46	4.2E-01	R13467.1	EST_HUMAN	ni69h01.s1 NCI_CGAP_P110 Homo sapiens cDNA clone IMAGE:997777 similar to gb:M33600 HLA CLASS II HISTOCOMPATIBILITY ANTIGEN, DR-1 BETA CHAIN (HUMAN);
5626	18423	31336	0.82	4.2E-01	BF242055.1	EST_HUMAN	y77e01.r1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:28278 5'
5693	18487	31408	1.53	4.2E-01	AW854162.1	EST_HUMAN	601879721F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4108493 5'
6112	18889	31858	1.01	4.2E-01	AL163247.2	NT	RC3-CT0254-060400-029-g04 CT0254 Homo sapiens cDNA
6852	19552	32582	10.8	4.2E-01	AU158472.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C047
6852	19552	32583	10.8	4.2E-01	AU158472.1	EST_HUMAN	AU158472 PLACE2 Homo sapiens cDNA clone PLACE2000470 3'
6911	25101	32694	2.15	4.2E-01	S82504.1	NT	AU158472 PLACE2 Homo sapiens cDNA clone PLACE2000470 3'
6993	19686	32734	7	4.2E-01	AL161547.2	NT	Brcal=breast cancer gene [rats, WF, spleen, Genomic, 419 nt, segment 2 of 2]
7891	20586	33715	2.21	4.2E-01	AW957448.1	EST_HUMAN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 47
7891	20586	33716	2.21	4.2E-01	AW957448.1	EST_HUMAN	EST369413 IMAGE resequences, IMAGE Homo sapiens cDNA
8106	20800	33932	0.61	4.2E-01		NT	EST369413 IMAGE resequences, IMAGE Homo sapiens cDNA
9870	22520		0.94	4.2E-01	AA705007.1	EST_HUMAN	Homo sapiens cytochrome c oxidase subunit VIc (COX6C), nuclear gene encoding mitochondrial protein, mRNA
10081	22729	35944	0.45	4.2E-01	AF181854.1	NT	z95f01.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:462849 3'
10393	23039	38256	1.78	4.2E-01	AW863666.1	EST_HUMAN	Lassa virus strain 803213 glycoprotein precursor and nucleoprotein genes, complete cds
10972	23648	36901	2.69	4.2E-01	AB023489.1	NT	MR3-SN0010-280300-103-h07 SN0010 Homo sapiens cDNA
11370	23977	37277	2.11	4.2E-01	BE066485.2	EST_HUMAN	Oryzias latipes OIGC7 mRNA for membrane guanylyl cyclase, complete cds
1072	13830	26488	1.83	4.1E-01	AI905481.1	EST_HUMAN	601660352R1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3906085 3'
							RC-BT091-210198-142 BT091 Homo sapiens cDNA

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Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1081	13839	26497	1.1	4.1E-01	AV705243.1	EST_HUMAN	AV705243 ADB Homo sapiens cDNA clone ADBAHF08 5'
1081	13839	26498	1.1	4.1E-01	AV705243.1	EST_HUMAN	AV705243 ADB Homo sapiens cDNA clone ADBAHF08 5'
2715	15422	28161	1.1	4.1E-01	7705283	NT	Homo sapiens anaphase-promoting complex subunit 7 (APC7), mRNA
2941	15706	28355	2.17	4.1E-01	AL161536.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 36
2941	15706	28356	2.17	4.1E-01	AL161536.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 36
3754	16506	29142	0.88	4.1E-01	AW961292.1	EST_HUMAN	EST1373364 MAGG resequences, MAGG Homo sapiens cDNA
3754	16506	29143	0.88	4.1E-01	AW961292.1	EST_HUMAN	EST1373364 MAGG resequences, MAGG Homo sapiens cDNA
4241	16982	29607	2.93	4.1E-01	AJ249207.1	NT	Rhodococcus sp. AD45 isoG, isoH, isoI, isoA, isoB, isoC, isoD, isoE and isoF genes
4271	17011		0.82	4.1E-01	AA909287.1	EST_HUMAN	om33402.s1 Soares_NFL_T_GBC S1 Homo sapiens cDNA clone NPCBDF10 5'
4618	17353	29688	1.46	4.1E-01	AV747890.1	EST_HUMAN	AV747890 NPC Homo sapiens cDNA clone NPCBDF10 5'
4868	18057	28708	2.48	4.1E-01	AA906344.1	EST_HUMAN	oj94b08.s1 Soares_NFL_T_GBC S1 Homo sapiens cDNA clone IMAGE:1505943 3'
5899	18684	31632	4.72	4.1E-01	BF681393.1	EST_HUMAN	602156690F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4297319 5'
7332	20014	33092	2.76	4.1E-01	U67635.1	NT	Methanococcus jannaschii section 77 of 150 of the complete genome
7935	20630	33757	1.38	4.1E-01	BF574604.1	EST_HUMAN	602133261F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4288238 5'
8988	21678	34827	1.39	4.1E-01	6755521	NT	Mus musculus signaling intermediate in Toll pathway-evolutionarily conserved (Slpec-pending), mRNA
9465	22075		0.67	4.1E-01	AF160597.1	NT	Volvaxo gymnocaudus Vgym560 cytochrome b (cytb) gene, complete cds; mitochondrial gene for
10163	22811		1.05	4.1E-01	AL139076.2	NT	Campylobacter jejuni NCTC11168 complete genome; segment 3/6
10310	22857	36173	0.91	4.1E-01	AV649579.1	EST_HUMAN	AV649579 GLC Homo sapiens cDNA clone GLCBVD12 3'
10404	23050	36267	0.61	4.1E-01	P18584	SWISSPROT	PROBABLE SERINE PROTEASE DO-LIKE PRECURSOR (59 KDA IMMUNOGENIC PROTEIN) (SK59)
10404	23050	36268	0.61	4.1E-01	P18584	SWISSPROT	PROBABLE SERINE PROTEASE DO-LIKE PRECURSOR (59 KDA IMMUNOGENIC PROTEIN) (SK59)
10478	23124		1.33	4.1E-01	BF349382.1	EST_HUMAN	CM2-HT0137-200999-010-608 HT0137 Homo sapiens cDNA
10743	23430	36673	80.48	4.1E-01	X58700.1	NT	Zea mays ZMPMS2 gene for 19 kDa zein protein
11366	23177	36404	2	4.1E-01	Q09470	SWISSPROT	VOL-TAGE-GATED POTASSIUM CHANNEL PROTEIN KV1.1 (HUK1)(HBK1)
12475	25360		2.62	4.1E-01	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
1016	13775	28435	0.82	4.0E-01	8404658	NT	Laqueus rubellus mitochondrion, complete genome
1316	14065	28739	0.95	4.0E-01	AF203478.1	NT	Drosophila melanogaster Dalmatian (dmt) mRNA, complete cds
1468	14216		4.05	4.0E-01		NT	Mus musculus platelet derived growth factor receptor, beta polypeptide (Pdgrfb), mRNA
1999	15583	27457	1.16	4.0E-01	Z96933.1	NT	Ascaris immitis masc2 gene
1999	15583	27458	1.16	4.0E-01	Z96933.1	NT	Ascaris immitis masc2 gene
2156	14886	27619	1.19	4.0E-01	AE001931.1	NT	Delnocooccus radiodurans R1 section 68 of 229 of the complete chromosome 1
2156	14886	27620	1.19	4.0E-01	AE001931.1	NT	Delnocooccus radiodurans R1 section 68 of 229 of the complete chromosome 1
2808	12852	25595	1.4	4.0E-01	6878490	NT	Mus musculus ubiquitin-protein ligase e3 component R-recogin (Ubr1), mRNA

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2968	15734	28383	1.1	4.0E-01	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
2968	16734	28384	1.1	4.0E-01	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
3683	16436	29080	1.98	4.0E-01	AF068903.1	NT	Streptococcus pneumoniae Y1C (Y1C), penicillin-binding protein 2x (pbp2x), and undecaprenyl-phosphate-UDP-MurNAc-pentapeptide phospho-MurNAc-pentapeptide transferase (mraY) genes, complete cds
3807	16559	29191	3.38	4.0E-01	AJ277511.1	NT	Ovis aries partial JD2 gene for T cell receptor delta chain (TORDJ2), exon 1
3807	16559	29192	3.38	4.0E-01	AJ277511.1	NT	Ovis aries partial JD2 gene for T cell receptor delta chain (TORDJ2), exon 1
4767	17499		7.97	4.0E-01	Q31949	SWISSPROT	NADH-PLASTOQUINONE OXIDOREDUCTASE CHAIN 5, CHLOROPLAST
5820	18609	31538	1.23	4.0E-01	AW970610.1	EST_HUMAN	EST382691 MAGE resequences, MAGK Homo sapiens cDNA
6345	19116	32104	0.94	4.0E-01	P27285	SWISSPROT	STRUCTURAL POLYPROTEIN (P130) [CONTAINS: COAT PROTEIN C; SPIKE GLYCOPROTEINS E3, E2 AND E1; 6 KD PEPTIDE]
7728	20391	33504	0.66	4.0E-01	P27546	SWISSPROT	MICROTUBULE-ASSOCIATED PROTEIN 4
7829	20524	33649	0.44	4.0E-01	BF092634.1	EST_HUMAN	MR4-TN0110-180900-202-g02 TN0110 Homo sapiens cDNA
7910	20605	33736	1.04	4.0E-01	AB016625.1	NT	Homo sapiens OCTN2 gene, complete cds
8904	21595	34736	1.17	4.0E-01	AA323289.1	EST_HUMAN	EST26066 Cerebellum II Homo sapiens cDNA 5' end similar to EST containing Alu repeat
11560	24159		2.03	4.0E-01	BF030262.1	EST_HUMAN	601558283F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3828092 5'
11721	24315		2.83	4.0E-01	L76080.1	NT	Synechocystis sp. PCC 9413 transposase gene, complete cds
12162	25222		2.26	4.0E-01	AL163300.2	NT	Homo sapiens chromosome 21 segment HS21C100
12684	24972		2.2	4.0E-01	P36049	SWISSPROT	HYPOTHETICAL 49.7 KD PROTEIN IN GIN2-STES INTERGENIC REGION
1366	14104	26780	1.85	3.9E-01	AF066618.1	NT	Gorilla gorilla carboxyl-ester lipase (CEL) gene, complete cds
2648	15358	28101	3.34	3.9E-01	AB033019.1	NT	Homo sapiens mRNA for KIAA1193 protein, partial cds
2709	15416	28153	4.27	3.9E-01	X82032.1	NT	H. sapiens B-myb gene
2709	15416	28154	4.27	3.9E-01	X82032.1	NT	H. sapiens B-myb gene
3093	15888	28499	4.73	3.9E-01	AJ225896.1	NT	Sinorhizobium meliloti egl, syrB2, cys3 genes and orf3
4059	16804	29435	1.05	3.9E-01	BF592611.1	EST_HUMAN	7/61401.x1 NCI_CGAP_Br16 Homo sapiens cDNA clone IMAGE:3339189 3'
4932	17680	30270	1.74	3.9E-01	BE728667.1	EST_HUMAN	601563948F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3833689 5'
5843	18631	31566	3.91	3.9E-01	BF208036.1	EST_HUMAN	601862362F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:4082055 5'
7854	20549	33674	0.92	3.9E-01	U79415.1	NT	Homo sapiens prepro dipeptidyl peptidase I (DPP-I) gene, complete cds
8760	21452	34600	0.81	3.9E-01	AW177011.1	EST_HUMAN	CM3-CT0105-170899-004-b08 CT0105 Homo sapiens cDNA
8769	21461		0.58	3.9E-01	BF346634.1	EST_HUMAN	602019944F1 NCI_CGAP_Brm87 Homo sapiens cDNA clone IMAGE:4155322 5'
9134	21822	34988	1.26	3.9E-01	AW195888.1	EST_HUMAN	xn86404.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2701351 3' similar to TR:O94821
9445	22122	35301	1.46	3.9E-01	A0937337.1	EST_HUMAN	wp76a02.x1 NCI_CGAP_Brm25 Homo sapiens cDNA clone IMAGE:2467658 3' similar to SW:RFX5_HUMAN P48882 BINDING REGULATORY FACTOR.;

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9778	22429	35635	3.03	3.9E-01	M19879.1	NT	Human clabindin 27 gene, exons 10 and 11, and L1 and Alu repeats
9845	22496		0.98	3.9E-01	11465620	NT	Porphyra purpurea mitochondrion, complete genome
10068	22714	35932	0.77	3.9E-01	D86722.1	NT	Nicotiana tabacum mRNA for TATA binding protein (TBP), complete cds
10722	23410		1.98	3.9E-01	AV695974.1	EST_HUMAN	AV695974 GK0 Homo sapiens cDNA clone GKCBQC11 5'
11753	24344	37874	1.47	3.9E-01	AV702623.1	EST_HUMAN	AV702623 ADB Homo sapiens cDNA clone ADBDBE06 5'
11948	25295		3.37	3.9E-01	AF304354.1	NT	Homo sapiens proteoglycan 3 (PRG3) gene, complete cds
12066	24581		2.08	3.9E-01	Q61670	SWISSPROT	HOMEOBOX PROTEIN HLX1
12559	24891		1.44	3.9E-01	11433335	NT	Homo sapiens hypothetical protein FLJ10583 (FLJ10583), mRNA
156	12971		8.33	3.8E-01	7019488	NT	Homo sapiens protein kinase PKNbeta (pknbeta), mRNA
1863	14601		1.03	3.8E-01	AE003870.1	NT	Xylella fastidiosa, section 16 of 229 of the complete genome
2460	15178	27918	1.28	3.8E-01	U41846.1	NT	Oeanorhabdus briggsae acetylcholinesterase (ace-1) gene, complete cds
2576	15280	28027	1.92	3.8E-01	AF214117.1	NT	Arabidopsis thaliana putative c-myc-like transcription factor (MYB3R-3) mRNA, complete cds
2638	15601	28092	3.96	3.8E-01	6878002	NT	Mus musculus solute carrier family 1, member 6 (Slc1a6), mRNA
3003	15769		1.14	3.8E-01	AJ251057.1	NT	Human immunodeficiency virus type 1 complete genome (isolate 98SE-MP1213)
3043	15809	28456	1.39	3.8E-01	AF043383.1	NT	Pleuroctes americanus aminopeptidase N (ampN) gene, partial cds
3477	16233	28887	7.98	3.8E-01	AL161518.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 30
3527	16283		0.79	3.8E-01	A1807219.1	EST_HUMAN	wf38b12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2357855 3'
3541	16283		1.22	3.8E-01	A1807219.1	EST_HUMAN	wf38b12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2357855 3'
3739	16492	28127	1.15	3.8E-01	BE154080.1	EST_HUMAN	PMO-HT0339-200400-010-G01 HT0339 Homo sapiens cDNA
3897	16847	29287	0.97	3.8E-01	6754095	NT	Mus musculus general transcription factor II J (GTF2j), mRNA
4043	16786	29416	0.74	3.8E-01	AJ271361.2	NT	Takifugu rubripes wnt2 (partial), frank1, cfr and frank2 (partial) genes
5522	18320	31221	1.42	3.8E-01	Q04888	SWISSPROT	TRANSCRIPTION FACTOR SOX-10
6247	19021		0.74	3.8E-01	S48825.1	NT	piron protein (mink, Genomic, 2446 nt)
6528	18294	32298	5.5	3.8E-01	BE072399.1	EST_HUMAN	QV3-BT0537-271299-049-e02 BT0537 Homo sapiens cDNA
6662	18579	32614	4.58	3.8E-01	AJ374601.1	EST_HUMAN	ta54f11.x1 Soares_total_fetus_Nb2HF8_gw Homo sapiens cDNA clone IMAGE:2047917 3' similar to
6840	19502	32527	1.25	3.8E-01	AL161513.2	NT	contains Alu repetitive element
7416	20093		4.42	3.8E-01	XG1597.1	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 25
8198	20890	34028	0.86	3.8E-01	M81385.1	NT	M.musculus gene for kallikrein-binding protein
8455	21147	34289	2.04	3.8E-01	AB046851.1	NT	Mouse liver receptor homologous protein (LRH-1) mRNA, complete cds
8523	21215	34358	1.02	3.8E-01	11441264	NT	Homo sapiens mRNA for KIAA1631 protein, partial cds
8716	21408	34551	1.28	3.8E-01	AL163279.2	NT	Homo sapiens FOS-like antigen-1 (FOSL1), mRNA
						EST_HUMAN	Homo sapiens chromosome 21 segment HS21C079
9461	22011		3.55	3.8E-01	T95413.1	EST_HUMAN	ye43h06.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:120539 5' similar to contains
							Alu repetitive element; contains P1R5 repetitive element;

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10895	23386		1.67	3.8E-01	AV755814.1	EST_HUMAN	AV755814 BM Homo sapiens cDNA clone BMFBCE07 5'
11521	24121		3.18	3.8E-01	BE719219.1	EST_HUMAN	RCO-HT0841-040800-032-b12 HT0841 Homo sapiens cDNA
11693	24288	37610	2.27	3.8E-01	R42550.1	EST_HUMAN	Y92h11.s1 Soares infant brain INIB Homo sapiens cDNA clone IMAGE:30289 3'
11693	24288	37611	2.27	3.8E-01	R42550.1	EST_HUMAN	Y92h11.s1 Soares infant brain INIB Homo sapiens cDNA clone IMAGE:30289 3'
12149	24636		4.76	3.8E-01	AE001124.1	NT	Borrelia burgdorferi (section 10 of 70) of the complete genome
12270	25316		2.08	3.8E-01	U94788.1	NT	Human p53 (TP53) gene, complete cds
12384	24779		3.39	3.8E-01	BE829256.1	EST_HUMAN	QV3-ET0063-190700-271-a05 ET0063 Homo sapiens cDNA
12723	24994		1.54	3.8E-01	U78031.1	NT	Mus musculus apoptosis inhibitor bel-x (bel-x) gene, exon 3 and complete cds
12771	25291		1.74	3.8E-01	AF291483.1	NT	Mus musculus vomeronasal receptor V1RA4 (V1ra4) gene, complete cds
12788	25040	30966	1.51	3.8E-01	AF194972.1	NT	Mus musculus developmental control protein mRNA, partial cds
2486	15203	27944	12.24	3.7E-01	AB037831.1	NT	Homo sapiens mRNA for KIAA1410 protein, partial cds
3453	16209	28860	9.64	3.7E-01	AF056336.1	NT	Danio rerio bone morphogenetic protein 4 precursor (BMP4) gene, complete cds
4204	16945	29572	7.99	3.7E-01	AJ218707.1	EST_HUMAN	pk39a07.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:1510188 3'
4286	17025	29651	1.3	3.7E-01	AW878037.1	EST_HUMAN	MR3-OT0007-080300-104-p02 OT0007 Homo sapiens cDNA
4357	17095	29730	2.55	3.7E-01	AE002408.1	NT	Neisseria meningitidis serogroup B strain MO58 section 50 of 206 of the complete genome
5676	18470	31386	1.15	3.7E-01	AF135187.1	NT	Homo sapiens interferon-induced protein p78 (MX1) gene, complete cds
5960	18647	31588	0.9	3.7E-01	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
6417	19185	32183	0.66	3.7E-01	M10806.1	NT	Chicken (White leghorn) delta-1 and delta-2 crystallin genes, complete cds
6436	19204		0.72	3.7E-01	L10353.1	NT	Mus saxicola hemoglobin mRNA, complete cds
7043	19734	32794	3.23	3.7E-01	11525943	NT	Homo sapiens tumor endothelial marker 7 precursor (TEM7) mRNA
7685	20349	33463	0.6	3.7E-01	T6802.1	EST_HUMAN	ye50a07.r3 Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:66324 5'
7719	20383	33497	0.56	3.7E-01	AW511326.1	EST_HUMAN	hd45d05.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2912457 3' similar to contains Alu repetitive element; contains L1 L2 L1 repetitive element;
8227	20921	34059	2.07	3.7E-01	11436739	NT	Homo sapiens chromosome 12 open reading frame 4 (C12ORF4), mRNA
8227	20921	34060	2.07	3.7E-01	11436739	NT	Homo sapiens chromosome 12 open reading frame 4 (C12ORF4), mRNA
8263	20957	34096	0.65	3.7E-01	AA02912.1	EST_HUMAN	ok43b11.s1 NCL CGAP Le12 Homo sapiens cDNA clone IMAGE:1516701 3'
9101	21769		1.31	3.7E-01	AJ271386.1	NT	Gallus gallus mRNA for beta-carotene 15,15'-dioxygenase (bCDO gene)
10069	22717		0.8	3.7E-01	K00691.1	NT	mouse Ig germline alpha membrane exons region
10110	22758	35970	4.12	3.7E-01	AJ336411.1	EST_HUMAN	q146b07.x1 Soares_fetal_lung_NbHL18W Homo sapiens cDNA clone IMAGE:1950997 3'
10764	23448	36690	1.98	3.7E-01	X05958.1	NT	Rabbit mRNA for fast skeletal muscle myosin heavy chain (MHC)
10957	23633	36882	2.81	3.7E-01	AJ297357.1	NT	Homo sapiens partial LIMD1 gene for LIM domains containing protein 1 and KIAA0851 gene
10957	23633	36883	2.81	3.7E-01	AJ297357.1	NT	Homo sapiens partial LIMD1 gene for LIM domains containing protein 1 and KIAA0851 gene
11443	23210	36441	2.75	3.7E-01	X04122.1	NT	Bovine mRNA for terminal deoxynucleotidyltransferase (TdT) (EC 2.7.7.31)
11676	24271	37593	1.43	3.7E-01	D79348.1	EST_HUMAN	HUM230A06B Human aorta polyA+ (TF-ujwara) Homo sapiens cDNA clone GEN-230A06 5'

Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11771	24362		2.87	3.7E-01	6677678	NT	Mus musculus retinoblastoma 1 (Rb1), mRNA
11869	24943		2.11	3.7E-01	J04982.1	NT	Human heart/skeletal muscle ATP/ADP translocator (ANT1) gene, complete cds
12033	24558		3.09	3.7E-01	AJ243525.1	NT	Chlamydomonas reinhardtii psittaci partial omp1 gene for outer membrane protein 1
12488	24847		1.9	3.7E-01	AL121154.1	EST_HUMAN	DKFZp762K075_r1 762 (synonym: hmel2) Homo sapiens cDNA clone DKFZp762K075 5'
12548	24886	30995	4.03	3.7E-01	Y18000.1	NT	Homo sapiens NF2 gene
254	13062	25701	2.17	3.6E-01	AJ009609.1	NT	Brassica napus mRNA for MAP4K alpha2 protein
975	13740		8.22	3.6E-01	U89241.1	NT	Human mlbp gene, partial cds
1291	14040	26713	3.83	3.6E-01	T80255.1	EST_HUMAN	y03a05.r1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:24443 5'
1291	14040	26714	3.83	3.6E-01	T80255.1	EST_HUMAN	y03a05.r1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:24443 5'
1909	14646	27356	6.73	3.6E-01	AW590184.1	EST_HUMAN	hg33102.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2947419 3'
1909	14646	27357	6.73	3.6E-01	AW590184.1	EST_HUMAN	hg33102.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2947419 3'
1944	14679	27393	5.7	3.6E-01	AF216207.1	NT	Mus musculus ribosomal protein S19 (Rps19) gene, complete cds
2047	14780		1.39	3.6E-01	AF066927.1	NT	Rattus norvegicus repeat element associated with the Rasgrf1 gene
2267	14993		1.05	3.6E-01	AB002321.1	NT	Human mRNA for KIAA0323 gene, partial cds
2389	15110		2.69	3.6E-01	X78725.1	NT	P. irregularis (P3804) gene for actin
2479	15197	27936	1.23	3.6E-01	L05435.1	NT	Rattus norvegicus synaptic vesicle protein (SV2) mRNA, complete cds
2479	15197	27937	1.23	3.6E-01	L05435.1	NT	Rattus norvegicus synaptic vesicle protein (SV2) mRNA, complete cds
2491	15208	27950	1.43	3.6E-01	AW812033.1	EST_HUMAN	RC5-ST0171-181099-011-g07 ST0171 Homo sapiens cDNA
2836	15348	28090	1.44	3.6E-01	P24206	SWISSPROT	PROTEIN-L-ISOASPARTATE O-METHYLTRANSFERASE (PROTEIN-BETA-ASPARTATE METHYLTRANSFERASE) (PIMT) (PROTEIN L-ISOASPARTYL METHYLTRANSFERASE) (L-ISOASPARTYL PROTEIN CARBOXYL METHYLTRANSFERASE)
2900	17884		7.16	3.6E-01	AF199485.1	NT	Drosophila melanogaster sugar transporter 3 (sug3) mRNA, complete cds
3462	16218	28871	2.16	3.6E-01	X78758.1	NT	H. sapiens serotonin transporter gene, exons 9 and 10
3462	16218	28872	2.16	3.6E-01	X78758.1	NT	H. sapiens serotonin transporter gene, exons 9 and 10
4375	17112	29745	1.3	3.6E-01	BE707883.1	EST_HUMAN	RC1-H10545-150600-014-b12 HT0545 Homo sapiens cDNA
4948	17875	30285	2.38	3.6E-01	AW339393.1	EST_HUMAN	ha02g04.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2872566 3'
5298	18103	30762	0.82	3.6E-01	AJ006565.1	NT	Homo sapiens lipo gene intron 5
5995	18776	31738	0.85	3.6E-01	P16431	SWISSPROT	FORMATE HYDROGENLYASE SUBUNIT 5 PRECURSOR (FHL SUBUNIT 5) (HYDROGENASE-3 COMPONENT E)
6396	19155	32154	1.74	3.6E-01	Y10196.1	NT	Homo sapiens PHF5 gene
7048	19739		3.2	3.6E-01	R94090.1	EST_HUMAN	y074a06.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:275987 5'
7193	19889	32843	1.9	3.6E-01	AW027174.1	EST_HUMAN	w72c10.x1 Soares thymus NHFTh Homo sapiens cDNA clone IMAGE:2513010 3' similar to TR:O15117
8123	20817	33953	0.58	3.6E-01	P98167	SWISSPROT	O15117 FYN BINDING PROTEIN. [1]; SCO-SPONDIN

Table 4

Single Exon Probes Expressed In Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8177	20871	34005	11.45	3.6E-01	AL161593.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 79
8900	21591	34731	2.74	3.6E-01	4504956	NT	Homo sapiens lysosomal-associated membrane protein 2 (LAMP2), transcript variant LAMP2A, mRNA
8900	21591	34732	2.74	3.6E-01	4504958	NT	Homo sapiens lysosomal-associated membrane protein 2 (LAMP2), transcript variant LAMP2A, mRNA
9091	21780	34944	1.17	3.6E-01	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
9299	21968	35139	1.04	3.6E-01	X17550.1	NT	D. melanogaster singed gene, exons 3, 4, 5 & 6
9299	21966	35140	1.04	3.6E-01	X17550.1	NT	D. melanogaster singed gene, exons 3, 4, 5 & 6
9369	21944		0.57	3.6E-01	X62825.1	NT	D. melanogaster singed gene, exons 3, 4, 5 & 6
9893	22543	35621	14.67	3.6E-01	Q53194	SWISSPROT	PROBABLE PEPTIDE ABC TRANSPORTER ATP-BINDING PROTEIN Y4TS
9893	22543	35735	0.51	3.6E-01	AW752901.1	EST_HUMAN	MR2-CT0222-211099-002-b10 CT0222 Homo sapiens cDNA
9893	22543	35736	0.51	3.6E-01	AW752901.1	EST_HUMAN	MR2-CT0222-211099-002-b10 CT0222 Homo sapiens cDNA
10884	23544	36791	3.31	3.6E-01	BE902390.1	EST_HUMAN	60187641BF1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3958997 5'
11052	23722	36993	4.12	3.6E-01	AB004293.1	NT	Arabidopsis thaliana mRNA for SigB, complete cds
11421	23188	36419	3.4	3.6E-01	AE000856.1	NT	Methanobacterium thermoautotrophicum from bases 702375 to 714311 (section 62 of 148) of the complete genome
11903	25415		1.83	3.6E-01	Y19210.1	NT	Homo sapiens h-hb5 gene for hair keratin, exons 1 to 9
11978	24522		1.4	3.6E-01	D90901.1	NT	Synechocystis sp. PCC6803 complete genome, 3/27, 271600-402289
11987	24528		3.89	3.6E-01	AE000335.1	NT	Escherichia coli K-12 MG1655 section 225 of 400 of the complete genome
12135	24624		4	3.6E-01	U66888.1	NT	Mus musculus Emr1 mRNA, complete cds
12493	24850		2.12	3.6E-01	11432598	NT	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (trithorax (Drosophila) homolog); translocated to, 10 (AF10), mRNA
12746	25363		2.23	3.6E-01	AW190229.1	EST_HUMAN	x60e11.x1 NCL CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2879116 3' similar to gb:K00558 TUBULIN ALPHA-1 CHAIN (HUMAN);
204	13017	25657	2.05	3.5E-01	6678933	NT	Mus musculus mannose receptor, C type 2 (Mrc2), mRNA
708	13482	26131	1.59	3.5E-01	7708136	NT	Homo sapiens GAP-like protein (LOC51306), mRNA
708	13482	26132	1.59	3.5E-01	7708136	NT	Homo sapiens GAP-like protein (LOC51306), mRNA
762	13535	26194	4.25	3.5E-01	BF129796.1	EST_HUMAN	601811060R1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4053951 3'
1615	14362	27053	1.1	3.5E-01	BF310688.1	EST_HUMAN	601894653F2 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4124244 5'
1636	14362	27069	1.96	3.5E-01	U35776.1	NT	Rattus norvegicus ADP-ribosylation factor-directed GTPase activating protein mRNA, complete cds
2281	15006	27747	1.35	3.5E-01	P06798	SWISSPROT	HOMEOBOX PROTEIN HOX-A4 (HOX-1.4) (MH-3)
2612	15600	28096	1.76	3.5E-01	AA223252.1	EST_HUMAN	z08409.s1 Stragene NT2 neuronal precursor 937230 Homo sapiens cDNA clone IMAGE:650872 3'

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Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3785	16537		0.85	3.5E-01	AA642138.1	EST_HUMAN	nr60403.s1 NCI_CGAP_Lyn3 Homo sapiens cDNA clone IMAGE:1172357 3'
4231	16972	29596	1.87	3.5E-01	AF071253.1	NT	Danio rerio homeobox protein (hoxb5b) gene, complete cds
4443	17179	29805	0.94	3.5E-01	BE146585.1	EST_HUMAN	RC5-HT0218-181099-011-g02 HT0218 Homo sapiens cDNA
4627	17362	29895	1.02	3.5E-01	Y18477.1	NT	Mus musculus Alox12b gene 5' flanking region
4880	17607	30230	4.58	3.5E-01	M18349.1	NT	Rat leukocyte common antigen (L-CA) gene, exons 1 through 5
5251	18057	30685	0.76	3.5E-01	Q96887	SWISSPROT	EARLY E2A DNA-BINDING PROTEIN
5251	18057	30686	0.76	3.5E-01	Q96887	SWISSPROT	EARLY E2A DNA-BINDING PROTEIN
5462	18261	31152	1.13	3.5E-01	D42045.1	NT	Human mRNA for KIAA0086 gene, complete cds
6143	18921		0.96	3.5E-01	AW863916.1	EST_HUMAN	PM4-SN0012-030400-001-a11 SN0012 Homo sapiens cDNA
6314	19085	32070	0.6	3.5E-01	AA431833.1	EST_HUMAN	zw7903.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:782429 5' similar to TR:G1068935
6359	19129	32124	0.96	3.5E-01	U37150.1	NT	Bos taurus peptide methionine sulfoxide reductase (msrA) mRNA, complete cds
6566	19331	32338	1.08	3.5E-01	O24357	SWISSPROT	GLUCOSE-6-PHOSPHATE 1-DEHYDROGENASE, CHLOROPLAST PRECURSOR (G6PD)
6956	19438		4.24	3.5E-01	X08505.1	NT	Sacchara mRNA for CD31 protein (PECAM-1)
7441	20118	33207	0.55	3.5E-01	P47281	SWISSPROT	HISTIDYL-TRNA SYNTHETASE (HISTIDINE-TRNA LIGASE) (HISRS)
7441	20118	33208	0.55	3.5E-01	P47281	SWISSPROT	HISTIDYL-TRNA SYNTHETASE (HISTIDINE-TRNA LIGASE) (HISRS)
7970	20665		2.19	3.5E-01	11448042	NT	Homo sapiens tumor protein p53-binding protein, 2 (TP53BP2), mRNA
7973	20688	33790	0.71	3.5E-01	BF368871.1	EST_HUMAN	RC4-ET0024-260600-014-c07 ET0024 Homo sapiens cDNA
8366	21059		0.63	3.5E-01	AF051561.1	NT	Rattus norvegicus Na-K-Cl cotransporter (Nkcc1) mRNA, complete cds
8825	21517	34662	1.17	3.5E-01	4507610	NT	Homo sapiens tyrosine kinase non-receptor 1 (TNK1), mRNA
9636	22288	35481	1.52	3.5E-01	Q02294	SWISSPROT	VOLTAGE-DEPENDENT N-TYPE CALCIUM CHANNEL ALPHA-1B SUBUNIT (CALCIUM CHANNEL, L TYPE, ALPHA-1 POLYPEPTIDE ISOFORM 5) (BRAIN CALCIUM CHANNEL III) (BIII)
9786	22437	35644	5.64	3.5E-01	Z28825.1	NT	X.laavis gene for albumin including HP1 enhancer
9867	22517	35713	0.96	3.5E-01	BE174794.1	EST_HUMAN	QV2-HT0577-080400-128-c07 HT0577 Homo sapiens cDNA
10635	23327	36564	2.76	3.5E-01	X61084.1	NT	C.griseus rhodopsin gene for opsin protein
10946	23625	36875	2.39	3.5E-01	AJ243178.1	NT	Gallus gallus SPARC gene for osteonectin, promoter and exon 1
10946	23625	36876	2.39	3.5E-01	AJ243178.1	NT	Gallus gallus SPARC gene for osteonectin, promoter and exon 1
11505	24106	37419	1.34	3.5E-01	U07000.1	NT	Human breakpoint cluster region (BCR) gene, complete cds
11585	24184	37499	1.64	3.5E-01	N77597.1	EST_HUMAN	yz90h12.r1 Soares_multiple_sclerosis_2NbhMSP Homo sapiens cDNA clone IMAGE:290375 5'
11619	24216		1.71	3.5E-01	M82885.1	NT	Drosophila melanogaster dual bar protein (BarH2) gene, exon 1
11684	24279	37601	1.51	3.5E-01	U05145.1	NT	Human glucokinase (GCK) gene, repeat polymorphism
11776	24367		1.36	3.5E-01	A064773.1	EST_HUMAN	HA0542 Human fetal liver cDNA library Homo sapiens cDNA
12063	24578		1.47	3.5E-01	X64585.1	NT	B.taurus atpA1 gene for F(0)F(1) ATP synthase alpha-subunit
12214	24676		2.32	3.5E-01	AE001774.1	NT	Thermotoga maritima section 86 of 136 of the complete genome

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Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12402	24787		1.4	3.5E-01	AE001691.1	NT	Thermotoga maritima section 3 of 136 of the complete genome
12703	26269	30723	3.33	3.5E-01	H80814.1	EST_HUMAN	ys64f11.r1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:219597 5'
12793	26269	30724	3.33	3.5E-01	H80814.1	EST_HUMAN	ys64f11.r1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:219597 5'
691	13466		1.85	3.4E-01	AJ242958.1	NT	Homo sapiens partial N-myc (exon 3), HPV45 L2, HPV45 L1, HPV45 E6, HPV45 E7 and HPV45 E1 genes isolated from IC4 cervical carcinoma cell line
955	13720	26386	7.61	3.4E-01	Y09738.2	NT	Pseudomonas fluorescens colR, colS genes,orf222 and partial inaA gene
1303	14052	26725	1.72	3.4E-01	Y00554.1	NT	Azotobacter vinelandii nifA gene for NifA protein (positive regulatory element)
2400	15121	27858	2.92	3.4E-01	D90909.1	NT	Synechocystis sp. PCC6803 complete genome, 11/27, 1311235-1430418
3007	15767	28415	0.85	3.4E-01	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
3001	15767	28416	0.85	3.4E-01	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
3146	15910	28555	1.08	3.4E-01	D90909.1	NT	Synechocystis sp. PCC6803 complete genome, 11/27, 1311235-1430418
3159	15922	28568	6.23	3.4E-01	U83905.1	NT	Canis familiaris rod photoreceptor cGMP-gated channel alpha-subunit (CNGC1) mRNA, complete cds
3338	16098	28749	0.9	3.4E-01	AF034862.1	NT	Homo sapiens pulmonary surfactant protein D, promoter region and exon 1
3522	16278	28933	3.48	3.4E-01	AF106835.1	NT	Methylovorus sp. strain SS1 putative GrpE (grpE), DnaK (dnaK), and putative DnaJ (dnaJ) genes, complete cds
3770	16522		1.69	3.4E-01	BF449010.1	EST_HUMAN	7n94a01.x1 NCL_CGAP_Ov18 Homo sapiens cDNA clone IMAGE:3572232 3' similar to TR:Q9UJ15 Q9UJ15 DJ18C9.1
4029	16774		2.38	3.4E-01	AA584198.1	EST_HUMAN	no11b10.s1 NCL_CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1100347 3'
4460	17196	29823	0.82	3.4E-01	AF166341.1	NT	Homo sapiens Integrin alpha 6 (ITGA6) gene, exons 12 through 23
4599	17334	29963	1.54	3.4E-01	BE069912.1	EST_HUMAN	MIR4-BT0403-230200-202-c01 BT0403 Homo sapiens cDNA
4898	17625		3.23	3.4E-01	A1240973.1	EST_HUMAN	q95c05.x1 NCL_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1867208 3' similar to contains Alu repetitive element
5143	17862		0.98	3.4E-01	U79746.1	NT	Homo sapiens serotonin transporter (hSERT) gene, promoter region, exons 1B and 2, and partial cds
5599	18394	31304	2.62	3.4E-01	AL161594.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 90
5721	18513		6.09	3.4E-01	AA085313.1	EST_HUMAN	zn12d11.s1 Stragene hNT neuron (#637233) Homo sapiens cDNA clone IMAGE:547221 3'
5917	18702		1.99	3.4E-01	L02971.1	NT	Echovirus 23 1AB, 1C, 1D, 2A, 2B, 2C, 3A, 3B, 3C, 3D proteins RNA, complete mature peptides and cds
5940	18722	31681	0.89	3.4E-01	BE748912.1	EST_HUMAN	601571811T1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:3838826 3'
6017	18798	31759	2.43	3.4E-01	AW204505.1	EST_HUMAN	UHH-B1-acl-e-12-0.U1.s1 NCL_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2719582 3'
6141	18919	31889	1.81	3.4E-01	AL120544.1	EST_HUMAN	DKFZp761A249_r1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761A249 5'
6644	19406		1.56	3.4E-01	N95225.1	EST_HUMAN	zb55e12.s1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:307342 3'

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6848	19548	32578	1.02	3.4E-01	AI468082.1	EST_HUMAN	hm83g05.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2162840 3' similar to gb:S37431
6959	10441	32456	0.59	3.4E-01	BF678702.1	EST_HUMAN	LAMININ RECEPTOR (HUMAN);
7806	20501		0.49	3.4E-01	AE000493.1	NT	602085283FT NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4249365 5'
8135	20829	33964	0.8	3.4E-01	Y14930.1	NT	Escherichia coli K-12 MG1655 section 383 of 400 of the complete genome
							Homo sapiens TCRAV28 gene, allele A4, partial
8188	20882		0.47	3.4E-01	BF449010.1	EST_HUMAN	7n84a01.x1 NCI_CGAP_Ovi18 Homo sapiens cDNA clone IMAGE:3572232 3' similar to TR:Q9UJ15
8386	21078		1.51	3.4E-01	AA337083.1	EST_HUMAN	Q9UJ15 DJ18C3.1;
8461	21153	34296	0.72	3.4E-01	L04690.1	NT	EST41765 Endometrial tumor Homo sapiens cDNA 5' end
8751	21443	34590	1.7	3.4E-01	9633624	NT	Oriculus griseus cholesterol 7-alpha-hydroxylase gene, complete cds
9112	21800	34954	4.42	3.4E-01	P26013	SWISSPROT	Bovine enterovirus strain K2577, complete genome
9112	21800	34965	4.42	3.4E-01	P26013	SWISSPROT	INTEGRIN BETA-8 PRECURSOR
9321	21988		0.51	3.4E-01	AB017510.1	NT	INTEGRIN BETA-8 PRECURSOR
9346	20417	33536	4.67	3.4E-01	U19492.1	NT	Ephydra fluviatilis mRNA for PLC-gamma8, complete cds
9346	20417	33537	4.67	3.4E-01	U19492.1	NT	Saccharomyces cerevisiae Maf1p (MAF1) gene, complete cds
9397	22059	35229	0.5	3.4E-01	AF193857.1	NT	Saccharomyces cerevisiae Maf1p (MAF1) gene, complete cds
9595	22248	35433	1.01	3.4E-01	U68763.1	NT	Dictyostellum discoideum putative CMF receptor CMFR1 mRNA, complete cds
9789	22440	35648	1.85	3.4E-01	AL225084.1	NT	Glycine max putative transcription factor SCOF-1 (sof-1) mRNA, complete cds
10376	23022		0.62	3.4E-01	AE004096.1	NT	Homo sapiens FAA gene, exon 16, 17 and 18
							Vibrio cholerae chromosome I, section 4 of 251 of the complete chromosome
10940	23620		4.72	3.4E-01	AE000891.1	NT	Methanobacterium thermoautotrophicum from bases 1018444 to 1029212 (section 87 of 148) of the complete genome
10984	23659	36912	2.6	3.4E-01	P06925	SWISSPROT	PROBABLE E4 PROTEIN
11032	23703	36971	2.17	3.4E-01	AF045981.1	NT	Rutillus arcasii cytochrome b (cytb) gene, mitochondrial gene encoding mitochondrial protein, partial cds
11253	23915	37207	1.61	3.4E-01	M25856.1	NT	Human von Willebrand factor gene, exons 38 and 37
11253	23915	37208	1.61	3.4E-01	M25856.1	NT	Human von Willebrand factor gene, exons 36 and 37
11483	24084	37396	1.88	3.4E-01	AB035507.1	NT	Rattus norvegicus mRNA for s-glycerin/MUC18, complete cds
11513	24113	37423	3.65	3.4E-01	AL161515.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 27
11786	24376	37706	1.72	3.4E-01	BF081948.1	EST_HUMAN	7k69d12.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:3480648 3'
11861	24445	37786	1.58	3.4E-01	U07000.1	NT	Human breakpoint cluster region (BCR) gene, complete cds
11881	24455		1.85	3.4E-01	U93604.1	NT	Citrus variegation virus putative replicase gene, partial cds
12197	24666		11.43	3.4E-01	L28339.1	NT	Human autoantigen mRNA, complete cds
12224	25192		1.61	3.4E-01	BE218652.1	EST_HUMAN	hiv2h08.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3176127 3' similar to contains PTR5.k3 PTR5 repetitive element;

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Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1280	25292		2.28	3.4E-01	9838361	NT	Beta vulgaris mitochondrion, complete genome
12391	24781	31036	2.2	3.4E-01	AJ287131.1	NT	Mus musculus SIL, MAP_17, CYP_a, SQL & CYP_b genes
12688	24974		1.82	3.4E-01	AF019413.1	NT	Homo sapiens HLA class III region containing tenascin X (tenascin-X) gene, partial cds; cytochrome P450 21-hydroxylase (CYP21B), complement component C4 (C4B) G11, helicase (SKI2W), RD, complement factor B (Bf), and complement component C2 (C2) genes,>
13	12840	25453	10.77	3.3E-01	X07990.1	NT	Rhizobium leguminosarum sym plasmid pRL5J1 nodX gene
103	12840	25453	4.4	3.3E-01	X07990.1	NT	Rhizobium leguminosarum sym plasmid pRL5J1 nodX gene
435	13221	25867	0.9	3.3E-01	AL181545.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 45
618	13397	26032	2.01	3.3E-01	7662485	NT	Homo sapiens KIAA1100 protein (KIAA1100), mRNA
1178	13931	26597	2.85	3.3E-01	Q12446	SWISSPROT	PROLINE-RICH PROTEIN LAS17
1284	14034	26705	3.76	3.3E-01	BF588880.1	EST_HUMAN	602184016T1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:4300261 3'
1336	14085	26760	1.2	3.3E-01	U43626.1	NT	Human chromosome 15q11-q13 putative DNA replication origin in the g-aminobutyric acid receptor b3 and a5 gene cluster
1601	14347	27036	1.47	3.3E-01	6753685	NT	Mus musculus disintegrin 5 (Dign5), mRNA
1731	14473		1.02	3.3E-01	AA332734.1	EST_HUMAN	EST36722 Embryo, 8 week (Homo sapiens cDNA 5' end
2022	14757		1.01	3.3E-01	AF031148.1	NT	Methylococcus capsulatus strain Bath outer membrane protein MopB (mopB) gene, complete cds
2404	15125		4.62	3.3E-01	4507834	NT	Homo sapiens uridine monophosphate synthetase (orotate phosphoribosyl transferase and orotidine-5'-decarboxylase) (UMPS) mRNA
2949	15715	28368	1.87	3.3E-01	AJ251805.1	NT	Bacteriophage phi-Ye03-12 complete genome
3051	15817	28462	1.49	3.3E-01	AJ007932.2	NT	Streptomyces argillaceus mitramycin biosynthetic genes
3486	16243	28599	1.07	3.3E-01	AB012922.1	NT	Homo sapiens MTA1-L1 gene, complete cds
3789	16541	29176	2.1	3.3E-01	O84645	SWISSPROT	EXODEOXYRIBONUCLEASE V BETA CHAIN
3799	16551	29183	0.97	3.3E-01	P22602	SWISSPROT	GENOME POLYPROTEIN [CONTAINS: N-TERMINAL PROTEIN (P1); HELPER COMPONENT PROTEINASE (HC-PRO); PROTEIN P3]
3932	16882	29323	1.03	3.3E-01	4757739	NT	Homo sapiens A kinase (PRKA) anchor protein 5 (AKAP5), mRNA
3947	16697	29336	1.47	3.3E-01	AL161498.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 10
3983	16731	29365	1.79	3.3E-01	AF200446.1	NT	Hypoxylon fragiforme chitin synthase gene, partial cds
4334	17073		1.6	3.3E-01	D31662.1	NT	Rattus norvegicus DNA for regucalcin, partial cds
4641	17375		1.23	3.3E-01	AI639114.1	EST_HUMAN	bp78b12.x1 NCI CGAP_U18 Homo sapiens cDNA clone IMAGE:2205407 3' similar to gp.X57522 ANTIGEN
4786	17517	30139	1.22	3.3E-01	D64003.1	NT	PEPTIDE TRANSPORTER 1 (HUMAN);
5146	17865		0.98	3.3E-01	AW937982.1	EST_HUMAN	Synechocystis sp. PCC6803 complete genome, 22/27, 2755703-2868766
5241	18047	30675	2.61	3.3E-01	X89819.1	NT	QVO-DT0047-170200-123-H08 DT0047 Homo sapiens cDNA
5241	18047	30676	2.61	3.3E-01	X89819.1	NT	R.norvegicus mRNA for 3'UTR of ubiquitin-like protein
							R.norvegicus mRNA for 3'UTR of ubiquitin-like protein

Table 4

Single Exon Probes Expressed In Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5700	18494	31417	0.74	3.3E-01	BF213873.1	EST_HUMAN	601848090F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4078823 5'
5856	18643	31582	1.9	3.3E-01	BE619650.1	EST_HUMAN	601472768T1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3875763 3'
5856	18643	31583	1.9	3.3E-01	BE619650.1	EST_HUMAN	601472768T1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3875763 3'
5947	18729	31688	1.18	3.3E-01	P05691	SWISSPROT	CIRCUMSPOROZOITE PROTEIN (CS)
6695	19612	32651	0.71	3.3E-01	AB034233.1	NT	Flexibacter litoralis gyrB gene for DNA gyrase B subunit, partial cds
6695	19612	32652	0.71	3.3E-01	AB034233.1	NT	Flexibacter litoralis gyrB gene for DNA gyrase B subunit, partial cds
6789	19533	32560	4.82	3.3E-01	AI628131.1	EST_HUMAN	ly84h01.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2285809 3' similar to contains Alu repetitive element; contains element L1 repetitive element
6789	19533	32561	4.82	3.3E-01	AI628131.1	EST_HUMAN	ly84h01.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2285809 3' similar to contains Alu repetitive element; contains element L1 repetitive element
7682	20346	33458	1.88	3.3E-01	N85146.1	EST_HUMAN	J2498F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone J2498 5' similar to TEGT
8460	21152	34295	18.62	3.3E-01	BF683954.1	EST_HUMAN	602140372F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4301800 5'
8659	21351	34497	0.48	3.3E-01	AU126115.1	EST_HUMAN	AU126115 NT2RP1 Homo sapiens cDNA clone NT2RP1000130 5'
8659	21351	34498	0.48	3.3E-01	AU126115.1	EST_HUMAN	AU126115 NT2RP1 Homo sapiens cDNA clone NT2RP1000130 5'
9012	21702	34852	0.81	3.3E-01	Q62925	SWISSPROT	MITOGEN-ACTIVATED PROTEIN KINASE KINASE 1 (MAPK/ERK KINASE 1) (MEK KINASE 1) (MEKK 1)
9278	22032	35203	0.81	3.3E-01	BE828491.1	EST_HUMAN	CM3-ET0041-180500-187-c10 ET0041 Homo sapiens cDNA
9278	22032	35204	0.81	3.3E-01	BE828491.1	EST_HUMAN	CM3-ET0041-180500-187-c10 ET0041 Homo sapiens cDNA
9411	22073	35244	2.62	3.3E-01	N69866.1	EST_HUMAN	za67h01.s1 Soares fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:297649 3'
9452	22002	35174	2.77	3.3E-01	BF378745.1	EST_HUMAN	RC4-TN0077-250800-071-g04 TN0077 Homo sapiens cDNA
9891	22541		2.27	3.3E-01	L41044.1	NT	Homo sapiens high-mobility group phosphoprotein (HMG1-C) gene, exons 1-3, complete cds
10622	23315	36554	3.13	3.3E-01	X63953.1	NT	D.mauritiana Adh gene
10622	23315	36555	3.13	3.3E-01	X63953.1	NT	D.mauritiana Adh gene
10951	23628		1.7	3.3E-01	BF526499.1	EST_HUMAN	902070802F1 NCL_CGAP_Bm64 Homo sapiens cDNA clone IMAGE:4213585 5'
11198	23861	37147	11.81	3.3E-01	BE219351.1	EST_HUMAN	ly51g02.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3176978 3'
11317	24008	37313	3.23	3.3E-01	P47953	SWISSPROT	GALECTIN-3 (GALACTOSE-SPECIFIC LECTIN 3) (MAC-2 ANTIGEN) (ICE-BINDING PROTEIN) (35 KD LECTIN) (CARBOHYDRATE BINDING PROTEIN 35) (CBP 35) (LAMININ-BINDING PROTEIN) (LECTIN L-26) (CBP30)
11719	24313		3.06	3.3E-01	AA806621.1	EST_HUMAN	db71g02.s1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1336860 3'
11741	12840	25453	1.87	3.3E-01	X07990.1	NT	Rhizobium leguminosarum sym plasmid pRL5.1 nodX gene
11977	24521	37266	1.71	3.3E-01	6598319	NT	Homo sapiens aldehyde oxidase 1 (AOX1), mRNA
12676	24967		3.34	3.3E-01	AF000002.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 287001-544000 nt. position (277)
444	13230		2.33	3.2E-01	AF018261.1	NT	Rattus norvegicus EH domain binding protein Epsin mRNA, complete cds

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Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
701	13476		1.43	3.2E-01	AL161561.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 61
1139	13894	26555	27.53	3.2E-01	AF047013.1	NT	Fusarium poae virus 1 RNA2 putative RNA dependent RNA polymerase gene, complete cds
1259	14008	26677	1.36	3.2E-01	Z50202.1	NT	P. vulgaris arc5-1 gene
1369	14117	26792	5.42	3.2E-01	Q48624	SWISSPROT	LACTOSE PERMEASE (LACTOSE-PROTON SYMPORT) (LACTOSE TRANSPORT PROTEIN)
1767	14509	27210	1.25	3.2E-01	Z36041.1	NT	S. cerevisiae chromosome II reading frame ORF YBR172c
1777	14519	27222	4.7	3.2E-01	AW957194.1	EST_HUMAN	EST369284 MAGC resequences, MAGD Homo sapiens cDNA
1777	14519	27223	4.7	3.2E-01	AW957194.1	EST_HUMAN	EST369284 MAGC resequences, MAGD Homo sapiens cDNA
1835	14574	27286	1.23	3.2E-01	AL111655.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
2157	14887	27621	2.52	3.2E-01	BF203817.1	EST_HUMAN	601868504F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4111512 5'
2543	15257		2.01	3.2E-01	7710079	NT	Mus musculus Pbx/knotted 1 homeobox (Pbxkx1), mRNA
2713	15420	28159	1.08	3.2E-01	AF060668.1	NT	Homo sapiens promyelocytic leukemia zinc finger protein (PLZF) gene, complete cds
3594	16347		0.77	3.2E-01	D10872.1	NT	Human h NAT allele 3-2 gene for arylamine N-acetyltransferase
4305	17044	29669	0.91	3.2E-01	4759195	NT	Homo sapiens synplekin (SYM) mRNA
4363	17101	29736	1.52	3.2E-01	M18818.1	NT	Rabbit beta-like globin gene cluster encoding the epsilon, gamma, delta (pseudogene) and beta globin polypeptides, complete cds
4464	17200	29826	1.21	3.2E-01	Q10268	SWISSPROT	HYPOTHETICAL 81.7 KD PROTEIN C13G7.04C IN CHROMOSOME 1 PRECURSOR
4688	17422		6.7	3.2E-01	BF693617.1	EST_HUMAN	602081972F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4246505 5'
4826	17557	30179	1.17	3.2E-01	Q57081	SWISSPROT	CYTADHERENCE HIGH MOLECULAR WEIGHT PROTEIN 3 (CYTADHERENCE ACCESSORY PROTEIN 3) (ACCESSORY ADHESIN PROTEIN 3) (P69)
4965	17690	30259	0.74	3.2E-01	BE782748.1	EST_HUMAN	601465591F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3868799 5'
5190	17998	30621	3.26	3.2E-01	BE173964.1	EST_HUMAN	CMO-HT0569-060300-269-f10 HT0569 Homo sapiens cDNA
5868	18655	31596	1.07	3.2E-01	L27221.1	NT	Giardia intestinalis pyruvate:flavodoxin oxidoreductase and flanking genes
6211	18986	31963	0.9	3.2E-01	AF018494.1	NT	Fugu rubripes gamma-aminobutyric acid receptor beta subunit gene, partial cds; 55kd erythrocyte membrane protein (P55), synaptic vesicle-associated integral membrane protein (VAMP-1), procollagen C-proteinase enhancer protein (PCOLCE) genes, complete c
6501	19266	32268	0.64	3.2E-01	AV718037.1	EST_HUMAN	AV718037 FH7A Homo sapiens cDNA clone FH7AABH01 5'
6634	19396		1.09	3.2E-01	AB002359.1	NT	Human mRNA for KIAA0361 gene, KIAA0361 protein
7755	20451	33575	0.51	3.2E-01	AJ277661.1	NT	Homo sapiens partial LMO1 gene for LIM domain only 1 protein, exon 1
8072	20766	33695	1.48	3.2E-01	M60266.1	NT	Rat ISO-alpha natriuretic factor gene, complete cds
8164	20858	33990	0.45	3.2E-01	AJ231001.1	NT	Rattus norvegicus repeat; map NOS-D12Wox1
8265	20959	34098	14.41	3.2E-01	X02508.1	NT	H-sapiens gene fragment for acetylcholine receptor (AChR) alpha subunit exons 8, 9 and 3' flanking region
8268	20962	34103	13.78	3.2E-01	BF311635.1	EST_HUMAN	601897107F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4126633 5'
8361	21054		1.38	3.2E-01	AL161574.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 70

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8398	21091	34226	1.24	3.2E-01	BF246771.1	EST_HUMAN	601855580F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4075627 5'
8398	21091	34227	1.24	3.2E-01	BF246771.1	EST_HUMAN	601855580F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4075627 5'
8471	21163	34306	2.65	3.2E-01	AE002015.1	NT	Deinococcus radiodurans R1 section 152 of 229 of the complete chromosome 1
8571	21263	34401	0.84	3.2E-01	U51026.1	NT	Oryctolagus cuniculus Ig H-chain pseudogene, V-region (VH6-a2) gene, partial cds
8571	21263	34402	0.84	3.2E-01	U51026.1	NT	Oryctolagus cuniculus Ig H-chain pseudogene, V-region (VH6-a2) gene, partial cds
8965	21656	34807	0.51	3.2E-01	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
8976	21666		2.18	3.2E-01	M86511.1	NT	Human monocyte antigen CD14 (CD14) mRNA, complete cds
9048	21737	34884	0.65	3.2E-01	AF041828.1	NT	Homo sapiens 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase (PF2K) gene, exons 12 and 13
9048	21737	34895	0.65	3.2E-01	AF041828.1	NT	Homo sapiens 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase (PF2K) gene, exons 12 and 13
9894	22544	35737	3.33	3.2E-01	U44914.1	NT	Borrelia burgdorferi plasmid cp32-2, erpC and erpD genes, complete cds; and unknown genes
10099	22747	35962	0.45	3.2E-01	BE326230.1	EST_HUMAN	h939f05.x1 NC1_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3181569 3'
10210	22858		3.41	3.2E-01	AB011399.1	NT	Homo sapiens gene for AF-6, complete cds
10566	23261	36498	3.94	3.2E-01	T08813.1	EST_HUMAN	EST04702 Fetal brain, Stragogene (cat#836206) Homo sapiens cDNA clone HFBD221
12010	25317		3.91	3.2E-01	L07288.1	NT	Drosophila melanogaster laminin A (Lam-A) mRNA, complete cds
12392	25374		1.44	3.2E-01	BE86846.1	EST_HUMAN	601507820F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3809532 5'
12524	24871		4.21	3.2E-01	O83217	SWISSPROT	ELONGATION FACTOR TU (EF-TU)
12655	24955		2.07	3.2E-01	L39874.1	NT	Homo sapiens deoxycytidylate deaminase gene, complete cds
12712	25354	30606	1.75	3.2E-01	BE385776.1	EST_HUMAN	601275480F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3616746 5'
2677	15386	28128	2.89	3.1E-01	R18051.1	EST_HUMAN	ye90h06.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:125051 5' similar to
2702	15532	28145	3.39	3.1E-01	7661971	NT	gb:M64241 QM PROTEIN (HUMAN);
2702	15532	28145	3.39	3.1E-01	7661971	NT	Homo sapiens KIAA0174 gene product (KIAA0174), mRNA
2702	15532	28146	3.39	3.1E-01	AW628036.1	EST_HUMAN	Homo sapiens KIAA0174 gene product (KIAA0174), mRNA
2862	15630		1.29	3.1E-01	AB029039.1	NT	h149h08.x1 Soares_NFL_I_GBC_S1 Homo sapiens cDNA clone IMAGE:2975391 3'
3170	15933		3.35	3.1E-01	AB029039.1	NT	Mus musculus gene for Ser/Thr kinase KKIAMRE, exon 6
3887	16637	29276	0.8	3.1E-01	AJ251588.1	NT	Daucus carota mRNA for transcription factor E2F (E2F gene)
4908	17636	30250	0.73	3.1E-01	AE003984.1	NT	Xylella fastidiosa, section 130 of 229 of the complete genome
5300	18190	30882	9.73	3.1E-01	AF176111.1	NT	Homo sapiens hepatocyte nuclear factor-3 alpha (HNF3A) gene, exon 1
5513	18311	31212	0.73	3.1E-01	P44132	SWISSPROT	HYPOTHETICAL PROTEIN H1236
5514	18312	31213	0.67	3.1E-01	Z74883.1	NT	S. cerevisiae chromosome XV reading frame ORF YOL1411w
5524	18322		0.88	3.1E-01	Y18278.1	NT	Mus musculus mRNA for polycystin
5685	18478	31396	2.11	3.1E-01	AF184122.1	NT	Homo sapiens filamin 2 (FLN2) gene, exons 10 through 22
6191	25087	31942	0.59	3.1E-01	R84322.1	EST_HUMAN	yc41104.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:198367 5'

Table 4

Single Exon Probes Expressed In Brain

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6374	19143	32140	1.34	3.1E-01	AW983549.1	EST_HUMAN	RC3-HN0001-310300-011-b04 HN0001 Homo sapiens cDNA
6439	19207	32203	1.01	3.1E-01	AI264458.1	EST_HUMAN	q33d01.x1 NCL_CGAP_Co8 Homo sapiens cDNA clone IMAGE:1874689 3'
6583	19346	32360	3.91	3.1E-01	X71887.1	NT	H.sapiens gene for immunoglobulin kappa light chain variable region A8 and A9
6873	25061	30545	2.41	3.1E-01	BE737392.1	EST_HUMAN	601306121F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3640420 5'
7579	20248	33354	0.77	3.1E-01	4885390	NT	Homo sapiens hyaluronan synthase 2 (HAS2), mRNA
8546	21238	34381	1.71	3.1E-01	R45318.1	EST_HUMAN	y94601.s1 Soares infant brain T1N1B Homo sapiens cDNA clone IMAGE:35639 3'
9802	22453	35855	0.54	3.1E-01	6679322	NT	Mus musculus phosphatidylinositol 4-phosphate 5-kinase, type 1 gamma (Pip5k1c), mRNA
9867	22615	35818	1.05	3.1E-01	BF696339.1	EST_HUMAN	602124743F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4281611 5'
9867	22615	35818	1.05	3.1E-01	BF696339.1	EST_HUMAN	602124743F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4281611 5'
10029	22677	35893	1.74	3.1E-01	AI244001.1	EST_HUMAN	q161e11.x1 NCL_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1863980 3' similar to gb:S55700 HYDROXYMETHYLGLUTARYL-COA LYASE PRECURSOR (HUMAN);
10201	22849		0.63	3.1E-01	T55925.1	EST_HUMAN	y647h08.s1 Stratagene fetal spleen (#937205) Homo sapiens cDNA clone IMAGE:74367 3' similar to similar to gb:U91036_rna2 HEMOGLOBIN GAMMA-A AND GAMMA-G CHAINS (HUMAN)
10741	23428	36672	1.26	3.1E-01	BF216117.1	EST_HUMAN	601883592F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4095814 5'
11524	24124	37430	2.56	3.1E-01	7662291	NT	Homo sapiens KIAA0764 gene product (KIAA0764), mRNA
12133	24623		1.48	3.1E-01	AF294308.1	NT	Anolis opalinus isolate QS NADH dehydrogenase subunit 2 (ND2) gene, complete cds; mitochondrial gene for mitochondrial product
12165	24647		3.03	3.1E-01	AF304162.1	NT	Stizostedion vitreum 40S ribosomal protein S11 mRNA, partial cds
12304	24729		2.92	3.1E-01	AF195953.1	NT	Homo sapiens membrane-bound aminopeptidase P (XNPEP2) gene, complete cds
12660	24960		3.46	3.1E-01	AF196779.1	NT	Homo sapiens transcription factor (GHM enhancer 3, JM11 protein, JM4 protein, JM5 protein, T54 protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synapophysin genes, complete cds; and L-type calcium channel α 2
12699	25347		1.35	3.1E-01	10946623	NT	Mus musculus peptidoglycan recognition protein-like (Pglyrp1-pending), mRNA
70	15512	25533	2.01	3.0E-01	6755083	NT	Mus musculus protein kinase C, epsilon (Pkc ϵ), mRNA
247	13056	25698	14.52	3.0E-01	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region, segment 1/2
1202	13954	26618	2.51	3.0E-01	AW300400.1	EST_HUMAN	xs63f08.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2774343 3'
1497	14244	26930	5.57	3.0E-01	AJ006755.1	NT	Balaenoptera physalus gene encoding atrial natriuretic peptide
2132	14862	27592	1.2	3.0E-01	AF237778.1	NT	Rattus norvegicus Ca2+/calmodulin-dependent protein kinase II, alpha subunit mRNA, 3' untranslated region
3206	15969		1.18	3.0E-01	AB030481.1	NT	Corynebacterium sp. ALY-1 alyPG gene for polyglutamate lyase, complete cds
3846	16587	28234	1.46	3.0E-01	AW817785.1	EST_HUMAN	PM1-ST0262-261199-001-g01 ST0262 Homo sapiens cDNA
4477	17212	29837	1.95	3.0E-01	AJ006755.1	NT	Balaenoptera physalus gene encoding atrial natriuretic peptide
5287	18073	30702	7.22	3.0E-01	BE741629.1	EST_HUMAN	601594960F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3948734 5'
5349	18182	30833	0.77	3.0E-01	AF229247.1	NT	Canis lupus familiaris hemagglutinin gene, complete cds

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5417	18216	30924	3.94	3.0E-01	BE693575.1	EST_HUMAN	RC3-BT0333-180700-111-e03 BT0333 Homo sapiens cDNA
5417	18216	30925	3.94	3.0E-01	BE693575.1	EST_HUMAN	RC3-BT0333-180700-111-e03 BT0333 Homo sapiens cDNA
5453	18252	31142	4.77	3.0E-01	U01247.1	NT	Mus musculus 129/sv Clara cell 10 kd protein (mCC10) gene, complete cds
6732	19566	32598	3.06	3.0E-01	D16313.1	NT	Mouse cytokeratin 15 gene, complete cds
6762	17931	30567	0.61	3.0E-01	U02369.1	NT	Strongylocentrotus purpuratus 34/67 kDa laminin-binding protein mRNA, partial cds
6827	19488	32510	0.85	3.0E-01	AF228247.1	NT	Canthalo orthopoxvirus hemagglutinin gene, complete cds
7021	19713	32770	0.71	3.0E-01	AL163206.2	NT	Homo sapiens chromosome 21 segment HS21C006
7227	19912	32985	2.77	3.0E-01	10947007	NT	Mus musculus midnolin (Mldn-pending), mRNA
7400	20078	33159	1.37	3.0E-01	AF071810.1	NT	Streptococcus pneumoniae strain DBL5 PspA (pspA) gene, partial cds
7827	20522	33648	1.3	3.0E-01	AE001755.1	NT	Thermotoga maritima section 87 of 136 of the complete genome
8271	20965		2.97	3.0E-01	9910161	NT	Mus musculus C-type (calcium dependent, carbohydrate recognition domain) lectin, superfamily member 9 (Clec4e), mRNA
8374	21067	34207	1.32	3.0E-01	BE566083.1	EST_HUMAN	601339079F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3681584 5'
8728	21420	34564	0.51	3.0E-01	AF141676.1	NT	Streptomyces sulfonofaciens isopenicillin N synthase (pcbc) gene, partial cds
8770	21462		0.8	3.0E-01	7661685	NT	Homo sapiens DKFZP586M0122 protein (DKFZP586M0122), mRNA
9118	21806	34972	0.81	3.0E-01	AF220507.1	NT	Anabaena PCC7120 cytosine-specific DNA methyltransferase (dmnB) gene, complete cds, putative
9856	22506		43.84	3.0E-01	BE001129.1	EST_HUMAN	anthranilate phosphoribosyltransferase gene, partial cds; and unknown gene
9868	22518	35714	1.25	3.0E-01	BF574612.1	EST_HUMAN	RC2-BN0074-240400-110-h12 BN0074 Homo sapiens cDNA
10042	22690	35908	0.49	3.0E-01	AF152598.3	NT	602133271F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4288336 5'
10042	22690						Adinobacillus actinomycetocornuans Tada (tada), TadaB (tadB), TadaC (tadC), TadaD (tadD), Tade (tade), TadeF (tadF), and TadeG (tadG) genes, complete cds
10294	22841	36155	0.84	3.0E-01	AW118111.1	EST_HUMAN	Adinobacillus actinomycetocornuans Tada (tada), TadaB (tadB), TadaC (tadC), Tade (tade), TadeF (tadF), and TadeG (tadG) genes, complete cds
10296	22943	36157	1.88	3.0E-01	AB030231.1	NT	xe03d410.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2606035 3'
10316	22963	36179	0.73	3.0E-01	BF683841.1	EST_HUMAN	Aspergillus oryzae bpaA gene for ER chaperone BiP, complete cds
10316	22963	36180	0.73	3.0E-01	BF683841.1	EST_HUMAN	602140133F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4301097 5'
10316	22963	36180	0.73	3.0E-01	BF683841.1	EST_HUMAN	602140133F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4301097 5'
11772	24363	37694	1.95	3.0E-01	H51029.1	EST_HUMAN	yp84b10.r1 Soares fetal liver spleen TNF1L Homo sapiens cDNA clone IMAGE:194107 5'
11772	24363	37695	1.95	3.0E-01	H51029.1	EST_HUMAN	yp84b10.r1 Soares fetal liver spleen TNF1L Homo sapiens cDNA clone IMAGE:194107 5'
12416	25302		2.52	3.0E-01	AJ297631.1	NT	Rattus norvegicus mRNA for glyceraldehyde-3-phosphate dehydrogenase type 2 (gapdh-2 gene)
12693	25345		5.51	3.0E-01	6877766	NT	Mus musculus ribose 5-phosphate isomerase A (RpiA), mRNA
2018	14793	27481	1.43	2.9E-01	AE000736.1	NT	Aquifex aeolicus section 68 of 109 of the complete genome
2245	14973	27710	1.16	2.9E-01	AF222718.1	NT	Chrysoidymus synnoides mitochondrion, complete genome
3246	16008	28658	2.73	2.9E-01	AW754239.1	EST_HUMAN	PM1-CT0326-171299-001-412 CT0326 Homo sapiens cDNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3246	16008	28659	2.73	2.9E-01	AW754239.1	EST_HUMAN	PM1-CT0328-171299-001-f12 CT0328 Homo sapiens cDNA
3877	16827	29265	0.72	2.9E-01	AI610836.1	EST_HUMAN	tp21a11.x1 NCL CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2188412 3' similar to gb:D15050 N1L-2-A
4052	16797	29427	0.73	2.9E-01	AB016426.1	NT	ZINC FINGER PROTEIN (HUMAN); contains element L1 repetitive element ;
4064	16809		0.77	2.9E-01	AW002902.1	EST_HUMAN	Cavia porcellus mRNA for glutathione s-transferase, complete cds
							wi02f10.x1 NCL CGAP_G08 Homo sapiens cDNA clone IMAGE:2480395 3'
4452	17188	29813	1.1	2.9E-01	AA284488.1	EST_HUMAN	zs57d12.r1 NCL CGAP_G0B1 Homo sapiens cDNA clone IMAGE:701691 5' similar to contains Alu repetitive element
5177	17986		1.66	2.9E-01	R37485.1	EST_HUMAN	yf77e12.s1 Soares infant brain T1N1B Homo sapiens cDNA clone IMAGE:28291 3'
5310	19507	32532	0.79	2.9E-01	AF321001.1	NT	Suaeda maritima subsp. salina S-adenosylmethionine synthetase 2 mRNA, complete cds
5677	18471	31387	5.19	2.9E-01	X56098.1	NT	B. subtilis levanase operon levD, levE, levF, levG and sacC (partial) genes for fructose phosphotransferase system polypeptides P16, P18, P20, P22 and P24
5677	18471	31388	5.19	2.9E-01	X56098.1	NT	B. subtilis levanase operon levD, levE, levF, levG and sacC (partial) genes for fructose phosphotransferase system polypeptides P16, P18, P20, P22 and P24
5689	18482	31401	6.4	2.9E-01	6679662	NT	Mus musculus Eph receptor A8 (EphA8), mRNA
5685	18747	31708	1.47	2.9E-01	AA418145.1	EST_HUMAN	z97b12.r1 Soares NIHMPu_S1 Homo sapiens cDNA clone IMAGE:767711 5'
6187	18664	31937	1.08	2.9E-01	AI797129.1	EST_HUMAN	w27c05.x1 NCL CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2342312 3' similar to contains L1, L1 L1 repetitive element ;
6233	19007	31984	2.4	2.9E-01	U03420.1	NT	Bos taurus myosin I mRNA, complete cds
6365	19135	32130	0.98	2.9E-01	R69194.1	EST_HUMAN	y93d08.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:141615 5'
6365	19135	32131	0.58	2.9E-01	R69194.1	EST_HUMAN	y93d08.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:141615 5'
6621	19383		0.58	2.9E-01	Z50156.1	NT	D. discoideum gene for 34 kD actin binding protein
6890	17966	33523	1.52	2.9E-01	AF142328.1	NT	Mus musculus Filin protein (Filin) gene, complete cds; and Ligh protein (Ligh) gene, partial cds
6966	19688	32737	2.95	2.9E-01	Q04399	SWISSPROT	PUTATIVE MULTICOPPER OXIDASE YDR506C
							Mus musculus major histocompatibility locus class II region: Fas-binding protein Daxx (DAXX) gene, partial cds; Bing1 (BING1), tapasin (tapasin), RalGDS-like factor (RLF), KE2 (KE2), BING4 (BING4), beta1, 3-galactosyl transferase (beta1, 3-galactosyl tr-
7059	19750	32813	2.06	2.9E-01	AF100956.1	NT	
7820	20515	33640	1.67	2.9E-01	BE540422.1	EST_HUMAN	601065830F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3452287 5'
7820	20515	33641	1.67	2.9E-01	BE540422.1	EST_HUMAN	601065830F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3452287 5'
8049	20743	33875	0.48	2.9E-01	AJ237937.1	NT	Bos taurus partial stat5A gene, exons 5-19
8049	20743	33876	0.48	2.9E-01	AJ237937.1	NT	Bos taurus partial stat5A gene, exons 5-19
8062	20756		0.94	2.9E-01	BF217743.1	EST_HUMAN	601882670F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4095113 5'
							Buchnera aphidicola plasmid pLeu isolate M1 2-isopropylmalate synthase (leuA) gene, partial cds; 3-isopropylmalate dehydrogenase (leuB) gene, complete cds; and isopropylmalate dehydratase subunit (leuC) gene, partial cds
8237	20931		0.49	2.9E-01	AF197456.1	NT	

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Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8493	21185	34328	0.84	2.9E-01	AU150910.1	EST_HUMAN	AU150910 NT2RP2 Homo sapiens cDNA clone NT2RP2003901 3'
8823	21616	34680	1.02	2.9E-01	AF225908.1	NT	Arabidopsis thaliana sulfonyleurea receptor-like protein mRNA, complete cds
8931	21822	34765	0.65	2.9E-01	M22452.1	NT	Baboon lymphocyte homing/adhesion receptor mRNA, complete cds
9145	21878	35040	0.76	2.9E-01	AJ248287.1	NT	Pyrococcus abyssi complete genome; segment 5/6
9145	21878	35041	0.76	2.9E-01	AJ248287.1	NT	Pyrococcus abyssi complete genome; segment 5/6
10810	23493	36728	1.93	2.9E-01	AF128843.1	NT	Trypanosoma cruzi stage-specific surface glycoprotein gp82 (gp82) mRNA, partial cds
11114	23784	37069	1.75	2.9E-01	V011394.1	NT	Torpedo californica mRNA encoding acetylcholine receptor gamma subunit
11114	23784	37069	1.75	2.9E-01	V011394.1	NT	Torpedo californica mRNA encoding acetylcholine receptor gamma subunit
11575	24174	37489	1.59	2.9E-01	AA095373.1	EST_HUMAN	ny35h02.s1 NCL CGAP_P12 Homo sapiens cDNA clone IMAGE:1273779 similar to contains LTR8.12 LTR8 repetitive element
11579	24178	37493	3.55	2.9E-01	AL139078.2	NT	Campylobacter jejuni NCTC11188 complete genome; segment 5/6
11600	24199	37519	1.62	2.9E-01	U35025.1	NT	Rattus norvegicus activin receptor-like kinase 7 (ALK7) mRNA, complete cds
11600	24199	37520	1.62	2.9E-01	U35025.1	NT	Rattus norvegicus activin receptor-like kinase 7 (ALK7) mRNA, complete cds
12452	24821	31024	4.05	2.9E-01	AF092453.1	NT	Homo sapiens TNF- α -inducible RNA binding protein (TIRP) gene, complete cds
12741	25007	30973	1.86	2.9E-01	Y08937.1	NT	Chlamydomonas reinhardtii mRNA for nitrite reductase structural locus
12741	25007	30974	1.86	2.9E-01	Y08937.1	NT	Chlamydomonas reinhardtii mRNA for nitrite reductase structural locus
555	13338		1.7	2.8E-01	U67136.1	NT	Rattus norvegicus A-kinase anchoring protein AKAP150 mRNA, complete cds
560	13342		1.01	2.8E-01	L28145.1	NT	Prune dwarf virus movement protein, complete cds, coat protein, complete cds
1061	13819	28481	3.69	2.8E-01	AF168050.1	NT	Guinea guinea oocyte maturation factor Mos (c-mos) gene, partial cds
1254	14003	28671	1.62	2.8E-01	BE313442.1	EST_HUMAN	601148733F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3163888 5'
1254	14003	28672	1.62	2.8E-01	BE313442.1	EST_HUMAN	601148733F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3163888 5'
1268	14017	28684	1.34	2.8E-01	D86550.1	NT	Human mRNA for serine/threonine protein kinase, complete cds
1651	14397	27087	1.11	2.8E-01	AF075238.1	NT	Hepatitis G virus isolate 80 (SZNAE12) polyprotein precursor, gene, partial cds
1720	14463	27163	2.04	2.8E-01	AW860020.1	EST_HUMAN	QV1-CT0364-120200-065-b05 CT0364 Homo sapiens cDNA
2006	14742	27467	2.35	2.8E-01	AL047620.1	EST_HUMAN	DKFZ58812321_r1 588 (synonym: hule1) Homo sapiens cDNA clone DKFZ58812321
2127	14858	27588	1.41	2.8E-01	AW511195.1	EST_HUMAN	hd44b03.x1 Soares_NFL_I_GBC_S1 Homo sapiens cDNA clone IMAGE:2912333 3'
2475	15193	27933	2.04	2.8E-01	AE000494.1	NT	Escherichia coli K-12 MG1655 section 384 of 400 of the complete genome
2475	15193	27934	2.04	2.8E-01	AE000494.1	NT	Escherichia coli K-12 MG1655 section 384 of 400 of the complete genome
2549	15264		1.89	2.8E-01	AL11685.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 65
2670	15380	28118	0.97	2.8E-01	AB020975.1	NT	Arabidopsis thaliana mRNA for lipoyltransferase, complete cds
2970	15796	28386	1.29	2.8E-01	AF179480.1	NT	Toxoplasma gondii 90kDa heat-shock protein (HSP90) mRNA, partial cds
2971	15737	28387	2.04	2.8E-01	Z14037.1	NT	B. taurus microsatellite (ETH121)
2971	15737	28387	2.04	2.8E-01	Z14037.1	NT	B. taurus microsatellite (ETH121)
3373	16132	28788	1.13	2.8E-01	AP000004.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 777001-994000 nt, position (4/7)

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3978	16726	26360	1.59	2.8E-01	AE001180.1	NT	Borrelia burgdorferi (section 66 of 70) of the complete genome
4174	16914		1.95	2.8E-01	AJ090868.1	EST_HUMAN	ov44g10.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1640226 3' similar to contains Alu repetitive element; contains element MER22 repetitive element ;
4422	17158	29789	0.99	2.8E-01	AL021127.2	NT	Mus musculus chromosome X contigA; putative Magea9 gene, Caltractin, NAD(P) steroid dehydrogenase and Zinc finger protein 185
4427	17163	29793	2.31	2.8E-01	AF13615	SWISSPROT	RNA POLYMERASE BETA SUBUNIT (LARGE STRUCTURAL PROTEIN) (L PROTEIN)
4772	17504	30126	1.19	2.8E-01	AF075238.1	NT	Hepatitis G virus isolate 60 (SZNAE12) polypeptide precursor, gene, partial cds
4777	17509	30131	2.67	2.8E-01	AF030154.1	NT	Bovine adenovirus 3 complete genome
4808	17539	30162	1.23	2.8E-01	BF528188.1	EST_HUMAN	602042601F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4180129 5'
4829	17660	30182	1.91	2.8E-01	AI272669.1	EST_HUMAN	q159c11.x1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:1876628 3' similar to contains Alu repetitive element; contains element LTR5 repetitive element ;
5228	25084	30680	24.95	2.8E-01	AA349697.1	EST_HUMAN	EST57072 Infant brain Homo sapiens cDNA 5' end
5519	18317	31218	3.07	2.8E-01	AB016825.1	NT	Homo sapiens OCTN2 gene, complete cds
5727	18519		0.95	2.8E-01	AW992593.1	EST_HUMAN	CM1-BN0024-150200-118-q12 BN0024 Homo sapiens cDNA
5848	18635		0.63	2.8E-01	AA404576.1	EST_HUMAN	zt41f01.11 Soares ovary tumor N6HOT Homo sapiens cDNA clone IMAGE:724921 5' similar to contains Alu repetitive element
6083	25418		0.85	2.8E-01	M36668.1	NT	Bovine 680 bp repeated unit of 1.723 satellite DNA
6123	18901	31869	1.53	2.8E-01	AF003124.1	NT	Mesembryanthemum crystallinum fructose-bisphosphate aldolase mRNA, complete cds
6123	18901	31870	1.53	2.8E-01	AF003124.1	NT	Mesembryanthemum crystallinum fructose-bisphosphate aldolase mRNA, complete cds
6632	19394	32409	8.34	2.8E-01	BF511215.1	EST_HUMAN	UHL-B14-act-f-04-0-UI.s1 NCI_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3085182 3'
7341	20022		1.17	2.8E-01	U05693.1	NT	Marsilea quadrifolia ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcl) gene, chloroplast gene encoding chloroplast protein, partial cds
7382	20062	33140	0.58	2.8E-01	X69980.1	NT	L. esculentum ypt2 mRNA for GTP-binding protein
7991	20696	33811	1.28	2.8E-01	A1346126.1	EST_HUMAN	qp48h01.x1 NCI_CGAP_Co8 Homo sapiens cDNA clone IMAGE:1926289 3' similar to gb:X06323_cds1 MITOCHONDRIAL 60S RIBOSOMAL PROTEIN L3 (HUMAN);
7991	20696	33812	1.28	2.8E-01	A1346126.1	EST_HUMAN	qp48h01.x1 NCI_CGAP_Co8 Homo sapiens cDNA clone IMAGE:1926289 3' similar to gb:X06323_cds1 MITOCHONDRIAL 60S RIBOSOMAL PROTEIN L3 (HUMAN);
8108	20802	33935	1.92	2.8E-01	U51688.1	NT	Homo sapiens lanosterol 14-alpha demethylase cytochrome P450 (CYP51) gene, exon 5'
8412	21105	34244	0.51	2.8E-01	AA911629.1	EST_HUMAN	o02h05.s1 NCI_CGAP_Co72 Homo sapiens cDNA clone IMAGE:1419993 3' similar to gb:M67789 IG GAMMA-1 CHAIN C REGION (HUMAN);
8498	21180		7.34	2.8E-01	BF347847.1	EST_HUMAN	602022987F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4158525 5'
9365	21941	35115	0.92	2.8E-01	U17251.1	NT	Neurospora crassa negative regulator sulfur controller-2 (scon-2) gene, complete cds
9611	22264		0.88	2.8E-01	L13654.1	NT	Lycopodium obscurum peroxidase (TPX1) mRNA, complete cds
9788	22439	35646	0.86	2.8E-01	AF132728.1	NT	Escherichia coli translocated intimin receptor Tir (tir) gene, complete cds

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Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9788	22439	35647	0.66	2.8E-01	AF132728.1	NT	Escherichia coli translocated intimin receptor Tir (tir) gene, complete cds
9850	22500	35700	0.52	2.8E-01	AF294393.1	NT	Rattus norvegicus glycerol-3-phosphate dehydrogenase gene, promoters A and B and exons 1a and 1b; nuclear gene for mitochondrial product
9980	22608	35813	3.35	2.8E-01	7706163	NT	Homo sapiens hypothetical protein (LOC51319), mRNA
10211	22859		1.47	2.8E-01	9626154	NT	Fujinami sarcoma virus, complete genome
10251	22899	36109	0.6	2.8E-01	BE959727.2	EST_HUMAN	601854822R1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:3839765 3'
10544	23335	36573	2.42	2.8E-01	BF241082.1	EST_HUMAN	601880794F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4109350 5'
10644	23335	36574	2.42	2.8E-01	BF241082.1	EST_HUMAN	601880794F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4109350 5'
10671	23362	36603	3.83	2.8E-01	BF695970.1	EST_HUMAN	601852148F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4076028 5'
10794	23477	36719	1.33	2.8E-01	AF051692.1	NT	Drosophila heteronema fruitless (fru) gene, alternative splice products, 5' flanking region, exons 1 through 7 and complete cds
11247	23909		4.51	2.8E-01	BF074023.1	EST_HUMAN	602137418F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4273853 5'
11583	24192	37510	17.85	2.8E-01	AL139074.2	NT	Campylobacter jejuni NC1C11168 complete genome; segment 116
12406	24789		15.41	2.8E-01	D83329.1	NT	Mus musculus DNA for prostaglandin D2 synthase, complete cds
12509	24861	31013	4.22	2.8E-01	BE178699.1	EST_HUMAN	PMA-HT0606-030400-001-e07 HT0606 Homo sapiens cDNA
12532	24877	31019	1.77	2.8E-01	BE900116.1	EST_HUMAN	601673020F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3955996 5'
12885	25306		2.52	2.8E-01	11433629	NT	Homo sapiens CDC42-binding protein kinase beta (DMPK-like) (CDC42BPB), mRNA
12806	25401		1.49	2.8E-01	AW025400.1	EST_HUMAN	wu89g05.x1 NCI_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:2627928 3'
464	13249	25890	3.97	2.7E-01	Y17324.1	NT	Rattus norvegicus CDK104 mRNA
599	13377	26007	3.25	2.7E-01	AA450061.1	EST_HUMAN	zx39b10.s1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:788827 3' similar to contains Alu repetitive element
1238	13987	26654	2.13	2.7E-01	AB004906.1	NT	Iponoea purpurea transposable element Tpi100 gene for transposase, complete cds
1617	14364		1.58	2.7E-01	X79815.1	NT	G.lambdla SR2 gene
1722	14465	27164	3.5	2.7E-01	W58067.1	EST_HUMAN	zid22h10.r1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:341443 5'
1769	14511	27212	2.56	2.7E-01	P03341	SWISSPROT	GAG POLYPROTEIN [CONTAINS: INNER COAT PROTEIN P12; CORE PROTEIN P16; CORE SHELL PROTEIN P30; NUCLEOPROTEIN P10]
2131	15588		2.25	2.7E-01	AF047575.1	NT	Rattus norvegicus vesicular monamine transporter type 2, promoter region and exon 1
2367	15089	27826	10.01	2.7E-01	Y13868.1	NT	Feline immunodeficiency virus env gene, isolate ITT0088PIU (M88), partial
2457	15175	27914	4.07	2.7E-01	A1310858.1	EST_HUMAN	ta43c11.x2 NCI_CGAP_Lu25 Homo sapiens cDNA clone IMAGE:2046836 3' similar to contains element L1 repetitive element
2899	15666	28314	1.2	2.7E-01	AF251276.1	NT	Mus musculus serine protease inhibitor 14 (Spi14) mRNA, complete cds
2983	15749		2.53	2.7E-01	BF088284.1	EST_HUMAN	CM1-HT0875-060900-385-e05 HT0875 Homo sapiens cDNA
3283	16044	28683	0.68	2.7E-01	8393620	NT	Rattus norvegicus Insulin receptor (Insr), mRNA
3992	16740	28374	1.97	2.7E-01	A1928015.1	EST_HUMAN	w092e11.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2462828 3'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4002	16749	29380	0.69	2.7E-01	AF216214.1	NT	Drosophila buzzatii alpha-esterase 6 (aE6) gene, partial cds
4002	16749	29381	0.69	2.7E-01	AF216214.1	NT	Drosophila buzzatii alpha-esterase 6 (aE6) gene, partial cds
4008	16754	29384	2.12	2.7E-01	U77569.1	NT	Homo sapiens DGeorge syndrome critical region, telomeric end
4980	17703		2.85	2.7E-01	AW856131.1	EST_HUMAN	RC1-CT0286-230200-016-c03 CT0286 Homo sapiens cDNA
5011	17733	30339	2.53	2.7E-01	AA100656.1	EST_HUMAN	z90a01.r1 Stratagene colon (#937204) Homo sapiens cDNA clone IMAGE:511848 5' similar to gb:X65488 cds1 HETEROGENOUS NUCLEAR RIBONUCLEOPROTEIN U (HUMAN);
5011	17733	30340	2.53	2.7E-01	AA100656.1	EST_HUMAN	z90a01.r1 Stratagene colon (#937204) Homo sapiens cDNA clone IMAGE:511848 5' similar to gb:X65488 cds1 HETEROGENOUS NUCLEAR RIBONUCLEOPROTEIN U (HUMAN);
5185	17963	30509	2.39	2.7E-01	P17277	SWISSPROT	HOMEOBOX PROTEIN HOX-A4 (CHOX-1.4)
5402	18202		0.85	2.7E-01	AB033171.1	NT	Astreopora myriophthalma mitochondrial cytb gene for cytochrome b, partial cds
6249	19023	31995	0.66	2.7E-01	Q00918	SWISSPROT	LATENT TRANSFORMING GROWTH FACTOR BETA BINDING PROTEIN 1 PRECURSOR (TRANSFORMING GROWTH FACTOR BETA-1 BINDING PROTEIN 1) (TGF-BETA1-BP-1) (TRANSFORMING GROWTH FACTOR BETA-1 MASKING PROTEIN, LARGE SUBUNIT)
6249	19023	31996	0.66	2.7E-01	Q00918	SWISSPROT	LATENT TRANSFORMING GROWTH FACTOR BETA BINDING PROTEIN 1 PRECURSOR (TRANSFORMING GROWTH FACTOR BETA-1 BINDING PROTEIN 1) (TGF-BETA1-BP-1) (TRANSFORMING GROWTH FACTOR BETA-1 MASKING PROTEIN, LARGE SUBUNIT)
6515	19280	32282	0.93	2.7E-01	AE001094.1	NT	Archaeoglobus fulgidus section 13 of 172 of the complete genome
6515	19280	32283	0.93	2.7E-01	AE001094.1	NT	Archaeoglobus fulgidus section 13 of 172 of the complete genome
6681	19598	32637	2.23	2.7E-01	Q61554	SWISSPROT	FIBRILLIN 1 PRECURSOR
6916	19653	32699	0.58	2.7E-01	U15967.1	NT	Drosophila melanogaster rfc40 protein, Rop protein (Rop), and small GTP binding protein (DRas2) genes, complete cds
6952	19434		0.79	2.7E-01	AI540070.1	EST_HUMAN	Id08h08.x1 NCJ_CGAP_GLI1 Homo sapiens cDNA clone IMAGE:2075103 3'
7256	19940	33015	0.74	2.7E-01	Q11079	SWISSPROT	HYPOTHETICAL 20.9 KD PROTEIN B0563.3 IN CHROMOSOME X
7461	20134	33225	0.75	2.7E-01	Q01168	SWISSPROT	NITROGEN REGULATORY PROTEIN NUT1
7461	20134	33226	0.75	2.7E-01	Q01168	SWISSPROT	NITROGEN REGULATORY PROTEIN NUT1
7588	20256	33363	2.16	2.7E-01	AF248054.1	NT	Bos taurus micromolar calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds
7588	20256	33364	2.16	2.7E-01	AF248054.1	NT	Bos taurus micromolar calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds
7638	20303	33411	0.94	2.7E-01	AA351121.1	EST_HUMAN	EST58740 Infant brain Homo sapiens cDNA 5' end similar to myosin-binding protein H
7638	20303	33412	0.94	2.7E-01	AA351121.1	EST_HUMAN	EST58740 Infant brain Homo sapiens cDNA 5' end similar to myosin-binding protein H
7694	20358	33472	0.71	2.7E-01	L01081.1	NT	Oryctolagus cuniculus UDP-glucuronosyltransferase (UGT2B13) mRNA, complete cds
7763	20459	33583	0.68	2.7E-01	AA013147.1	EST_HUMAN	ze35b11.s1 Soares, retina N2b44-IR Homo sapiens cDNA clone IMAGE:360957 3' similar to contains Alu repetitive element;

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7925	20620		0.53	2.7E-01	AF048820.1	NT	Carassius auratus pituitary adenylate cyclase activating polypeptide type 1 receptor precursor mRNA, complete cds
8086	20780	33909	0.51	2.7E-01	R39257.1	EST_HUMAN	yc91h06.s1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:23511 3'
8190	20884	34022	0.8	2.7E-01	AL161552.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 52
8657	21349	34494	0.59	2.7E-01	Q14764	SWISSPROT	MAJOR VAULT PROTEIN (MVP) (LUNG RESISTANCE-RELATED PROTEIN)
8925	21616	34760	0.46	2.7E-01	X03216.1	NT	Staphylococcus aureus transposon Tn554
9232	21911	35084	10.41	2.7E-01	O83809	SWISSPROT	THREONYL-TRNA SYNTHETASE (THREONINE-TRNA LIGASE) (THRRS)
9232	21911	35085	10.41	2.7E-01	O83809	SWISSPROT	THREONYL-TRNA SYNTHETASE (THREONINE-TRNA LIGASE) (THRRS)
9235	21914		2	2.7E-01	P37928	SWISSPROT	FIMBRIAE W PROTEIN
9700	22351	35546	0.61	2.7E-01	D89660.1	NT	Rattus norvegicus DNA for peroxisome assembly factor-2, exon 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17 and complete cds
9981	22629	35838	0.74	2.7E-01	AF091848.1	NT	Oryctolagus cuniculus calgranulin C mRNA, partial cds
10018	22666	35882	3.09	2.7E-01	AF097434.1	NT	Mus musculus transcription factor NF-ATc isoform a (NF-ATc) mRNA, complete cds
10149	22797	36012	0.57	2.7E-01	AF156539.1	NT	Homo sapiens xeroderma pigmentosum complementation group C (XPC) gene, intron 9
10149	22797	36013	0.57	2.7E-01	AF156539.1	NT	Homo sapiens xeroderma pigmentosum complementation group C (XPC) gene, intron 9
10714	23403	36642	1.62	2.7E-01	AV705043.1	EST_HUMAN	AV705043 ADB Homo sapiens cDNA clone ADBCOD05 5'
10714	23403	36643	1.62	2.7E-01	AV705043.1	EST_HUMAN	AV705043 ADB Homo sapiens cDNA clone ADBCOD05 5'
10724	23412	36653	3.13	2.7E-01	AJ133269.1	NT	Homo sapiens cavedin-1/-2 locus, Contig 1, D7S522, genes CAV2 (exons 1, 2a, and 2b), CAV1 (exons 1 and 2)
11820	24406		1.5	2.7E-01	O14181	SWISSPROT	PUTATIVE 60S RIBOSOMAL PROTEIN C4F8.05C
12482	25190		1.49	2.7E-01	AB008782.1	NT	Arabidopsis thaliana mRNA for sulfate transporter, complete cds
12665	24863		2.83	2.7E-01	AF217491.1	NT	Homo sapiens fragile 16D oxido reductase (FOR) gene, exon 6
12811	25054	30929	1.95	2.7E-01	AV742419.1	EST_HUMAN	AV742419 CB Homo sapiens cDNA clone CBMAXF02 5'
457	15542	25883	2.03	2.6E-01	P78411	SWISSPROT	IROQUOIS-CLASS HOMEODOMAIN PROTEIN IRX-2
468	13254		1.38	2.6E-01	D16459.1	NT	Bos taurus mRNA for mb-1, complete cds
1372	14120	26795	1.66	2.6E-01	BE865087.1	EST_HUMAN	601510838F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3912345 5'
1417	14165	26848	1.14	2.6E-01	AB013290.1	NT	Glycine max pseudogene for Bd 30K
1889	14626	27335	4.33	2.6E-01	AL161472.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 2
1889	14626	27336	4.33	2.6E-01	AL161472.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 2
							bb04d10.x1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:2958451 3' similar to gb:M36072 60S RIBOSOMAL PROTEIN L7A (HUMAN); gb:M14689_cds1 Mouse surfeit locus surfeit 3 protein gene (MOUSE);
2086	14818		10.48	2.6E-01	AW733152.1	EST_HUMAN	Human prealbumin gene, complete cds
2148	14878	27613	3.7	2.6E-01	M11844.1	NT	B. maritimus rbcL gene
2476	15194		1.62	2.6E-01	Y12996.1	NT	

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2548	15263		8.87	2.6E-01	BE272440.1	EST_HUMAN	601126016F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:2980043 5'
3568	16323	28971	8.99	2.6E-01	M22342.1	NT	Bacteriophage T2 DNA-(adenine-N6)methyltransferase (dam) gene, complete cds
3634	16387	29028	2.02	2.6E-01	AF229118.1	NT	Homo sapiens acetylcholinesterase collagen-like tail subunit (COLQ) gene, exons 1A, 2, 3, 4, and 5
4079	16823	29449	0.96	2.6E-01	AW959510.1	EST_HUMAN	EST371580 MAGE resequences, MAGF Homo sapiens cDNA
4134	16876	29506	16.7	2.6E-01	BE080598.1	EST_HUMAN	QV1-BT0630-040400-132-e03 BT0630 Homo sapiens cDNA
4324	17063	29691	1.2	2.6E-01	AF175293.1	NT	Enterococcus faecium strain N97-330 vanD glycopeptide resistance gene cluster, complete cds; and unknown gene
4459	17195	29821	0.8	2.6E-01	AB021180.1	NT	Gallus gallus mRNA for skeletal myosin heavy chain, complete cds
4459	17195	29822	0.8	2.6E-01	AB021180.1	NT	Gallus gallus mRNA for skeletal myosin heavy chain, complete cds
4511	17246	29881	1.46	2.6E-01	AA457617.1	EST_HUMAN	aa89d07.1 Stratagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:838477 5'
4601	17336	29865	1.77	2.6E-01	U01103.1	NT	Arabidopsis thaliana PSI type III chlorophyll a/b-binding protein (Lhca3*) mRNA, complete cds
4687	17401	30035	1.18	2.6E-01	AF142703.1	NT	Ophrestia radicea metatranscriptase-like protein (metK) gene, complete cds; chloroplast gene for chloroplast product
4910	17638	30252	0.95	2.6E-01	AF153350.1	NT	Mus musculus metalloprotease disintegrin (Adam28) mRNA, complete cds
4914	17642	30257	3.6	2.6E-01	H04858.1	EST_HUMAN	y51e05.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:152288 5'
5257	18063		1.06	2.6E-01	AB035972.1	NT	Paramecium caudatum gene for PAP, complete cds
5484	18283		0.68	2.6E-01	AI862398.1	EST_HUMAN	td16a03.x1 NCL_CGAP_Cot16 Homo sapiens cDNA clone IMAGE:2075788 3' similar to contains element MER35 repetitive element
5698	18481	31400	0.73	2.6E-01	AF207550.1	NT	Homo sapiens protein translocase, JM26 protein, UDP-galactose translocator, pim-2 protooncogene homolog pim-2h, and shal-type potassium channel genes, complete cds; JM12 protein and transcription factor (GHM enhancer 3 genes, partial cds; and unknown g>
5980	25417		2.35	2.6E-01	AE001811.1	NT	Thermotoga maritima section 123 of 136 of the complete genome
6108	18885	31854	2.28	2.6E-01	AI582557.1	EST_HUMAN	ts02e12.x1 NCL_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2227438 3' similar to SW:NDF1_RAT Q64289 NEUROGENIC DIFFERENTIATION FACTOR 1; contains element LTR1 repetitive element
6108	18885	31855	2.26	2.6E-01	AI582557.1	EST_HUMAN	ts02e12.x1 NCL_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2227438 3' similar to SW:NDF1_RAT Q64289 NEUROGENIC DIFFERENTIATION FACTOR 1; contains element LTR1 repetitive element
6328	19098	32086	0.91	2.6E-01	AL162757.2	NT	Neisseria meningitidis serogroup A strain Z2491 complete genome; segment 6/7
6570	19334	32344	0.73	2.6E-01	BE792052.1	EST_HUMAN	601581754F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3936156 5'
6570	19334	32345	0.73	2.6E-01	BE792052.1	EST_HUMAN	601581754F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3936156 5'
6938	19973	32719	0.9	2.6E-01	AI914380.1	EST_HUMAN	wid48c04.x1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2331366 3' similar to gb:M37721 PEPTIDYL-GLYCINE ALPHA-AMIDATING MONOOXYGENASE PRECURSOR (HUMAN);

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7289	19972	33050	0.82	2.6E-01	BE148961.1	EST_HUMAN	CMO-HT0245-031 199-085-f04 HT0245 Homo sapiens cDNA
7329	25110		0.79	2.6E-01	AL139077.2	NT	Campylobacter jejuni NCTC11168 complete genome; segment 4/8
7363	20044		0.89	2.6E-01	AA196149.1	EST_HUMAN	zp92a01.r1 Stratagene HeLa cell s3 937216 Homo sapiens cDNA clone IMAGE:627672 5'
7639	20304	33413	1.9	2.6E-01	R10365.1	EST_HUMAN	yf37a03.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:129004 3' similar to gb:X12517 U1 SMALL NUCLEAR RIBONUCLEOPROTEIN C (HUMAN);
7687	20351	33465	0.66	2.6E-01	Q09855	SWISSPROT	HYPOTHETICAL TRP-ASP REPEATS CONTAINING PROTEIN C29E6.01 IN CHROMOSOME 1
7748	20444	33568	1.3	2.6E-01	R02411.1	EST_HUMAN	ye82a07.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:124212 5'
7804	20499	33620	1.15	2.6E-01	BE144331.1	EST_HUMAN	MRO-HT0168-181199-003-d12 HT0168 Homo sapiens cDNA
8040	20735	33867	0.64	2.6E-01	X82641.1	NT	D.melanogaster mRNA for alpha 1,2 mannosidase (Berlin)
8040	20736	33868	0.64	2.6E-01	X82641.1	NT	D.melanogaster mRNA for alpha 1,2 mannosidase (Berlin)
8232	20926	34064	3.05	2.6E-01	BF343588.1	EST_HUMAN	602014422F1 NCJ CGAP_Bm84 Homo sapiens cDNA clone IMAGE:4150396 5'
8309	21003	34140	2.13	2.6E-01	Q10199	SWISSPROT	HYPOTHETICAL 75.2KD PROTEIN C11C11.02 IN CHROMOSOME 11
8594	21286	34424	4.32	2.6E-01	BE830339.1	EST_HUMAN	RC8-ET0082-310500-021-F10 ET0082 Homo sapiens cDNA
8594	21286	34425	4.32	2.6E-01	BE830339.1	EST_HUMAN	RC8-ET0082-310500-021-F10 ET0082 Homo sapiens cDNA
9367	21942	35116	0.96	2.6E-01	X17604.1	NT	S. occidentalis INV gene for invertase (EC 3.2.1.26)
9639	22291		0.62	2.6E-01	AF057121.1	NT	Lontra canadensis cytochrome b (cytb) gene, mitochondrial gene encoding mitochondrial protein, complete cds
9768	22419	35626	1.19	2.6E-01	P87366	SWISSPROT	GREEN-SENSITIVE OPSIN (GREEN CONE PHOTORECEPTOR PIGMENT) (KHF-G)
9788	22419	35627	1.19	2.6E-01	P87366	SWISSPROT	GREEN-SENSITIVE OPSIN (GREEN CONE PHOTORECEPTOR PIGMENT) (KHF-G)
9930	22578		0.48	2.6E-01	U67581.1	NT	Methanococcus jannaschii section 123 of 160 of the complete genome
10090	22738		0.74	2.6E-01	Q28295	SWISSPROT	VON WILLEBRAND FACTOR PRECURSOR (VWF)
10406	23052		0.9	2.6E-01	Y10196.1	NT	Homo sapiens PHEX gene
10467	23113		0.45	2.6E-01	AB015355.1	NT	Homo sapiens NRAMP2 gene for natural resistance-associated macrophage protein 2, complete cds
11400	24006	37310	1.78	2.6E-01	P48280	SWISSPROT	CELL DIVISION PROTEIN FTSW HOMOLOG
11511	24111		66.41	2.6E-01	X51755.1	NT	Human lambda-immunoglobulin constant region complex (germline)
11996	24534		1.71	2.6E-01	10190855	NT	Mus musculus Jerky (Jrk), mRNA
12177	25309		3.1	2.6E-01	BE883491.1	EST_HUMAN	601511052F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3912612 5'
12242	24693	31077	2.81	2.6E-01	AF316896.1	NT	Homo sapiens Na/K-ATPase gamma subunit (FXVD2) gene, complete cds, alternatively spliced
12565	24895		1.56	2.6E-01	D88425.1	NT	Cavia cobaya mRNA for serine/threonine kinase, complete cds
12725	24996		2.19	2.6E-01	P47285	SWISSPROT	HYPOTHETICAL PROTEIN MG039
234	13045	25684	2.55	2.5E-01	4502296	NT	Homo sapiens ATP synthase, H ⁺ -transporting, mitochondrial F1 complex, delta subunit (ATP5D), nuclear gene encoding mitochondrial protein, mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
235	13045	25684	2.39	2.5E-01	4502296	NT	Homo sapiens ATP synthase, H ⁺ transporting, mitochondrial F1 complex, delta subunit (ATP5D), nuclear
248	13057		3.32	2.5E-01	M26501.1	NT	Starfish (P. ochraceus) cytoplasmic actin gene, complete cds
813	13584	26250	1.35	2.5E-01	U09984.1	NT	Mus musculus ICR/Swiss glycerinaldehyde 3-phosphate dehydrogenase (Gapdh-S) gene, complete cds
1038	13788		1.2	2.5E-01	AE002156.1	NT	Ureaplasma urealyticum section 57 of 59 of the complete genome
1099	13857	28517	6.42	2.5E-01	T89837.1	EST_HUMAN	ye11g07.r1 Stralagene lung (#937210) Homo sapiens cDNA clone IMAGE:117468 5'
1509	14255	26941	0.9	2.5E-01	AL115624.1	NT	Bovine chereia strain T4 cDNA library under conditions of nitrogen deprivation
1721	14464		4.79	2.5E-01	4885406	NT	Homo sapiens hyperpolarization activated cyclic nucleotide-gated potassium channel 4 (HCN4) mRNA
1876	15581	27323	1.88	2.5E-01	BE696604.1	EST_HUMAN	PM4-CT0400-310700-005-408 CT0400 Homo sapiens cDNA
1876	15581	27324	1.58	2.5E-01	BE696604.1	EST_HUMAN	PM4-CT0400-310700-005-408 CT0400 Homo sapiens cDNA
2407	15128		16	2.5E-01	AE000675.1	NT	Aquifex acidicus section 7 of 109 of the complete genome
2500	15217		1.08	2.5E-01	AA251987.1	EST_HUMAN	zs11a12.r1 NCI_QGAP_GCB1 Homo sapiens cDNA clone IMAGE:684862 5'
3370	16129		0.84	2.5E-01	BF698193.1	EST_HUMAN	602125525F1 NIH_MGC 58 Homo sapiens cDNA clone IMAGE:4282279 5'
3407	16165		3.04	2.5E-01	AW97347.1	EST_HUMAN	EST365464 IMAGE resequences, MAGM Homo sapiens cDNA
3524	16280	28935	1.25	2.5E-01	AF233875.1	NT	Danio rerio peptide YY precursor gene, complete cds
3537	16293	28942	7.54	2.5E-01	AL161517.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 29
3828	16579	29211	1.53	2.5E-01	AI741483.1	EST_HUMAN	wg11c07.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2364780 3'
3828	16579	29212	1.53	2.5E-01	AI741483.1	EST_HUMAN	wg11c07.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2364780 3'
4283	17022		0.97	2.5E-01	Q03314	SWISSPROT	RHIB PROTEIN
4700	17434		1.25	2.5E-01	Q27225	SWISSPROT	MOLT-INHIBITING HORMONE PRECURSOR (Mih)
4706	17438	30070	3.98	2.5E-01	AF007768.1	NT	Charistoneura fumiferana diapause associated protein 2 (DAP2) mRNA, complete cds
4732	17484	30101	2.01	2.5E-01	AE004416.1	NT	Vibrio cholerae chromosome II, section 73 of 93 of the complete chromosome
4751	17483		3.7	2.5E-01	AJ230113.1	NT	Mus musculus annexin V gene, intron 4 segment containing 5' LTR and gag portion of MuERV-L (murine endogenous retrovirus) element
4781	17513	30135	1.09	2.5E-01	BE896785.1	EST_HUMAN	601437468F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3922600 5'
4987	17710	30315	0.71	2.5E-01	AW879588.1	EST_HUMAN	h08211.x1 Soares_NFL_I_GBC_S1 Homo sapiens cDNA clone IMAGE:3041997 3' similar to
5243	18049	30678	13.48	2.5E-01	S83390.1	NT	WP_Y71F9A_294.D CE22858
5870	18657	31598	0.73	2.5E-01	AJ006345.1	NT	T3 receptor-associated cofactor-1 [human, fetal liver, mRNA, 2930 nt]
5871	18658		0.98	2.5E-01	AL163207.2	NT	Homo sapiens KVLQ1 gene
6529	19295	32299	0.95	2.5E-01	AJ251973.1	NT	Homo sapiens chromosome 21 segment HS21C007
6945	19427	32442	0.79	2.5E-01	8394138	NT	Homo sapiens partial steerin-1 gene
							Rattus norvegicus rablin 3 (RABIN3), mRNA

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Table 4
Single Exon Probes Expressed In Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7252	19936	33011	0.88	2.5E-01	U13992.1	NT	Feline calicivirus CFI69 RNA helicase/cysteine protease/RNA-dependent RNA polymerase polyprotein precursor and capsid protein precursor, genes, complete cds; and unknown gene
7278	19962		1.29	2.5E-01	AF134119.1	NT	Mus musculus SKD1 (Skd1) gene, complete cds
7494	20167	33259	0.83	2.5E-01	AL161506.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 18
7536	20206	33303	3.6	2.5E-01	AL163282.2	NT	Homo sapiens chromosome 21 segment HS21C082
7744	20440	33564	2.47	2.5E-01	BF109040.1	EST_HUMAN	7157a03.x1 Soares NSF F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3525389 3'
7754	20450	33574	0.8	2.5E-01	BE960712.1	EST_HUMAN	601653391R2 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3826198 3'
8125	20819	33955	1.87	2.5E-01	BF038595.1	EST_HUMAN	601469238F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3862809 5'
8298	20890	34128	0.7	2.5E-01	P04492	SWISSPROT	E1B PROTEIN, SMALL T-ANTIGEN (E1B 19K)
8534	21226	34368	3.87	2.5E-01	H53236.1	EST_HUMAN	yq84f07.r1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:202501 5'
8774	21466	34613	0.79	2.5E-01	M88626.1	NT	Mouse testis-specific protein (TPX-1) gene, exon 10
9416	22094	35265	15.72	2.5E-01	U89651.2	NT	Homo sapiens matrix metalloproteinase MMP Rasi-1 gene, promoter region
9416	22094	35266	15.72	2.5E-01	U89651.2	NT	Homo sapiens matrix metalloproteinase MMP Rasi-1 gene, promoter region
9472	22081	35253	2.06	2.5E-01	AF085164.1	NT	Hordeum vulgare receptor-like kinase LRK10 gene, partial cds
9472	22081	35254	2.06	2.5E-01	AF085164.1	NT	Hordeum vulgare receptor-like kinase LRK10 gene, partial cds
9998	22646	35858	1.39	2.5E-01	AW581997.1	EST_HUMAN	RC3-ST0186-130100-015-a07 ST0186 Homo sapiens cDNA
10441	23087	36315	2.13	2.5E-01	AW152246.1	EST_HUMAN	xg40c10.x1 NCJ_CGAP_U11 Homo sapiens cDNA clone IMAGE:2630034 3' similar to contains Alu repetitive element/contains element MSR1 repetitive element ;
10444	23090	36319	1.21	2.5E-01	X58491.1	NT	Mouse L1Md LINE DNA
11013	23685	36945	3.43	2.5E-01	D50914.1	NT	Human mRNA for KIAA0124 gene, partial cds
11647	24244		1.61	2.5E-01	AF027153.1	NT	Homo sapiens sodium/myo-inositol cotransporter (SLC5A3) gene, complete cds
11803	24393	37727					
11832	24490	37808	1.29	2.5E-01	U46315.1	NT	Litomosoides sigmodontis microfilarial sheath protein SHP1a precursor (shp1a) gene, complete cds
11960	25386		5.12	2.5E-01	AF200528.1	NT	Zea mays cellulose synthase-4 (Cesa-4) mRNA, complete cds
12365	24798		6.13	2.5E-01	AL161541.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 41
12412	25233	30821	1.37	2.5E-01	AF000003.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 544001-777000 nt, position (3/7)
540	13323	25955	1.69	2.5E-01	AF170072.1	NT	Spodoptera frugiperda CALNUC mRNA, complete cds
828	13598	26269	3.34	2.4E-01	AA936316.1	EST_HUMAN	on70d04.st Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1562023 3'
1281	14031	26700	33.63	2.4E-01	BF576124.1	EST_HUMAN	602132442F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4271578 5'
1281	14031	26701	33.63	2.4E-01	AJ289880.1	NT	Homo sapiens KIAA0851 gene (partial), XT3 gene and LZTFL1 gene
1363	14111	26785	1.03	2.4E-01	AJ289880.1	NT	Homo sapiens KIAA0851 gene (partial), XT3 gene and LZTFL1 gene
1843	14581		32.88	2.4E-01	AF267753.1	NT	Homo sapiens FLI-1 gene, partial
1893	14630	27340	1.33	2.4E-01	AF251708.1	NT	Mesembryanthemum crystallinum putative potassium channel protein Mkt1p mRNA, complete cds
							Zacays dhumnades fructose-1,6-bisphosphatase mRNA, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2134	14864	27594	1.1	2.4E-01	AF111188.2	NT	Homo sapiens serine palmitoyl transferase, subunit II gene, complete cds; and unknown genes
2165	14894		1.44	2.4E-01	P46394	SWISSPROT	IMMUNOGLOBULIN A1 PROTEASE PRECURSOR (IGAT1 PROTEASE)
2258	14985	27725	2.28	2.4E-01	AE000890.1	NT	Aquifex acidicus section 12 of 109 of the complete genome
2382	15104	27843	1.38	2.4E-01	BF002171.1	EST_HUMAN	7h23d04.x1 NCI_CGAP_Co16 Homo sapiens cDNA clone IMAGE:3316807 3' similar to SW:PRSB_XENLA
2539	15254	27994	2.46	2.4E-01	Z36534.1	NT	O42586 26S PROTEASE REGULATORY SUBUNIT 6A ;
2765	15470	28213	2.16	2.4E-01	X71783.1	NT	D.discoideum (Ax3-K) porA gene
2789	15494	28234	2.84	2.4E-01	AF030154.1	NT	S.pombe swf6 gene
						NT	Bovine adenovirus 3 complete genome
3129	15894		2.94	2.4E-01	U72726.1	NT	Oryza longistaminata receptor kinase-like protein, family member D, and retrofit (gag/pol) genes, complete cds
3145	15909	28554	1.48	2.4E-01	X74209.1	NT	H.sapiens AGT gene, PstI fragment of intron 4
3743	16498	29131	0.73	2.4E-01	AE000312.1	NT	Escherichia coli K-12 MG1655 section 202 of 400 of the complete genome
4010	16756		0.74	2.4E-01	D29960.1	NT	Rattus norvegicus mRNA for alphaB crystallin-related protein, complete cds
4883	17610		1.09	2.4E-01	AL161589.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 85
4989	17712	30317	0.96	2.4E-01	D00944.1	NT	Hepatitis C virus genomic RNA for polyprotein, complete cds
5375	18175	30865	0.98	2.4E-01	A1925707.1	EST_HUMAN	w033405.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2457129 3'
5375	18175	30868	0.98	2.4E-01	A1925707.1	EST_HUMAN	w033405.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2457129 3'
5397	18197	30891	0.8	2.4E-01	D50871.1	NT	Glycine max mRNA for mitotic cyclin b1-type, complete cds
5569	18366	31275	8.16	2.4E-01	AF091216.1	NT	Mus musculus Wrm protein (Wrm) gene, complete cds
5569	18366	31276	8.16	2.4E-01	AF091216.1	NT	Mus musculus Wrm protein (Wrm) gene, complete cds
5597	18392		0.77	2.4E-01	M83377.1	NT	Gallus gallus brain-derived neurotrophic factor (BDNF) gene, 5' end
5799	25076		0.99	2.4E-01	AJ133836.2	NT	Branchiostoma floridae mRNA for calmodulin 2 (cam2) gene
						EST_HUMAN	7154d04.x1 NCI_CGAP_Br16 Homo sapiens cDNA clone IMAGE:3338503 3' similar to SW:SFR4_HUMAN
5805	18595	31520	2.22	2.4E-01	BF502336.1	EST_HUMAN	Q08170 SPLICING FACTOR, ARGININE/SERINE-RICH 4, contains element TAR1 TARI repetitive element
5895	18680	31627	3	2.4E-01	AF035546.1	NT	Drosophila melanogaster p38a MAP kinase gene, complete cds
5999	18780	31741	2.53	2.4E-01	7661801	NT	Homo sapiens HSPC142 protein (HSPC142), mRNA
6050	18830	31793	0.67	2.4E-01	AV733787.1	EST_HUMAN	AV733787 cda Homo sapiens cDNA clone cdAADE11 5'
						EST_HUMAN	wc62c11.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2323220 3' similar to gb.J03464
6441	19209	32206	2.23	2.4E-01	A1698989.1	EST_HUMAN	PROCOLLAGEN ALPHA 2(I) CHAIN PRECURSOR (HUMAN);
7243	19928	33004	9.5	2.4E-01	L43001.1	NT	Bos taurus guanylyl cyclase-activating protein 2 (guca2) mRNA, complete cds
7404	20081	33163	0.55	2.4E-01	N48732.1	EST_HUMAN	yy55c11.r1 Soares_multiple sclerosis 2N6HMSF Homo sapiens cDNA clone IMAGE:277460 5'
7625	20291	33400	0.81	2.4E-01	AF229044.1	NT	Mus musculus DXImx48e protein (DXImx48e) mRNA, complete cds
8247	20941	34076	1.61	2.4E-01	AJ012685.1	NT	Tetrahymena thermophila macronuclear gene encoding ribosomal protein L3, exons 1-2

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8497	21189	34332	1.02	2.4E-01	BF242794.1	EST_HUMAN	601877679F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4106298 5'
8552	21244		0.47	2.4E-01	BF678275.1	EST_HUMAN	602086188F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4250372 5'
9030	21720	34874	0.49	2.4E-01	AL139077.2	NT	Campylobacter jejuni NGTC11168 complete genome; segment 4/6
9030	21720	34876	0.49	2.4E-01	AL139077.2	NT	Campylobacter jejuni NGTC11168 complete genome; segment 4/6
9463	22013	35181	7.01	2.4E-01	AF693515.1	EST_HUMAN	wd43e02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2330906 3' similar to contains
9603	22256	35441	0.88	2.4E-01	AF220067.1	NT	MER22.b1 TAR1 repetitive element ;
9603	22256	35442	0.88	2.4E-01	AF220067.1	NT	Drosophila melanogaster SKPB gene, complete cds
10337	22984	36202	1.68	2.4E-01	Q03692	SWISSPROT	Drosophila melanogaster SKPB gene, complete cds
10667	23358	36598	4.6	2.4E-01	AL161494.2	NT	COLLAGEN ALPHA 1(X) CHAIN PRECURSOR
10739	23428	36671	1.39	2.4E-01	AF030196.1	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 6
11158	23825		2.09	2.4E-01	Z21847.1	NT	Mus musculus type 1 sigma receptor gene, complete cds
11840	24424	37765	1.32	2.4E-01	BE617538.1	EST_HUMAN	P.asiatica mosaic virus genomic RNA
11891	24461	37801	1.75	2.4E-01	AF217491.1	NT	601441421T1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3845836 3'
12019	25180		2.34	2.4E-01	AF004213.1	NT	Homo sapiens fragile 16D oddo reductase (FOR) gene, exon 6
12080	24588		2.74	2.4E-01	AJ278191.1	NT	Arabidopsis thaliana ethylene-insensitive3-like1 (EIL1) mRNA, complete cds
12287	25162		1.97	2.4E-01	V01507.1	NT	Mus musculus mRNA for putative mc7 protein (mc7 gene)
12400	25201		2.06	2.4E-01	BF184642.1	EST_HUMAN	Gallus gallus gene coding for a-actin
12720	24992		3.66	2.4E-01	AL183281.2	NT	601842848F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4083739 5'
380	13167	25810	1.06	2.3E-01	S75898.1	NT	Homo sapiens chromosome 21 segment HS21C081
622	13401		5	2.3E-01	U39713.1	NT	aromatase [Poephila guttata=zabira finches, ovary, mRNA, 3188 nt]
652	13430	26069	33.31	2.3E-01	U67596.1	NT	Mycoplasma genitalium section 35 of 51 of the complete genome
913	13680	26341	4.19	2.3E-01	BE311893.1	EST_HUMAN	Methanococcus jannaschii section 138 of 150 of the complete genome
1558	14305		1.12	2.3E-01	U22837.2	NT	601142073F1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:3505818 5'
1599	14345	27035	1.23	2.3E-01	AJ245480.1	NT	Yersinia pestis HmsH (hmsH), HmsF (hmsF), HmsR (hmsR), and HmsS (hmsS) genes, complete cds
1628	14374	27063	2.74	2.3E-01	Y10887.2	NT	Brassica napus sig gene for S-locus glycoprotein, cultivar T2
2038	14772		1.51	2.3E-01	AJ235563.1	NT	Mus musculus cds5 gene, exon 1, partial
2447	15166	27903	2.66	2.3E-01	BE297718.1	EST_HUMAN	Homo sapiens partial intron 3 of the wild type AF-4FEL gene
2657	15367	28105	1.59	2.3E-01	M11319.1	NT	601175562F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3531015 5'
2827	14114	26789	3.38	2.3E-01	AB015033.1	NT	Human erythropoietin gene, complete cds
2963	15726	28379	1.36	2.3E-01	AA601379.1	EST_HUMAN	Marinibacteria agarovorans gyrB gene for DNA gyrase subunit B, partial cds, strain:FO 14957
3082	15847		7.07	2.3E-01	R21732.1	EST_HUMAN	no16d06.s1 NCI_CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1100843 3' similar to contains Alu repetitive element; contains element T1-R repetitive element ;
							yh21b07.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:130357 3'

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3363	16122	28780	1.14	2.3E-01	H68836.1	EST_HUMAN	Y97H10.1 Soares fetal liver spleen 1NFSL Homo sapiens cDNA clone IMAGE:213283 5'
3821	16573	29205	1.01	2.3E-01	S82821.1	NT	GSTA5-glutathione S-transferase Yc2 subunit (5' region, intron 1) [rats, Morris hepatoma cell line, Genomic, 2212 nt, segment 1 of 3]
3914	16664		5.22	2.3E-01			
4316	17055	29680	1.1	2.3E-01	R82252.1	EST_HUMAN	Homo sapiens KIAA0450 gene product (KIAA0450), mRNA
4368	17106		1.98	2.3E-01	L78789.1	NT	Y11701.1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:149017 5'
4417	17163	29784	1.03	2.3E-01	D90899.1	NT	Mus musculus renin (Ren-1c) gene, promoter region
4454	17190	29816	2.51	2.3E-01	AF092535.1	NT	Synechocystis sp. PC08803 complete genome, 1/27, 1-133859
4517	17252	29887	6.19	2.3E-01	503184	NT	Homo sapiens mitogen-activated protein kinase p38delta (PRKM13) mRNA, complete cds
4988	17711	30316	0.84	2.3E-01	AB032400.1	NT	Homo sapiens nuclear transport factor 2 (placental protein 15) (PP15) mRNA
5221	18028	30654	2.53	2.3E-01	AB040945.1	NT	Mus musculus tujip 1 mRNA, complete cds
							Homo sapiens mRNA for KIAA1512 protein, partial cds
5343	18146	30825	2.08	2.3E-01	BF058381.1	EST_HUMAN	7k30b06.x1 NCL CGAP_OV18 Homo sapiens cDNA clone IMAGE:3476999 3' similar to SW.GAG_SMSAV
5443	18242	31130	4.58	2.3E-01	X96587.1	NT	P03330 GAG POLYPROTEIN [CONTAINS: CORE PROTEIN P15; INNER COAT PROTEIN P12; CORE SHELL PROTEIN P30; NUCLEOPROTEIN P10]. ;
5563	18360		0.94	2.3E-01	L39112.1	NT	C.familiaris tom1 gene
5665	18460	31374	0.76	2.3E-01	S60371.1	NT	Vitiforma cornutum small subunit ribosomal RNA gene
5851	18638	31575	1.59	2.3E-01	A1708840.1	EST_HUMAN	23S rRNA [Leuconostoc carnosum, Genomic, 2866 nt]
							as27e12.x1 Barstead aorta HPLRB6 Homo sapiens cDNA clone IMAGE:2318446 3' similar to gb.X13238
5851	18638	31576	1.59	2.3E-01	A1708840.1	EST_HUMAN	CYTTOCHROME C OXIDASE POLYPEPTIDE VIC PRECURSOR (HUMAN);
							as27e12.x1 Barstead aorta HPLRB6 Homo sapiens cDNA clone IMAGE:2318446 3' similar to gb.X13238
6558	19323	32330	0.93	2.3E-01	AF198089.1	NT	CYTTOCHROME C OXIDASE POLYPEPTIDE VIC PRECURSOR (HUMAN);
							Oryctolagus cuniculus cytochrome oxidase subunit VIa (coxVIa2) mRNA, complete cds; nuclear gene for mitochondrial product
6778	19522	32549	4.33	2.3E-01	A1718148.1	EST_HUMAN	as42f12.x1 Barstead aorta HPLRB6 Homo sapiens cDNA clone IMAGE:2319887 3' similar to contains Alu repetitive element
7011	19703	32759	1.08	2.3E-01	8923323	NT	Homo sapiens hypothetical protein FLJ20345 (FLJ20345), mRNA
7188	19874	32947	0.9	2.3E-01	AF000227.1	NT	Secale cereale omega secalin gene, complete cds
7315	19998	33077	3.14	2.3E-01	AF175389.1	NT	Glycine max resistance protein LM17 precursor RNA, partial cds
7318	20001	33079	0.64	2.3E-01	AV719681.1	EST_HUMAN	AV719681 GLC Homo sapiens cDNA clone GLCDB08 5'
7318	20001	33080	0.64	2.3E-01	AV719681.1	EST_HUMAN	AV719681 GLC Homo sapiens cDNA clone GLCDB08 5'
7508	20179		2.94	2.3E-01	6754779	NT	Mus musculus myosin XV (Myo15), mRNA
7513	20184	33278	1.38	2.3E-01	BE888071.1	EST_HUMAN	601511573F1 NIH_MGC-71 Homo sapiens cDNA clone IMAGE:3812859 5'
7652	20316		2.73	2.3E-01	N80083.1	EST_HUMAN	zat12608.r1 Soares fetal liver spleen 1NFSL Homo sapiens cDNA clone IMAGE:292358 5'
7750	20446	33569	0.71	2.3E-01	AL161558.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 58

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7892	20587	33717	2.16	2.3E-01	M68931.1	NT	Oxyfiche nova macronuclear telomere-binding protein alpha subunit (tel-alpha alanine version) gene, complete cds
8391	21084	34217	0.47	2.3E-01	U57899.1	NT	Mus musculus prosaposin (psap) (SGP-1) gene, complete cds
8671	21363	34510	0.66	2.3E-01	AW090541.1	EST_HUMAN	xc90e06.x1 NCI CGAP_Brn35 Homo sapiens cDNA clone IMAGE:2591554 3'
8786	21478	34627	0.45	2.3E-01	AW964460.1	EST_HUMAN	EST376533 IMAGE resequences, MAGH Homo sapiens cDNA
9039	21729	34883	1.02	2.3E-01	AA372164.1	EST_HUMAN	EST84061 Rhabdomyosarcoma Homo sapiens cDNA 5' end similar to DnaJ homolog (GB:X63368)
9039	21729	34884	1.02	2.3E-01	AA372164.1	EST_HUMAN	EST84061 Rhabdomyosarcoma Homo sapiens cDNA 5' end similar to DnaJ homolog (GB:X63368)
9480	22133	35313	0.62	2.3E-01	6679318	NT	Mus musculus phosphatidylinositol 3-kinase catalytic subunit delta (PIK3cd), mRNA
9609	22262	35448	0.62	2.3E-01	U77974.1	NT	Tribolium castaneum transcription factor homolog (Tc-efe) gene, complete cds
9628	22281	35471	0.5	2.3E-01	BE277860.1	EST_HUMAN	601120110F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2966739 5'
9682	22334	35528	0.59	2.3E-01	AW864460.1	EST_HUMAN	EST376533 IMAGE resequences, MAGH Homo sapiens cDNA
9731	22382	35584	1.02	2.3E-01	X62124.1	NT	Haemophilus influenzae genes for HincII restriction-modification system (HincII methyltransferase (EC 2.1.1.72) and HincII endonuclease (EC 3.1.21.4))
9767	22418	35625	0.56	2.3E-01	AW364633.1	EST_HUMAN	PM2-D70036-281299-001-r04 DT0036 Homo sapiens cDNA
9834	22485	35686	2.45	2.3E-01	BE173080.1	EST_HUMAN	MRO-HT0569-240400-014-g11 HT0559 Homo sapiens cDNA
9882	22542	35734	2.75	2.3E-01	AJ293261.1	NT	Rhizobium leguminosarum partial genomic DNA for exopolysaccharide biosynthesis genes
10340	22687	36205	0.84	2.3E-01	AF201928.1	NT	Murine hepatitis virus strain 2, complete genome
10351	22898		5.11	2.3E-01	BF133577.1	EST_HUMAN	601846156R2 NIH_MGC_59 Homo sapiens cDNA clone IMAGE:4102092 3'
10937	23617	36867	1.49	2.3E-01	AF004833.1	NT	Mus musculus tissue factor pathway inhibitor (TFPI) mRNA, complete cds
10937	23617	36868	1.49	2.3E-01	AF004833.1	NT	Mus musculus tissue factor pathway inhibitor (TFPI) mRNA, complete cds
11144	23811	37092	1.77	2.3E-01	AJ250189.1	NT	Mus musculus partial mRNA for muscle protein 534 (mg534 gene)
11144	23811	37093	1.77	2.3E-01	AJ250189.1	NT	Mus musculus partial mRNA for muscle protein 534 (mg534 gene)
11324	24015	37318	3.03	2.3E-01	AE002167.2	NT	Chlamydia pneumoniae AR39, section 4 of 94 of the complete genome
11815	24403		1.75	2.3E-01	AV709736.1	EST_HUMAN	AV709736 ADC Homo sapiens cDNA clone ADCAGH01 5'
11855	24439		1.33	2.3E-01		NT	Homo sapiens integrin, alpha 3 (anigen CD49C, alpha 3 subunit of VLA-3 receptor) (ITGA3), transcript variant b, mRNA
12004	24539		4.47	2.3E-01	U45426.1	NT	Borrelia burgdorferi 2.9-6 locus, ORF-A-D genes, complete cds and REP+ gene, partial cds
12088	24583		4.88	2.3E-01	T27231.1	EST_HUMAN	HCOEST44 HT29M8 Homo sapiens cDNA clone HCOE44 5'
12120	24612		1.52	2.3E-01	AW863940.1	EST_HUMAN	PM4-SN0012-030400-001-b06 SN0012 Homo sapiens cDNA
12173	25319	30711	2.88	2.3E-01	AW303623.1	EST_HUMAN	xc21d07.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2813773 3' similar to TR:Q9Z175
12206	25366	30613	8.63	2.3E-01	BE882464.1	EST_HUMAN	Q9Z175 LYSYL OXIDASE-RELATED PROTEIN 2, contains PTR5.b2 TAR1 repetitive element ;
12255	24701		2.51	2.3E-01	BF663319.1	EST_HUMAN	602144459F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4297719 5'

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ-ID NO:	Exon SEQ-ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12303	24728		2.35	2.3E-01	AJ006519.1	NT	Rattus norvegicus mRNA for acid gated ion channel
12398	24784		1.76	2.3E-01	U49845.1	NT	Pleurodeles waltl distal-less like protein PwDlx-3 (PwDlx-3) mRNA, complete cds
12403	24728		1.55	2.3E-01	AJ006519.1	NT	Rattus norvegicus mRNA for acid gated ion channel
12847	24952		2	2.3E-01	BF475611.1	EST_HUMAN	nec39h12.x1 Lupsaki_sciatric_nerve Homo sapiens cDNA clone IMAGE:3395950 3' similar to contains element MER38 repetitive element:
88	12914	25552	1.63	2.2E-01	AI052190.1	EST_HUMAN	oz14et10.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1675290 3' similar to TR:Q13040 Q13040 ATP-BINDING CASSETTE PROTEIN;
1557	14304	26993	1.64	2.2E-01	AF187850.1	NT	Homo sapiens PPAR delta gene, promoter region
2082	14814	27547	2.52	2.2E-01	M34640.1	NT	Fresh-water sponge Emfri alpha collagen (COLF1) gene
2402	15123	27860	6.3	2.2E-01	BF877538.1	EST_HUMAN	602085608F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4249989 5'
2594	15308	28044	2.02	2.2E-01	BE618258.1	EST_HUMAN	601462629F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3866190 5'
2594	15308	28045	2.02	2.2E-01	BE618258.1	EST_HUMAN	601462629F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3866190 5'
2884	15651	28294	4.36	2.2E-01	BE155625.1	EST_HUMAN	PM2-HT0353-281289-003-a12 HT0353 Homo sapiens cDNA
2884	15651	28295	4.36	2.2E-01	BE155625.1	EST_HUMAN	PM2-HT0353-281289-003-a12 HT0353 Homo sapiens cDNA
2921	15687		1.57	2.2E-01	AF020503.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHIT) gene, exon 5
3387	16146		1.97	2.2E-01	AL161562.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 62
3794	16546		1.12	2.2E-01	AF155728.1	NT	Xiphophorus maculatus truncated Rex1 retrotransposon reverse transcriptase (RT) pseudogene
4105	18848		0.72	2.2E-01	U68174.1	NT	Mus musculus breast/ovarian cancer susceptibility protein (BRCA1) mRNA, complete cds
4194	18935	29562	6.45	2.2E-01	AF155142.1	NT	Mus musculus mixed lineage kinase 3 (Mlk3) and two pore domain K+ channel subunit (Kcnk6) genes, complete cds
4232	18973	29597	2.11	2.2E-01	AF117340.1	NT	Mus musculus MAP kinase kinase kinase 1 (Mekk1) mRNA, complete cds
4232	18973	29598	2.11	2.2E-01	AF117340.1	NT	Mus musculus MAP kinase kinase kinase 1 (Mekk1) mRNA, complete cds
4323	17062	29689	1.21	2.2E-01	U01307.1	NT	Human scRNA (BC200 beta) pseudogene
4323	17062	29690	1.21	2.2E-01	U01307.1	NT	Human scRNA (BC200 beta) pseudogene
4775	17507		1.36	2.2E-01	D50604.1	NT	Human beta-cytoplasmic actin (ACTBP9) pseudogene
4779	17511	30133	2.1	2.2E-01	AA211216.1	EST_HUMAN	zq87c05.r1 Stragene hNT neuron (#937233) Homo sapiens cDNA clone IMAGE:648968 5'
4982	17705		1.1	2.2E-01	L13296.1	NT	Mus musculus vinculin gene, exon 3
5062	17781		0.93	2.2E-01	S57565.1	NT	histamine H2-receptor [rats, Genomic, 1928 nt]
5140	17858	30474	2.64	2.2E-01	5835974	NT	Vidia chalybeata mitochondrion, complete genome
5659	18454	31368	2.07	2.2E-01	5803002	NT	Homo sapiens diaphanous (Drosophila, homolog) 2 (DIAPH2), transcript variant 156, mRNA
5669	18484		4.5	2.2E-01	D64000.1	NT	Synechocystis sp. PCC6803 complete genome, 19/27, 2392729-2538999
5910	18694	31646	0.56	2.2E-01	U67087.1	NT	Gallus gallus T-box containing protein (Ch-TbxT) mRNA, complete cds
5910	18694	31647	0.56	2.2E-01	U67087.1	NT	Gallus gallus T-box containing protein (Ch-TbxT) mRNA, complete cds

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Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6608	19369	32381	0.73	2.2E-01	AB039490.1	NT	Homo sapiens gene for fukutin, complete cds
6926	19662	32708	10.21	2.2E-01	AV756238.1	EST_HUMAN	AV756238 BM Homo sapiens cDNA clone BMFAHC06 5'
7029	19721	32777	1.28	2.2E-01	AF082738.1	NT	Streptococcus pyogenes phosphatidyglycerophosphate synthase (pgsA) and ABC transporter ATP-binding protein (stpA) genes, complete cds; and unknown genes
7029	19721	32778	1.28	2.2E-01	AF082738.1	NT	Streptococcus pyogenes phosphatidyglycerophosphate synthase (pgsA) and ABC transporter ATP-binding protein (stpA) genes, complete cds; and unknown genes
7191	19877	32950	1.86	2.2E-01	M24136.1	NT	Human glycophorin B gene, exon 4
7191	19877	32951	1.86	2.2E-01	M24136.1	NT	Human glycophorin B gene, exon 4
7386	20066	33144	0.83	2.2E-01	AE000035.2	NT	Mycoplasma pneumoniae M129 section 45 of 63 of the complete genome
7628	20284	33402	0.86	2.2E-01	AB024553.1	NT	Bacillus halodurans DNA, complete and partial cds, strain: C-125
7919	20614	33402	2.04	2.2E-01	AF155143.1	NT	Mus musculus nm23-M1 gene, promoter region
7987	20682	33808	1.01	2.2E-01	Z49933.1	NT	E.coli sepA and sepB genes
8449	21141	34279	0.54	2.2E-01	AJ132918.1	NT	Pan troglodytes MeCP2 gene 3'UTR
8794	21486	34632	3.53	2.2E-01	AE001713.1	NT	Thermidoga maritima section 25 of 136 of the complete genome
8920	21611	34853	4.35	2.2E-01	AW855039.1	EST_HUMAN	PM3-CT0263-241298-009-b07 CT0263 Homo sapiens cDNA
9013	21703	34853	1.45	2.2E-01	8393247	NT	Mus musculus deformed epidermal autoregulatory factor 1 (Drosophila) (Dera1), mRNA
9098	21786	34952	1.04	2.2E-01	BF376354.1	EST_HUMAN	MR1-TN0045-110900-006-c02 TN0045 Homo sapiens cDNA
9189	21859	35024	1.36	2.2E-01	W02988.1	EST_HUMAN	Za0408.r1 Soares melanocyte 2N9HM Homo sapiens cDNA clone IMAGE:291591 5'
9207	22086	35259	13.43	2.2E-01	P48634	SWISSPROT	LARGE PROLINE-RICH PROTEIN BAT2 (HLA-B-ASSOCIATED TRANSCRIPT 2)
9252	21931	35104	0.69	2.2E-01	AJ009839.1	NT	Xenopus laevis mRNA for kinesin-like protein 3 (xklp3)
9263	22017	35185	0.81	2.2E-01	7657428	NT	Mus musculus osteoblast specific factor 2 (OSF-2), mRNA
9276	22030	35200	3.95	2.2E-01	M89643.1	NT	Brachydanio rerio ependymin beta and gamma chains (Epd) gene, complete cds
9521	22174	35358	0.58	2.2E-01	Q90980	SWISSPROT	CYCLOIC NUCLEOTIDE GATED CHANNEL, ROD PHOTORECEPTOR, ALPHA SUBUNIT (CNG CHANNEL 3) (CNG-3) (CNG3)
9715	22366	35564	3.4	2.2E-01	AF197941.1	NT	Funaria hygrometrica chloroplast-localized small heat shock protein (CPsHSP21) mRNA, complete cds;
9853	22503	35703	1.85	2.2E-01	BF206507.1	EST_HUMAN	nuclear gene for chloroplast product
10076	22724	35941	0.85	2.2E-01	9625671	NT	601869724F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4100189 5'
10232	22880	36092	0.6	2.2E-01	T59472.1	EST_HUMAN	Human herpesvirus 5, complete genome
10232	22880	36093	0.6	2.2E-01	T59472.1	EST_HUMAN	y63d08.r1 Stratagene ovary (y637217) Homo sapiens cDNA clone IMAGE:75855 5'
							y63d08.r1 Stratagene ovary (y637217) Homo sapiens cDNA clone IMAGE:75855 5'
							Pseudomonas aeruginosa quinolone ethanol dehydrogenase (exaA) gene, partial cds; cytochrome c550 precursor (exaB), NAD+ dependent acetaldehyde dehydrogenase (exaC), and pyroloquinone
10268	22916	36126	0.58	2.2E-01	AF068264.1	NT	synthesis A (pqqA) genes, complete cds; and pyroloquin>
10341	22988		0.61	2.2E-01	AF071001.1	NT	Mus musculus PHR1 (Phr1) gene, partial cds

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Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10387	23033	36247	0.8	2.2E-01	AE001562.1	NT	Helicobacter pylori, strain J99 section 123 of 132 of the complete genome
10387	23033	36248	0.8	2.2E-01	AE001562.1	NT	Helicobacter pylori, strain J99 section 123 of 132 of the complete genome
10520	23166	36394	0.48	2.2E-01	AF049720.1	NT	Homo sapiens neuronal nitric oxide synthase (NOS1) gene, alternative exons 11 and AS
11070	23740	37014	1.56	2.2E-01	AF257772.1	NT	Homo sapiens RNA binding protein MCG10 gene, complete cds, alternatively spliced
11164	23831	37110	1.48	2.2E-01	AB021083.1	NT	TT virus ORF1 gene, isolate TS4-11, partial cds
11398	24005	37309	4.83	2.2E-01	X01918.1	NT	Drosophila 88C glue gene cluster
11438	23205	38437	5.22	2.2E-01	7706215	NT	Homo sapiens H-2K binding factor-2 (LOC51580), mRNA
11935	24493		1.66	2.2E-01	BE870959.1	EST_HUMAN	801446957F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3850670 5'
12040	25380						Homo sapiens chromosome Xq28 melanoma antigen family A2a (MAGEA2A), melanoma antigen family A12 (MAGEA12), melanoma antigen family A2b (MAGEA2B), melanoma antigen family A3 (MAGEA3), calreticulin (CALT), NAD(P)H dehydrogenase-like protein (NSDHL), and LIP
12123	24615		2.21	2.2E-01	U82871.2	NT	Vitis vinifera cultivar Pinot Noir plasma membrane aquaporin (PIP1a) mRNA, complete cds
12225	17904	30591	3.87	2.2E-01	AF188843.1	NT	RC1-CT0249-141199-021-g04 CT0249 Homo sapiens cDNA
12226	24681		1.6	2.2E-01	AW661922.1	EST_HUMAN	hi17b02.x1 NCI_OGAP_GU1 Homo sapiens cDNA clone IMAGE:2972523 3'
12731	25371		2.58	2.2E-01	AV694801.1	EST_HUMAN	AV694801 GKC Homo sapiens cDNA clone GKCAHB02 5'
950	13716	26382	2.12	2.1E-01	AA569289.1	EST_HUMAN	nm31e11.s1 NCI_OGAP_Lip2 Homo sapiens cDNA clone IMAGE:1061804
953	13718	26384	0.77	2.1E-01	AL161504.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 18
1102	13859		2.75	2.1E-01	AE002314.2	NT	Chlamydia muridarum, section 45 of 85 of the complete genome
1176	13929	26593	1.15	2.1E-01	6754289	NT	Mus musculus interferon (alpha and beta) receptor 2 (Ifnar2), mRNA
1176	13929	26594	1.15	2.1E-01	6754289	NT	Mus musculus interferon (alpha and beta) receptor 2 (Ifnar2), mRNA
1908	14643	27353	2.07	2.1E-01	AA906824.1	EST_HUMAN	ok73e02.s1 NCI_OGAP_GC4 Homo sapiens cDNA clone IMAGE:1519610 3' similar to gb:K02765
2152	14882	27616	4.2	2.1E-01	BF695073.1	EST_HUMAN	COMPLEMENT C3 PRECURSOR (HUMAN);
2485	15598	27942	1	2.1E-01	H73968.1	EST_HUMAN	602083129F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4247503 5'
2485	15598	27943	1	2.1E-01	H73968.1	EST_HUMAN	yu04f07.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:232837 3'
2558	15270	28005	0.91	2.1E-01	AF022814.1	NT	yu04f07.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:232837 3'
							Fugu rubripes transcription factor (SLP-1) and heme-oxygenase genes, complete cds
2925	15691	28335	2.3	2.1E-01		NT	Homo sapiens potassium voltage-gated channel, subfamily H (eag-related), member 4 (KCNH4), mRNA
3786	16538		6.08	2.1E-01	9838361	NT	Beta vulgaris mitochondrion, complete genome
4032	16777	29408	1.1	2.1E-01	P11675	SWISSPROT	IMMEDIATE-EARLY PROTEIN IE180
4032	16777	29409	1.1	2.1E-01	P11675	SWISSPROT	IMMEDIATE-EARLY PROTEIN IE180
4343	17082		1.77	2.1E-01	AB033041.1	NT	Homo sapiens mRNA for KIAA1215 protein, partial cds
4537	17272	29904	1.23	2.1E-01	AB010273.1	NT	Homo sapiens pshsp47 gene, complete cds
5013	17734	30341	1.4	2.1E-01	Q01338	SWISSPROT	ALPHA-2A ADRENERGIC RECEPTOR (ALPHA-2A ADRENOCEPTOR) (ALPHA-2AAR)

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Single Exon Probes Expressed in Brain

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5090	17809	30425	1.09	2.1E-01	AE001528.1	NT	Helicobacter pylori, strain J99 section 87 of 132 of the complete genome
5218	18028	30650	6.24	2.1E-01	BF672695.1	EST_HUMAN	602152001F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4293001 5'
6787	18531	32559	1.4	2.1E-01	AJ23392.1	NT	Dato fragilis mitochondrial 16S rRNA gene, partial
6798	19459	32481	1.92	2.1E-01	U04642.1	NT	Human olfactory receptor (OR17-2) gene, partial cds
7306	19889	33065	0.65	2.1E-01	Q01956	SWISSPROT	VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV3.3 (KSHIID)
7306	19889	33066	0.65	2.1E-01	Q01956	SWISSPROT	VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV3.3 (KSHIID)
7317	20000		2.38	2.1E-01	AE000972.1	NT	Archaeoglobus fulgidus section 135 of 172 of the complete genome
7606	20272	33380	1.94	2.1E-01	AF000949.1	NT	Cantis familiaris keratin (KRT9) gene, complete cds
7651	20315	33425	1.22	2.1E-01	AF088897.1	NT	Glycine max malate dehydrogenase (Mdh-2) gene, nuclear gene encoding mitochondrial protein, partial cds
7651	20315	33426	1.22	2.1E-01	AF088897.1	NT	Glycine max malate dehydrogenase (Mdh-2) gene, nuclear gene encoding mitochondrial protein, partial cds
7971	20668		1.21	2.1E-01	7305030	NT	Mus musculus erythrocyte protein band 4.1-like 3 (Epb4.13), mRNA
8400	21093	34229	4.44	2.1E-01	U68399.1	NT	Haemophilus influenzae hmcD, putative haemocin processing protein (hmcC), putative ABC transporter (hmcB), putative haemocin structural protein (hmcA), and haemocin immunity protein (hmcI) genes, complete cds
8696	21388	34531	0.86	2.1E-01	AL040537.1	EST_HUMAN	DKFZp434H0814_r1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434H0814 5'
8696	21388	34532	0.86	2.1E-01	AL040537.1	EST_HUMAN	DKFZp434H0814_r1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434H0814 5'
8857	21548		0.45	2.1E-01	AB022524.1	NT	Homo sapiens APC1 gene, exon 9
8936	21626	34768	5.58	2.1E-01	Z35768.1	NT	S.cerevisiae chromosome II reading frame ORF YBL025w
9404	22066	35237	0.57	2.1E-01	N42536.1	EST_HUMAN	yy11e10.r1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:270954 5'
9404	22066	35238	0.57	2.1E-01	N42536.1	EST_HUMAN	yy11e10.r1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:270954 5'
9413	22091	35282	2.31	2.1E-01	X97378.1	NT	A.italiana mRNA for AIRanBP1b protein
9518	22171	35354	1.13	2.1E-01	AB038529.1	NT	Homo sapiens p53R2 gene for ribonucleotide reductase, exon 6
10227	22875	36088	1.47	2.1E-01	Z97087.1	NT	Beta vulgaris mRNA for elongation factor 1-beta
10258	22806	36116	2.5	2.1E-01	P52824	SWISSPROT	DIACYLGLYCEROL KINASE, DELTA (DIGLYCERIDE KINASE) (DGK-DELTA) (DAG KINASE DELTA)
10264	22912	36122	0.97	2.1E-01	BF574254.1	EST_HUMAN	602131427F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4270831 5'
11554	24153		2.19	2.1E-01	11036647	NT	Homo sapiens pericardial polypeptide 2 (PPY2), mRNA
11572	24171	37487	1.59	2.1E-01	BE180422.1	EST_HUMAN	RC3-H10622-040500-013-611 HT0622 Homo sapiens cDNA
11870	24944		1.38	2.1E-01	X57624.1	NT	Drosophila melanogaster ALA-E6 DNA, repeat region
12377	24775		2.07	2.1E-01	AF217490.1	NT	Homo sapiens fragile 18D oxidoreductase (FOR) gene, exons 8, 9, and partial cds
12578	25287		1.47	2.1E-01	L32588.1	NT	Human granulysin gene
12635	24935		1.42	2.1E-01	BE622149.1	EST_HUMAN	601440712F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3915675 5'

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12758	25019	30960	1.79	2.1E-01	BE672330.1	EST_HUMAN	7a59e02.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:3223034 3'
195	13008	26650	2.43	2.0E-01	AB017437.1	NT	Gallus gallus mRNA for avian, complete cds
521	13305		3.11	2.0E-01	7705601	NT	Homo sapiens CGI-18 protein (LOC51008), mRNA
683	13458	26103	1.24	2.0E-01	M77085.1	NT	O. cuniculus germine IgH heavy chain V-H pseudogene, allotype V-Ha2
792	13984	26225	2.19	2.0E-01	AF027865.1	NT	Mus musculus Major Histocompatibility Locus class II region
991	13753	26414	1.09	2.0E-01	D90905.1	NT	Synechocystis sp. PCC6803 complete genome, 7/27, 781449-920915
1103	13960	26519	2.47	2.0E-01	AL163213.2	NT	Homo sapiens chromosome 21 segment HS21C013
1232	13981	26851	1.77	2.0E-01	AJ132695.5	NT	Homo sapiens rac1 gene
1285	14035	26706	1.63	2.0E-01	AW384837.1	EST_HUMAN	PM1-HT0422-291299-002-c06 HT0422 Homo sapiens cDNA
1443	14190		1.52	2.0E-01	AJ243957.1	NT	Plum pox virus strain M, complete genome, isolate PS
1470	14217	26904	14.63	2.0E-01	4503408	NT	Homo sapiens dysstrobrevin, alpha (DTNA), mRNA
1544	14280	26977	1.97	2.0E-01	AB007874.1	NT	Homo sapiens mRNA, chromosome 1 specific transcript KIAA0505
1550	14296	26983	1.01	2.0E-01	AF260700.1	NT	Homo sapiens sodium iodide symporter mRNA, partial cds
1692	14436	27132	1.4	2.0E-01	U22346.1	NT	Human bradykinin B1 receptor (bradyr1) gene, complete cds
1712	14455		1.67	2.0E-01	AF111170.3	NT	Homo sapiens 14q32 Jagger2 gene, complete cds; and unknown gene
1752	14494		4.33	2.0E-01	U67525.1	NT	Methanococcus Jannaschii section 67 of 150 of the complete genome
1883	14620	27328	1.12	2.0E-01	BE871330.1	EST_HUMAN	601449441F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3853330 5'
1883	14620	27330	1.12	2.0E-01	BE871330.1	EST_HUMAN	601449441F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3853330 5'
2347	15070		1.63	2.0E-01	X82877.1	NT	H. sapiens Na+ D-glucose cotransport regulator gene
3555	16310		0.71	2.0E-01	AW238005.1	EST_HUMAN	xp15b02.x1 NCI_CGAP_HN9 Homo sapiens cDNA clone IMAGE:2740395 3' similar to contains element
3693	16447	29087	0.89	2.0E-01	P34641	SWISSPROT	MER21 repetitive element ;
3822	16574	29206	1.12	2.0E-01	AL163204.2	NT	CEB-11 PROTEIN
3936	16886	29327	0.76	2.0E-01	Z46906.1	NT	Homo sapiens chromosome 21 segment HS21C004
4528	17263		8.49	2.0E-01	BE828165.1	EST_HUMAN	Sus scrofa
4979	17702	30309	5.28	2.0E-01	8922080	NT	QV4-EN0032-190500-223-e03 EN0032 Homo sapiens cDNA
5009	16237	28893	0.8	2.0E-01	P46607	SWISSPROT	Homo sapiens hypothetical protein ASH1 (ASH1), mRNA
5359	18161	30845	2.63	2.0E-01	X56600.1	NT	HOMEBOX PROTEIN GLABRA2 (HOMEBOX-LEUCINE ZIPPER PROTEIN ATHB-10) (HD-ZIP PROTEIN ATHB-10)
5655	18450	31363	1.94	2.0E-01	11432540	NT	Rat SOD-2 gene for manganese-containing superoxide dismutase
5750	18542	31464	0.76	2.0E-01	X91856.1	NT	Homo sapiens dual oxidase-like domains 2 (DUOX2), mRNA
5969	18751	31712	6.3	2.0E-01	U19300.1	NT	F. rubripes DNA encoding for valyl-tRNA synthetase
6081	18860		0.73	2.0E-01	M75967.1	NT	Saccharomyces cerevisiae Hal5p (HAL5) mRNA, complete cds
6182	18988	31943	0.78	2.0E-01	P02467	SWISSPROT	Human hepatocyte growth factor gene, exon 1
							COLLAGEN ALPHA 2(I) CHAIN PRECURSOR

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6335	19105	32094	3.2	2.0E-01	X61033.1	NT	Mauratus mu class glutathione transferase gene
6435	19203	32200	4.02	2.0E-01	AW360885.1	EST_HUMAN	PM1-CT0247-141099-001-g06 CT0247 Homo sapiens cDNA
7194	19880	32954	1.28	2.0E-01	AF250371.1	NT	Mus musculus phosphofructokinase-1 C isozyme (Pfkf) gene, exons 3 through 7
7345	20026	33102	0.68	2.0E-01	P94422	SWISSPROT	GAMMA-GLUTAMYL TRANSPEPTIDASE PRECURSOR
7675	20339	33452	0.84	2.0E-01	V00726.1	NT	Mouse germ line gene coding for beta-globin (Y2)
7853	20548		5.8	2.0E-01	AF028026.1	NT	Andes virus strain O123133 glycoprotein G1 and G2 precursor, gene, partial cds
8100	20794	33925	2.95	2.0E-01	X91151.1	NT	M.musculus scp2 gene exon 14
8624	21316		0.99	2.0E-01	BE562247.1	EST_HUMAN	601344848F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3677794 5'
9251	21930	35103	0.82	2.0E-01	U82511.1	NT	Dicystostellum discoideum random slug cDNA19 protein (rsc19) mRNA, partial cds
9290	21957	35129	0.68	2.0E-01	U71122.1	NT	Arabidopsis pyruvate decarboxylase-2 (Pdc2) gene, complete cds
9456	22006		4.97	2.0E-01	AE001278.1	NT	Chlamydia trachomatis section 5 of 87 of the complete genome
9646	22298	35493	0.65	2.0E-01	P11420	SWISSPROT	DAUGHTERLESS PROTEIN
9646	22298	35494	0.65	2.0E-01	P11420	SWISSPROT	DAUGHTERLESS PROTEIN
9791	22442		2.11	2.0E-01	AF146892.1	NT	Homo sapiens filamin 2 (FLN2) mRNA, complete cds
9941	22889	35792	1.98	2.0E-01	AF086907.1	NT	Arabidopsis thaliana root gravitropism control protein (PIN2) gene, complete cds
9941	22889	35793	1.98	2.0E-01	AF086907.1	NT	Arabidopsis thaliana root gravitropism control protein (PIN2) gene, complete cds
10067	22715	35933	0.68	2.0E-01	AF157814.1	NT	Homo sapiens cAMP specific phosphodiesterase (PDE4C) gene, exons 2 through 12
10067	22715	35934	0.68	2.0E-01	AF157814.1	NT	Homo sapiens cAMP specific phosphodiesterase (PDE4C) gene, exons 2 through 12
10114	22782		0.69	2.0E-01	X78388.1	NT	D.melanogaster DNA mobile element (hoppe)
10305	22952	36167	2.78	2.0E-01	X97121.1	NT	R.norvegicus mRNA for NTR2 receptor
10744	23431	36674	1.56	2.0E-01	D89088.1	NT	Salvelinus pluvius mRNA for transferrin, complete cds
10744	23431	36675	1.56	2.0E-01	D89088.1	NT	Salvelinus pluvius mRNA for transferrin, complete cds
11609	24207	37530	1.4	2.0E-01		NT	Chlorella vulgaris chloroplast, complete genome
11609	24207	37531	1.4	2.0E-01		NT	Chlorella vulgaris chloroplast, complete genome
12358	24762		1.51	2.0E-01	AF206637.2	NT	Pinophytes promelas liver glucose-6-phosphate-1-dehydrogenase mRNA, partial cds
12545	25210		1.39	2.0E-01	AF302773.1	NT	Homo sapiens ninein-Lm isoform (ninein) mRNA, complete cds
12556	25139	30894	1.36	2.0E-01	AW975297.1	EST_HUMAN	EST1387405 IMAGE sequences, MAGN Homo sapiens cDNA
12594	24950	30885	3.58	2.0E-01	A1023592.1	EST_HUMAN	ov60a10.st Soares, testes_NHT Homo sapiens cDNA clone IMAGE:1643610 3'
12618	24924		2.68	2.0E-01	AF078164.2	NT	Homo sapiens Ku70-binding protein (KUB3) mRNA, partial cds
12753	25014	30678	1.87	2.0E-01		NT	Mus musculus fructosamine 3 kinase (Fn3k) mRNA
108	12929		3.9	1.9E-01	7549743	NT	Rattus norvegicus Aryl hydrocarbon receptor nuclear translocator 1 (Arlt1), mRNA
342	13143	25781	6.86	1.9E-01	AF004353.1	NT	Mus musculus pale ear (ep) gene, wild type allele, 3' region, partial cds
641	13420	26058	1.43	1.9E-01	U32581.2	NT	Homo sapiens lambda/delta protein kinase C-interacting protein mRNA, complete cds
641	13420	26059	1.43	1.9E-01	U32581.2	NT	Homo sapiens lambda/delta protein kinase C-interacting protein mRNA, complete cds

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
648	13427	26068	5.97	1.9E-01	BE070801.1	EST_HUMAN	RC3-BT0502-251199-011-d01 BT0502 Homo sapiens cDNA
649	13427	26068	8.46	1.9E-01	BE070801.1	EST_HUMAN	RC3-BT0502-251199-011-d01 BT0502 Homo sapiens cDNA
965	13730		1.73	1.9E-01	7305180	NT	Mus musculus interleukin 2 receptor, gamma chain (IL2rg), mRNA
1082	13840	26499	13.43	1.9E-01	AA358813.1	EST_HUMAN	EST67784 Fetal lung II Homo sapiens cDNA 5' end
1349	14097	26772	1.78	1.9E-01	AF061282.1	NT	Sorghum bicolor 22 kDa kafirin cluster
1414	14162		2.51	1.9E-01	AF184623.1	NT	Plasmodium vivax reticulocyte binding protein-2 (bbp-2) gene, complete cds
2380	15102	27841	3.61	1.9E-01	U60066.1	NT	Homo sapiens hypothetical protein FLJ10581 (FLJ10581), mRNA
2923	15689	28333	3.43	1.9E-01	U60066.1	NT	Sigmodon hispidus p53 gene, partial cds
2939	15704		5.68	1.9E-01	J00922.1	NT	Gallus gallus ovalbumin (Y) gene, complete cds
3002	15788	28417	0.96	1.9E-01	U28148.1	NT	Rattus norvegicus brush border myosin-I (BBMI) mRNA, partial cds
3390	16149	28803	4.28	1.9E-01	D13197.1	NT	Mouse gene for Immunoglobulin diversity region D1
3473	16229	28883	4.44	1.9E-01	R16467.1	EST_HUMAN	1/42710.1 Soares fetal liver spleen 1NF1S Homo sapiens cDNA clone IMAGE:129547 5'
3816	16588	29108	1.33	1.9E-01	P39768	SWISSPROT	PAIR-RULE PROTEIN ODD-PAIRED
3973	16722	29356	3.15	1.9E-01	AB006784.1	NT	Schizosaccharomyces pombe DNA for cytoplasmic dynein heavy chain, complete cds
4063	16808	29438	1.28	1.9E-01	AW754106.1	EST_HUMAN	CM3-CT0315-271199-045-b11 CT0315 Homo sapiens cDNA
4206	16947	29573	1.09	1.9E-01	BE834943.1	EST_HUMAN	MR1-FN0010-290700-007-004 FN0010 Homo sapiens cDNA
4950	17677		1.05	1.9E-01	AF223842.1	NT	Rattus norvegicus chemokine receptor CXCR3 mRNA, complete cds
5517	18315		4.88	1.9E-01	AW130149.1	EST_HUMAN	x29a07.x1 NCL CGAP_UH1 Homo sapiens cDNA clone IMAGE:2619444 3' similar to gb:M73779 RETINOIC ACID RECEPTOR ALPHA-1 (HUMAN);
5558	18355	31265	7.87	1.9E-01	AF127937.1	NT	Homo sapiens DNA polymerase epsilon catalytic subunit protein (POLE1) gene, exon 1a
5749	18541	31463	0.7	1.9E-01	AF091216.1	NT	Mus musculus Wrm protein (Wrm) gene, complete cds
5795	18596		2.56	1.9E-01	AU133116	EST_HUMAN	AU133116 NT2RP4 Homo sapiens cDNA clone NT2RP4001328 5'
6235	19009	31985	0.75	1.9E-01	A1762391.1	EST_HUMAN	wi54h02.x1 NCL CGAP_Co16 Homo sapiens cDNA clone IMAGE:2394089 3'
6294	19067	32050	1.03	1.9E-01	AW148452.1	EST_HUMAN	SYNTHASE BETA CHAIN, MITOCHONDRIAL PRECURSOR (HUMAN);
6878	17952	30548	1.69	1.9E-01	R43212.1	EST_HUMAN	yq09a12.x1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:31863 3' similar to contains MER13 repetitive element ;
6900	19638	32852	0.69	1.9E-01	AF034920.1	NT	Homo sapiens tubby like protein 1 (TULP1) gene, exons 9-11
6900	19638	32853	0.69	1.9E-01	AF034920.1	NT	Homo sapiens tubby like protein 1 (TULP1) gene, exons 9-11
7160	19847	32917	0.62	1.9E-01	U73846.1	NT	Drosophila melanogaster testis-specific RNA-binding protein (bruno) mRNA, complete cds
7391	20070	33149	1.38	1.9E-01	U80922.1	NT	Arabidopsis thaliana serine/threonine protein phosphatase type one (TOPP8) gene, complete cds
7436	20113	33201	3.11	1.9E-01	AF072724.1	NT	Zea mays starch branching enzyme 1 (sbe1) gene, complete cds
7885	20580	33709	1.46	1.9E-01	AL161557.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 57
8586	21278	34417	10.77	1.9E-01	AB033024.1	NT	Homo sapiens mRNA for KIAA1198 protein, partial cds

Table 4

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8844	21536	34681	1.24	1.9E-01	M14568.1	NT	Marupial cat beta-globin gene mRNA, partial cds
8844	21536	34682	1.24	1.9E-01	M14568.1	NT	Marupial cat beta-globin gene mRNA, partial cds
9775	22426	35632	0.61	1.9E-01	AA912486.1	EST_HUMAN	o96g10.s1 NCL_CGAP_PNS1 Homo sapiens cDNA clone IMAGE:1537506 3' similar to contains Alu repetitive element;
10142	22790	36005	0.85	1.9E-01	BE830353.1	EST_HUMAN	RC5-ET0082-060700-022-A02 ET0082 Homo sapiens cDNA
10142	22790	36006	0.85	1.9E-01	BE830353.1	EST_HUMAN	RC5-ET0082-060700-022-A02 ET0082 Homo sapiens cDNA
10540	23237	36470	2.48	1.9E-01	AL161503.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 15
10540	23237	36471	2.48	1.9E-01	AL161503.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 15
10655	23346	36583	2.09	1.9E-01	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
10966	23661	36915	1.34	1.9E-01	AA912480.1	EST_HUMAN	o9602.s1 NCL_CGAP_PNS1 Homo sapiens cDNA clone IMAGE:1537487 3' similar to gb.L21696_cds1 PROTHYMOSIN ALPHA (HUMAN); contains element OFR repetitive element;
10966	23661	36916	1.34	1.9E-01	AA912480.1	EST_HUMAN	o9602.s1 NCL_CGAP_PNS1 Homo sapiens cDNA clone IMAGE:1537487 3' similar to gb.L21696_cds1 PROTHYMOSIN ALPHA (HUMAN); contains element OFR repetitive element;
11487	24088	37399	1.53	1.9E-01	M22253.1	NT	Rattus norvegicus sodium channel I mRNA, complete cds
11726	24320	37645	2.77	1.9E-01	AJ243213.1	NT	Homo sapiens partial 5-HT4 receptor gene, exons 2 to 5
11752	24343	37873	1.6	1.9E-01	L07344.1	NT	Influenza A/Guangdong/243/72 nucleoprotein (seg 5) gene, 5' end
11847	24431	37772	1.3	1.9E-01	AF287263.1	NT	Mus musculus ATP-binding cassette 1, sub-family A, member 1 (Abca1) gene, complete cds
12399	24785		1.67	1.9E-01	AF055900.1	NT	Drosophila melanogaster clathrin light chain mRNA, complete cds
30	12558	25475	2.61	1.8E-01	U73200.1	NT	Mus musculus p116Rip mRNA, complete cds
253	15539	25700	0.9	1.8E-01	AB022090.1	NT	Mus musculus Cctg gene for chaperonin containing TCP-1 gamma subunit, partial cds
361	13159	25802	1.76	1.8E-01	4502532	NT	Homo sapiens calcium channel, voltage-dependent, beta 2 subunit (CACNB2) mRNA, and translated products
729	13503	26158	1.01	1.8E-01	AB021490.2	NT	Oryzias latipes gene for membrane guanylyl cyclase OIGC1, complete cds
961	13728	26390	0.94	1.8E-01	AB021212.1	EST_HUMAN	wd71102.XT NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2337051 3'
1069	13826	26485	1.63	1.8E-01	AF000580.1	NT	Dictyostelium discoideum plasmid Ddp5, complete genome
1268	14015	26683	8.28	1.8E-01	AL117189.1	NT	Yersinia pestis plasmid pCD1
1492	14239	26925	1.97	1.8E-01	6753947	NT	Mus musculus guanylate nucleotide binding protein 1 (Gbp1), mRNA
1492	14239	26926	1.97	1.8E-01	6753947	NT	Mus musculus guanylate nucleotide binding protein 1 (Gbp1), mRNA
1839	14577		1.2	1.8E-01	4505036	NT	Homo sapiens latent transforming growth factor beta binding protein 4 (LTBP4) mRNA
1859	14597		1.58	1.8E-01	AI733708.1	EST_HUMAN	q922410.x5 NCL_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1761811 3' similar to TR:O75936 O75936 GAMMA BUTYROBETAINE HYDROXYLASE;

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1908	14945	27355	1.75	1.8E-01	AB051897.1	NT	Mus musculus Scya6, Scya9, Scya16-ps, Scya5 genes for small inducible cytokine A6 precursor, small inducible cytokine A9 precursor, Scya16 pseudogene, small inducible cytokine A5 precursor, complete cds
2897	15408		2.36	1.8E-01	AW835728.1	EST_HUMAN	QV3-DT0018-081299-036-g04 DT0018 Homo sapiens cDNA
2898	15665		1.89	1.8E-01	AF184589.1	NT	Jonopsidium acutale LEAFY protein (LEAFY2) gene, partial cds
2804	15670	28319	1.29	1.8E-01	AW182300.1	EST_HUMAN	X41a03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2659758 3'
3121	15886	28528	1.76	1.8E-01	AW995178.1	EST_HUMAN	QV0-BN0041-070300-147-c04 BN0041 Homo sapiens cDNA
3610	16363	28005	0.98	1.8E-01	H03369.1	EST_HUMAN	Y45e01.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:151704 3' similar to contains Alu repetitive element;
3610	16363	29008	0.98	1.8E-01	H03369.1	EST_HUMAN	Y45e01.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:151704 3' similar to contains Alu repetitive element;
4299	17038		1.43	1.8E-01	D37954.1	NT	Bovine NB25 mRNA for MHC class II (BoLA-DQB), complete cds
4519	17254	29888	5.94	1.8E-01	AL161556.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 56
4721	17453	30087	2.9	1.8E-01	AB051897.1	NT	Mus musculus Scya6, Scya9, Scya16-ps, Scya5 genes for small inducible cytokine A6 precursor, small inducible cytokine A9 precursor, Scya16 pseudogene, small inducible cytokine A5 precursor, complete cds
4754	17486	30114	0.94	1.8E-01	X92179.1	NT	S. tuberosum mRNA for alcohol dehydrogenase
4964	17707	30311	2.03	1.8E-01	AW814270.1	EST_HUMAN	MR3-ST0203-151299-112-g08 ST0203 Homo sapiens cDNA
4999	17722	30325	1.06	1.8E-01	A1792382.1	EST_HUMAN	en28g07.y5 Gessler Wilms tumor Homo sapiens cDNA
5035	17794	30367	4.66	1.8E-01	AF181258.1	NT	Mesocricetus auratus Na-taurocholeate cotransporting polypeptide mRNA, partial cds
5718	18510	31431	0.82	1.8E-01	AL161594.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 90
5835	18624	31558	0.68	1.8E-01	N28629.1	EST_HUMAN	Y38h08.r1 Soares melanocyte 2NBHM Homo sapiens cDNA clone IMAGE:264083 5'
6037	18817	31777	1.18	1.8E-01	6678428	NT	Mus musculus Tnf receptor-associated factor 6 (Traf6), mRNA
6419	19187	31778	1.18	1.8E-01	6678428	NT	Mus musculus Tnf receptor-associated factor 6 (Traf6), mRNA
6483	19230	32185	1.15	1.8E-01	Q9QY14	SWISSPROT	FORHEAD BOX PROTEIN E3
6906	19644	32889	2.06	1.8E-01	N94853.1	EST_HUMAN	Y62h02.r1 Soares multiple sclerosis_2NBHMS Homo sapiens cDNA clone IMAGE:278163 6'
6906	19644	32690	1.18	1.8E-01	AB018561.1	NT	Citullus lanatus mRNA for wsus, complete cds
7346	20027	33103	0.7	1.8E-01	AB018561.1	NT	Citullus lanatus mRNA for wsus, complete cds
9242	21921	35091	1.26	1.8E-01	AF001511.1	NT	Bacillus halodurans genomic DNA, section 5/14
9274	22028	35198	1.22	1.8E-01	M73258.1	NT	Human cellular DNA/Human papillomavirus proviral DNA
9391	22053		0.5	1.8E-01	AA493751.1	EST_HUMAN	Bacteriophage like, complete genome
9473	22126	35305	0.94	1.8E-01	P15272	SWISSPROT	nh02a05.s1 NCJ_CGAP_Thy1 Homo sapiens cDNA clone IMAGE:943088 similar to contains L1.13 L1 repetitive element;
							AMP NUCLEOSIDASE

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9473	22126	35306	0.94	1.8E-01	P15272	SWISSPROT	AMP NUCLEOSIDASE
9514	22167	35348	0.91	1.8E-01	M26019.1	NT	S. commune oridine-5'-phosphate decarboxylase (URA1) gene, complete cds
9514	22167	35349	0.91	1.8E-01	M26019.1	NT	S. commune oridine-5'-phosphate decarboxylase (URA1) gene, complete cds
9679	22331	35526	0.75	1.8E-01	P08123	SWISSPROT	COLLAGEN ALPHA 2(I) CHAIN PRECURSOR
9683	22335	35530	0.77	1.8E-01	U67548.1	NT	Methanococcus jannaschii section 90 of 150 of the complete genome
10033	22681		0.78	1.8E-01	AF200252.1	NT	Aquarius amplius cytochrome oxidase subunit I (COI) gene, partial cds; mitochondrial gene for mitochondrial product
10268	22914	36124	1.48	1.8E-01	X63440.1	NT	M. musculus mRNA for P19-protein tyrosine phosphatase
10533	23230	36465	3.08	1.8E-01	X77336.1	NT	A. thaliana mRNA for ribonucleotide reductase R2
10577	23272	36508	7.28	1.8E-01	U39908.1	NT	Bacteriophage rIT integrase, repressor protein (rro), dUTPase, holin and lysis genes, complete cds
10637	19644	32689	2.61	1.8E-01	AB018561.1	NT	Citullus lanatus mRNA for wsus, complete cds
10637	19644	32690	2.61	1.8E-01	AB018561.1	NT	Citullus lanatus mRNA for wsus, complete cds
10638	23329	36567	5.69	1.8E-01	AF019107.1	NT	Dicystellum discoideum unknown (DG1041) gene, complete cds
10942	23621	36870	2.64	1.8E-01	M59257.1	NT	Human carcinoembryonic antigen (CEA) gene, exon 4
11439	23206	36438	4.04	1.8E-01	X57033.1	NT	B. laurus mRNA for potassium channel
11767	24356	37691	3.45	1.8E-01	8394421	NT	Rattus norvegicus Thromboxane receptor (Tbx2r), mRNA
11967	24514		1.59	1.8E-01	10086561	NT	Bovine ephemeral fever virus, complete genome
12025	24553	31111	2.04	1.8E-01	BF348623.1	EST_HUMAN	602019928F1 NCL CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4155318 5'
12476	24899		3.28	1.8E-01	Q96682	SWISSPROT	DNA TERMINAL PROTEIN (BELLETT PROTEIN) (PTP PROTEIN)
12585	24908		1.91	1.8E-01	R24494.1	EST_HUMAN	yn48h10.1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:133027 5'
12628	24931		2.3	1.8E-01	Y11114.1	NT	E. dispar mRNA for hexokinase (hpk1)
12745	25324		1.61	1.8E-01	X16635.1	NT	Rattus norvegicus CaBP9k gene
563	13345	25972	1.57	1.7E-01	BE385164.1	EST_HUMAN	601274604F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3615768 5'
787	13559	28221	2.32	1.7E-01	X53330.1	NT	P. dumerilii histone gene cluster for core histones H2A, H2B, H3 and H4
941	13708		2.21	1.7E-01	P35616	SWISSPROT	NEUROFILAMENT TRIPLET L PROTEIN (NEUROFILAMENT LIGHT POLYPEPTIDE) (NF-L)
1036	13796	28455	1.89	1.7E-01	AF081810.1	NT	Lymantia dispar nucleopolydnavirus, complete genome
1036	13796	28456	1.89	1.7E-01	AF081810.1	NT	Lymantia dispar nucleopolydnavirus, complete genome
1874	14710		2.6	1.7E-01	AF255051.1	NT	Homo sapiens BNIP3H (BNIP3H) gene, complete cds; nuclear gene for mitochondrial product
2863	15631	28275	2.28	1.7E-01	AF000716.1	NT	Vibrio cholerae hypoxanthine phosphoribosyltransferase (hpt) gene, partial cds, hemagglutinin/protease regulatory protein (hapR) gene, complete cds, and YRAL_VIBCO gene, partial cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2883	15631	28276	2.29	1.7E-01	AF000716.1	NT	Vibrio cholerae hypoxanthine phosphoribosyltransferase (hpt) gene, partial cds, hemagglutinin/protease regulatory protein (hpr) gene, complete cds, and YRAL VIBCO gene, partial cds
2927	15693	28338	1.55	1.7E-01	AA336909.1	EST_HUMAN	EST41651 Endometrial tumor Homo sapiens cDNA 5' end
2995	15761	28409	1.33	1.7E-01	AJ238736.1	NT	Naja naja atra ctk-1 gene, exons 1-3
2995	15761	28410	1.33	1.7E-01	AJ238736.1	NT	Naja naja atra ctk-1 gene, exons 1-3
3103	15868	28508	1.24	1.7E-01	AF081514.1	NT	Taxus canadensis geranylgeranyl diphosphate synthase mRNA, complete cds
3439	16195	28845	1.74	1.7E-01	AJ269505.1	NT	Anabaena sp. ORF4 (partial), ORF3, ORF2, ORF1, adpA gene, adpB gene, adpC gene, adpD gene, adpE gene and adpF gene
3595	16348	28889	1.04	1.7E-01	AJ224877.1	NT	Homo sapiens hapt1 gene, complete CDS
3616	16369		0.92	1.7E-01	5031886	NT	Homo sapiens LIM domain-containing preferred translocation partner in lipoma (LPP) mRNA
3918	16668	29309	4.84	1.7E-01	AJ235377.1	NT	Homo sapiens derivative 11 breakpoint fragment: partial intron 10 of the ALL-1/MLL/HRX gene fused to intron 5 of the AF-4/TEL gene
4522	17257		1.69	1.7E-01	X53936.1	NT	Schistosoma gregaria alpha repetitive DNA
4787	17518	30140	1.08	1.7E-01	AJ247635.1	EST_HUMAN	qh57e09.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1848808 3' similar to contains ORF.b1 ORF repetitive element;
5054	17773		1.11	1.7E-01	AF072725.1	NT	Zea mays starch branching enzyme IIb (ae) gene, complete cds
5122	17840	30456	0.75	1.7E-01	D37951.1	NT	Rattus norvegicus mRNA for MIBP1 (c-myc intron binding protein 1), complete cds
5323	18128	30785	2	1.7E-01	AA470686.1	EST_HUMAN	ne13a02.s1 NCI_CGAP_Co3 Homo sapiens cDNA clone IMAGE:381066 3' similar to gb:M17886 60S ACIDIC RIBOSOMAL PROTEIN P1 (HUMAN);
5323	18128	30786	2	1.7E-01	AA470686.1	EST_HUMAN	ne13a02.s1 NCI_CGAP_Co3 Homo sapiens cDNA clone IMAGE:381066 3' similar to gb:M17886 60S ACIDIC RIBOSOMAL PROTEIN P1 (HUMAN);
5508	18304	31205	0.82	1.7E-01	U43599.1	NT	Brugia pahangi microfilarial sheath protein SHP3 (shp3) gene, complete cds
6237	19011	31988	13.23	1.7E-01	H72118.1	EST_HUMAN	ys02g06.s1 Soares_fetal_liver_spleen_1NFLS Homo sapiens cDNA clone IMAGE:213658 3'
6293	19066	32048	0.97	1.7E-01	AJ370976.1	EST_HUMAN	ta29c11.x1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:2045492 3'
6293	19066	32049	0.97	1.7E-01	AJ370976.1	EST_HUMAN	ta29c11.x1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:2045492 3'
6753	17922	30557	0.65	1.7E-01	BE300286.1	EST_HUMAN	60094406771 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2960248 3'
6780	19524		2.28	1.7E-01	AF026552.3	NT	Mesorhynchus auratus oviductin precursor (OV) gene, complete cds
6902	19640		0.88	1.7E-01	Z92910.1	NT	Homo sapiens HFE gene
7120	19808	32874	1.1	1.7E-01	AF000422.1	NT	Escherichia coli O157:H7 genomic DNA, Sakai-VT2 prophage inserted region
7197	19883	32957	8.8	1.7E-01	AF000422.1	EST_HUMAN	601569022F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3843964 5'
7380	20060	33139	1.37	1.7E-01	P16724	SWISSPROT	PROBABLE PROCESSING AND TRANSPORT PROTEIN UL56 (HFLF0 PROTEIN)
7396	25112	33153	0.71	1.7E-01	Q01965	SWISSPROT	COLLAGEN ALPHA 3(IV) CHAIN PRECURSOR
7760	20456	33580	1.32	1.7E-01	AF000573.1	NT	Homo sapiens homogentisate 1,2-dioxygenase gene, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7863	20558	33684	0.82	1.7E-01	AF150689.1	NT	Pseudomonas putida long-chain-fatty-acid-CoA ligase (fadD) gene, complete cds
8175	20869	34001	6.19	1.7E-01	7708428	NT	Homo sapiens cleavage and polyadenylation specificity factor 3, 73kD subunit (CPSF3), mRNA
8175	20869	34002	6.19	1.7E-01	7708428	NT	Homo sapiens cleavage and polyadenylation specificity factor 3, 73kD subunit (CPSF3), mRNA
8598	21280	34431	0.47	1.7E-01	AW992873.1	EST_HUMAN	RC2-BN0032-120200-011-a10 BN0032 Homo sapiens cDNA
8628	21320	34482	2.09	1.7E-01	D00384.1	NT	Rat (SHR strain) SX1 gene
8743	21435	34580	0.75	1.7E-01	AF217413.1	NT	Homo sapiens neuroigin 3 isoform gene, complete cds, alternatively spliced
8743	21435	34581	0.75	1.7E-01	AF217413.1	NT	Homo sapiens neuroigin 3 isoform gene, complete cds, alternatively spliced
9066	21755	34918	0.48	1.7E-01	BE253142.1	EST_HUMAN	601116672F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3357184 5'
9066	21755	34917	0.48	1.7E-01	BE253142.1	EST_HUMAN	601116672F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3357184 5'
9490	22143	35323	7.85	1.7E-01	AP001508.1	NT	Bacillus halodurans genomic DNA, section 2/14
9597	22250	35435	0.51	1.7E-01	AW977455.1	EST_HUMAN	EST389584 MAGIE resequences, MAGO Homo sapiens cDNA
9597	22250	35436	0.51	1.7E-01	AW977455.1	EST_HUMAN	EST389584 MAGIE resequences, MAGO Homo sapiens cDNA
9615	22288	35455	3.14	1.7E-01	U16288.1	NT	Human class IV alcohol dehydrogenase (ADH7) gene, exon 3
9708	22359	35555	0.63	1.7E-01	AJ251749.1	NT	Drosophila melanogaster mRNA for serine protease inhibitor (serpin-6), (sp6 gene)
10133	22781		2.4	1.7E-01	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
10283	22940	36154	1.4	1.7E-01	11427203	NT	Homo sapiens solute carrier family 7 (cationic amino acid transporter, y* system), member 2 (SLC7A2), mRNA
10295	22942	36156	1.72	1.7E-01	AA627872.1	EST_HUMAN	ng60e07.s1 NCI_CGAP_C09 Homo sapiens cDNA clone IMAGE:1148292 3' similar to gb:U25081
10501	23147		0.45	1.7E-01	AL161542.2	NT	TRANSFORMING PROTEIN RHOC (HUMAN);
10578	23274	36511	8.78	1.7E-01	BE390835.1	EST_HUMAN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 42
10709	23398	36637	2.85	1.7E-01	AA814617.1	EST_HUMAN	601286547F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3613258 5'
11055	23725	36995	9.13	1.7E-01	7106300	NT	af43a03.s1 NCI_CGAP_CNS1 Homo sapiens cDNA clone IMAGE:1428924 3'
11055	23725	36996	9.13	1.7E-01	7106300	NT	Mus musculus adenomatosis polyposis cell binding protein Eb1 (Eb1), mRNA
11146	23813	37098	1.62	1.7E-01	Y08391.1	NT	Mus musculus adenomatosis polyposis cell binding protein Eb1 (Eb1), mRNA
11348	24038	37341	1.88	1.7E-01	AA883375.1	EST_HUMAN	S.pombe pop1+ gene
11712	24307		1.83	1.7E-01	P16272	SWISSPROT	ak45709.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1480297 3'
11712	24307		1.83	1.7E-01	P16272	SWISSPROT	AMP NUCLEOSIDASE
11748	24337	37663	1.62	1.7E-01	P55899	SWISSPROT	IGG RECEPTOR FORN LARGE SUBUNIT P51 PRECURSOR (FCRN) (NEONATAL FC RECEPTOR)
11748	24337	37664	1.62	1.7E-01	P55899	SWISSPROT	IGG FC FRAGMENT RECEPTOR TRANSPORTER, ALPHA CHAIN
11874	24453	37799	2.62	1.7E-01	11418157	NT	IGG RECEPTOR FORN LARGE SUBUNIT P51 PRECURSOR (FCRN) (NEONATAL FC RECEPTOR)
12000	25320		1.95	1.7E-01	AL163278.2	NT	Homo sapiens calcium channel, voltage-dependent, alpha 11 subunit (CAGNA11), mRNA
							Homo sapiens chromosome 21 segment HS21C078

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12288	25167		1.95	1.7E-01	A1824404.1	EST_HUMAN	b69g05.x1 NCL CGAP_U11 Homo sapiens cDNA clone IMAGE:2274872 3' similar to gb:M73779 RETINOIC
12552	24889	30996	18.27	1.7E-01	U01317.1	NT	ACID RECEPTOR ALPHA-1 (HUMAN);
122	12940	25582	2.38	1.6E-01	AF217532.1	NT	Human beta globin region on chromosome 11
684	15518	26081	1.51	1.6E-01	R31497.1	EST_HUMAN	Homo sapiens mevalonate kinase gene, exon 6 and 7
1493	14240	26927	1.16	1.6E-01	AA548863.1	EST_HUMAN	h75f12.1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:135599 5'
1512	14258	26944	3.92	1.6E-01	AF298117.1	NT	h28d12.s1 NCL CGAP_Cot1 Homo sapiens cDNA clone IMAGE:1014839 3'
1917	14654	27364	1.86	1.6E-01	P22063	SWISSPROT	Homo sapiens homeobox protein OTX2 gene, complete cds
1977	14713		1.51	1.6E-01	U10334.1	NT	AXONIN-1 PRECURSOR (AXONAL GLYCOPROTEIN TAG-1)
2383	15593	27844	1.35	1.6E-01	X94232.1	NT	Crassostrea gigas RNA polymerase II largest subunit mRNA, partial cds
2497	15214	27957	1.4	1.6E-01	AB037729.1	NT	H. sapiens mRNA for novel T-cell activation protein
2894	15661	28307	10.17	1.6E-01	AF185589.1	NT	Homo sapiens mRNA for KIAA1308 protein, partial cds
2894	15661	28308	10.17	1.6E-01	AF185589.1	NT	Homo sapiens cytochrome P450 3A4 (CYP3A4) gene, promoter region
3624	16377	29018	1.21	1.6E-01	AJ003165.1	NT	Homo sapiens cytochrome P450 3A4 (CYP3A4) gene, promoter region
3624	16377	29019	1.21	1.6E-01	AJ003165.1	NT	Populus trichocarpa cv. Trichobel ABI3 gene
3982	16730		2.49	1.6E-01	AE004413.1	NT	Populus trichocarpa cv. Trichobel ABI3 gene
4294	17033	29661	9.42	1.6E-01	AF179880.1	NT	Vibrio cholerae chromosome II, section 70 of 93 of the complete chromosome
4423	17159		3.07	1.6E-01	AW56860.1	EST_HUMAN	Homo sapiens apelin gene, complete cds
4431	17167		4.35	1.6E-01	6753319	NT	EST380677 MAGE resequences, MAGJ Homo sapiens cDNA
							Mus musculus chaperonin subunit 3 (gamma) (Cct3), mRNA
4869	17596	30219	0.7	1.6E-01	P40631	SWISSPROT	MICRONUCLEAR LINKER HISTONE POLYPROTEIN (MIC LH) [CONTAINS: LINKER HISTONE
							PROTEINS ALPHA, BETA, DELTA AND GAMMA]
4892	17619	30237	1.38	1.6E-01	AA098343.1	EST_HUMAN	z184h09.s1 Stratagene colon (#937204) Homo sapiens cDNA clone IMAGE:511361 3' similar to TR:E221955
4911	17639	30253	1.54	1.6E-01	AJ008356.1	NT	E221955 38,856 BP SEGMENT OF CHROMOSOME XIV ;
4911	17639	30254	1.54	1.6E-01	AJ008356.1	NT	Lycopodium obscurum Real fragment 2, satellite region
5303	18108	30768	0.99	1.6E-01	L40808.1	NT	Lycopodium obscurum Real fragment 2, satellite region
							Plasmodium falciparum (strain Dd2) variant-specific surface protein (var-1) gene, complete cds
5435	18234	30947	2.95	1.6E-01	AW187496.1	EST_HUMAN	xm43f01.x1 NCL CGAP_GC6 Homo sapiens cDNA clone IMAGE:2686969 3' similar to TR:O75984 O75984
							HYPOTHETICAL 127.6 KD PROTEIN ;
5435	18234	30948	2.95	1.6E-01	AW187496.1	EST_HUMAN	xm43f01.x1 NCL CGAP_GC6 Homo sapiens cDNA clone IMAGE:2686969 3' similar to TR:O75984 O75984
5447	18246	31134	2.15	1.6E-01	AF034716.1	NT	HYPOTHETICAL 127.6 KD PROTEIN ;
5938	18720	31679	0.83	1.6E-01	BE925803.1	EST_HUMAN	Rattus norvegicus CCAA/Tenhancer binding protein epsilon (cebpe) gene, complete cds
6162	18939	31909	0.71	1.6E-01	BF183584.1	EST_HUMAN	RC3-BN0034-113-h01 BN0034 Homo sapiens cDNA
6162	18939	31910	0.71	1.6E-01	BF183584.1	EST_HUMAN	601809725R1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:4040335 3'
							601809725R1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:4040335 3'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8334	19104	32092	2.37	1.6E-01	AL161588.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 84
8334	19104	32093	2.37	1.6E-01	AL161588.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 84
6885	19602	32841	0.55	1.6E-01	AA3398047.1	EST_HUMAN	2189404.1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:729511 5'
6867	17644	30539	5.32	1.6E-01	AW291215.1	EST_HUMAN	UI-H-B12-agi-b-06-Q-UI.s1 NCI CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2724418 3'
7676	20340	33453	1.66	1.6E-01	AW246359.1	EST_HUMAN	2822248.5 prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2822248 5'
7703	20366		0.74	1.6E-01	AU136525.1	EST_HUMAN	AU136525 PLACE1 Homo sapiens cDNA clone PLACE1004468 5'
7768	20464	33589	1.81	1.6E-01	L49349.1	NT	Gorilla gorilla androgen receptor gene, partial exon
7924	20619		0.51	1.6E-01	BE244087.1	EST_HUMAN	TCBAP1E0607 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP0607
8018	20713	33844	0.87	1.6E-01	U38243.1	NT	Bacteroides vulgatus beta-lactamase (ctxA) gene, complete cds and mobilization protein (mcbA) gene, complete cds
8530	21222	34364	0.88	1.6E-01	Z96119.1	NT	Bacillus subtilis complete genome (section 16 of 21): from 2997771 to 3213410
8725	21417	34561	0.63	1.6E-01	R13673.1	EST_HUMAN	yf60h08.1 Soares Infant brain T1NB Homo sapiens cDNA clone IMAGE:26873 5'
8831	21523		0.59	1.6E-01	L36861.1	NT	Homo sapiens guanylate cyclase activating protein (GCAP) gene exons 1-4, complete cds
8870	21561	34706	1.72	1.6E-01	Z49501.1	NT	S.cerevisiae chromosome X reading frame ORF YJR001w
9009	21699		0.83	1.6E-01	AF111167.2	NT	Homo sapiens Jun dimerization protein gene, partial cds; cfos gene, complete cds; and unknown gene
9551	22204		2.09	1.6E-01	BF375171.1	EST_HUMAN	RC3-ST0200-041199-011-h01 ST0200 Homo sapiens cDNA
9554	22207	35391	1.7	1.6E-01	Z49501.1	NT	S.cerevisiae chromosome X reading frame ORF YJR001w
9589	22242		0.97	1.6E-01	BE155684.1	EST_HUMAN	PM2-HT0353-270100-004-f11 HT0353 Homo sapiens cDNA
10553	23249	36488	3.3	1.6E-01	AW850853.1	EST_HUMAN	IL3-C10220-11199-028-G01 CT0220 Homo sapiens cDNA
10918	23598	36845	1.59	1.6E-01	O14647	SWISSPROT	CHROMODOMAIN-HELICASE-DNA-BINDING PROTEIN 2 (CHD-2)
10918	23598	36846	1.59	1.6E-01	O14647	SWISSPROT	CHROMODOMAIN-HELICASE-DNA-BINDING PROTEIN 2 (CHD-2)
10923	23603	36852	1.55	1.6E-01	BE259849.1	EST_HUMAN	601145793F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3161183 5'
11059	23729		4.28	1.6E-01	AF105064.1	NT	Plasmodium falciparum calcium-dependent protein kinase-3 (cdpk3) gene, complete cds
11388	23894	37296	7.28	1.6E-01	6671562	NT	Mus musculus adaptor-related protein complex AP-1, beta 1 subunit (Ap1b1), mRNA
11706	24301		1.26	1.6E-01	BF527237.1	EST_HUMAN	602039465F2 NCI CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4177073 5'
11886	25331		1.64	1.6E-01	6678466	NT	AV719585 GLC Homo sapiens cDNA clone G1CEMF07 5'
12002	24538	37273	5.28	1.6E-01	AV719585.1	EST_HUMAN	Rat convertase P05 mRNA, 5' end
12292	24721	31052	1.72	1.6E-01	L14933.1	NT	RC1-LT0074-120200-014-h01_1 LT0074 Homo sapiens cDNA
12321	24740		1.5	1.6E-01	AW839711.1	EST_HUMAN	Cucumis sativus KS mRNA for ent-kaurene synthase, complete cds
12418	25149		287.76	1.6E-01	AB045310.1	NT	Homo sapiens mRNA for FLJ00104 protein, partial cds
12574	24901		2.4	1.6E-01	AK024496.1	NT	

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Table 4

Single Exon Probes Expressed in Brain

Single Exon Probes Expressed in Brain							
Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12681	24961		1.72	1.6E-01	AF287344.1	NT	Fuchsia hybrid cultivar Qiu 94208 ribosomal protein S10 gene, partial cds; nuclear gene for mitochondrial product
12687	24973	30992	1.7	1.6E-01	9506522	NT	Rattus norvegicus chondroitin sulfate proteoglycan 5 (neuroglycan C) (Ospg5), mRNA
12786	25046		1.52	1.6E-01	BF672698.1	EST_HUMAN	602152004F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4293145 5'
241	13050	26889	1.4	1.5E-01	BE710087.1	EST_HUMAN	IL3-HT0819-040700-197-E05 HT0619 Homo sapiens cDNA
241	13050	25690	1.4	1.5E-01	BE710087.1	EST_HUMAN	IL3-HT0819-040700-197-E05 HT0619 Homo sapiens cDNA
573	15517		9.31	1.5E-01	AV711696.1	EST_HUMAN	AV711696 DCA Homo sapiens cDNA clone DCAADH06 5'
768	13539	26198	1.09	1.5E-01	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
1070	13828	26487	1.01	1.5E-01	AJ009735.1	NT	Cyprinus carpio mRNA for EGG322 myosin heavy chain, 3'UTR
1075	13833	26491	2.75	1.5E-01	AJ251885.1	NT	Homo sapiens partial SLC22A2 gene for organic cation transporter (OCT2), exon 1
1091	13849		1.42	1.5E-01	L36125.1	NT	Rattus norvegicus insulin-responsive glucose transporter (GLUT4) gene, 5' end
1194	13946	26610	0.82	1.5E-01	AW195516.1	EST_HUMAN	hs39d11.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2698085 3'
1252	14001	26688	2.98	1.5E-01	D26535.1	NT	Human gene for dihydropyrimidine succinyltransferase, complete cds (exon 1-15)
1252	14001	26689	2.98	1.5E-01	D26535.1	NT	Human gene for dihydropyrimidine succinyltransferase, complete cds (exon 1-15)
1465	14212	26901	1.88	1.5E-01	AF117340.1	NT	Human gene for dihydropyrimidine succinyltransferase, complete cds (exon 1-15)
1901	14638	27347	1	1.5E-01	AW444451.1	EST_HUMAN	Human gene for dihydropyrimidine succinyltransferase, complete cds (exon 1-15)
2716	15423	28162	1.98	1.5E-01	BF695381.1	EST_HUMAN	Human gene for dihydropyrimidine succinyltransferase, complete cds (exon 1-15)
2914	15680		1.15	1.5E-01	AW572516.1	EST_HUMAN	xw58a02.x2 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:4247537 5'
3048	15814	28459	0.74	1.5E-01	O78687	SWISSPROT	THYROID HORMONE RECEPTOR ALPHA-1 (HUMAN);
3347	16106	28761	5.06	1.5E-01	AA935049.1	EST_HUMAN	NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4
3361	16120	28777	0.82	1.5E-01	Z23104.1	NT	oc68d06.s1 NCI_CGAP_GC4 Homo sapiens cDNA clone IMAGE:1571337 3' similar to gb:M11433
3361	16120	28778	0.82	1.5E-01	Z23104.1	NT	RETINOL-BINDING PROTEIN 1, CELLULAR (HUMAN);
				1.5E-01	Z23104.1	NT	L.stagnalis mRNA for G protein-coupled receptor
				1.5E-01		NT	L.stagnalis mRNA for G protein-coupled receptor
3738	18491	29128	2.11	1.5E-01	U09964.1	NT	Mus musculus ICR/Swiss glyceraldehyde 3-phosphate dehydrogenase (Gapd-S) gene, complete cds
3752	16504	29140	0.74	1.5E-01	7108358	NT	Homo sapiens pyruvate dehydrogenase kinase, isoenzyme 1 (PDK1), nuclear gene encoding mitochondrial protein, mRNA
3848	16599	29238	2.55	1.5E-01	AW685983.1	EST_HUMAN	h310f06.x1 Soares NFL_I_GBC_S1 Homo sapiens cDNA clone IMAGE:2981411 3'
4028	16773	29405	1.1	1.5E-01	AW366659.1	EST_HUMAN	RC2-HT0149-191099-012-09 HT0149 Homo sapiens cDNA
4161	16901	29630	8.35	1.5E-01	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
4676	17410	30046	1.57	1.5E-01	BF687865.1	EST_HUMAN	602087192F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4066223 5'
4703	15423	28162	1.92	1.5E-01	BF695381.1	EST_HUMAN	602093289F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4247537 5'
5132	17850	30467	1.55	1.5E-01	Z72808.1	NT	S.cerevisiae chromosome VII reading frame ORF YGL086w

Table 4

Single Exon Probes Expressed In Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5146	17864	30480	1.05	1.5E-01	AF056313.1	NT	Morone saxatilis gonadotropin-releasing hormone type II gene, complete cds
5176	17984	30499	2.16	1.5E-01	P07998	SWISSPROT	THROMBOSPONDIN 1 PRECURSOR
5203	18011	30632	1.15	1.5E-01	AF256652.1	NT	Calman crocodilus MHC class II beta chain (hellbeta) gene, complete cds
5245	18051		6.92	1.5E-01	P15196	SWISSPROT	SEX HORMONE-BINDING GLOBULIN PRECURSOR (SHBG) (SEX STEROID-BINDING PROTEIN) (ABP)
5451	18250	31139	5.08	1.5E-01	AW850754.1	EST_HUMAN	IL3-CT0219-160200-064-F10 CT0219 Homo sapiens cDNA
5492	18291	31188	8.42	1.5E-01	U65016.1	NT	Mus musculus transforming growth factor alpha (TGFA) mRNA, complete cds
5492	18291	31189	8.42	1.5E-01	U65016.1	NT	Mus musculus transforming growth factor alpha (TGFA) mRNA, complete cds
5915	18700	31653	3.09	1.5E-01	6753659	NT	Mus musculus DNA methyltransferase 2 (Dnmt2), mRNA
5915	18700	31654	3.09	1.5E-01	6753659	NT	Mus musculus DNA methyltransferase 2 (Dnmt2), mRNA
5952	18734	31693	1.93	1.5E-01	AJ276605.1	NT	Mus musculus genomic fragment, 279 Kb, chromosome 7
6102	18880	31847	3.1	1.5E-01	BE727658.1	EST_HUMAN	601564322F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3833981 5'
6152	18929		1.77	1.5E-01	4506356	NT	Homo sapiens RAD54 (S.cerevisiae)-like (RAD54L) mRNA
6251	19025	31999	2.09	1.5E-01	AF134907.1	NT	Influenza B virus (B/Nanchang/480/94) NB protein gene, complete cds; and neuraminidase gene, partial cds
6409	25089	32176	2.21	1.5E-01	AE001039.1	NT	Archaeoglobus fulgidus section 68 of 172 of the complete genome
6437	19205	32201	4.99	1.5E-01	11417236	NT	Homo sapiens chromosome 5 open reading frame 3 (CSORF3), mRNA
6448	19216	32214	1.95	1.5E-01	P48508	SWISSPROT	GLUTAMATE-CYSTEINE LIGASE REGULATORY SUBUNIT (GAMMA-GLUTAMYL CYSTEINE SYNTHETASE) (GAMMA-ECS) (GCS LIGHT CHAIN)
6493	19259	32260	2.35	1.5E-01	Q28462	SWISSPROT	AMELOGENIN
6585	19348	32361	1.25	1.5E-01	AA714760.1	EST_HUMAN	hw30d10.s1 NCI CGAP_GCB0 Homo sapiens cDNA clone IMAGE:1241971 3'
6612	19375	32389	1.66	1.5E-01	P30143	SWISSPROT	HYPOTHETICAL 51.7 KD PROTEIN IN THRC-TALB INTERGENIC REGION (ORF8)
6882	17958	30554	6.82	1.5E-01	AW970295.1	EST_HUMAN	EST382376 IMAGE resequences, MAGK Homo sapiens cDNA
6918	25102		0.79	1.5E-01	AA811545.1	EST_HUMAN	0673102.s1 NCI CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1337019 3' similar to contains element LTR2 repetitive element;
7115	19803		2.07	1.5E-01	AF210842.1	NT	Homo sapiens HARP (HARP) gene, exon 17 and complete cds
7290	19973	33051	2.96	1.5E-01	A973157.1	EST_HUMAN	wf52c08.x1 NCI CGAP_U11 Homo sapiens cDNA clone IMAGE:2491310 3'
7490	20162	33254	2.04	1.5E-01	AF299073.1	NT	Bos taurus Niemann-Pick type C1 disease protein (NPC1) mRNA, complete cds
7490	20162	33255	2.04	1.5E-01	AF299073.1	NT	Bos taurus Niemann-Pick type C1 disease protein (NPC1) mRNA, complete cds
7499	20171	33262	2.04	1.5E-01	AF600811.1	EST_HUMAN	UI-HF-BND-akk-d-05-0-UI.1 NIH_MGC_60 Homo sapiens cDNA clone IMAGE:3077409 5'
7499	20171	33263	2.04	1.5E-01	AF600811.1	EST_HUMAN	UI-HF-BND-akk-d-05-0-UI.1 NIH_MGC_60 Homo sapiens cDNA clone IMAGE:3077409 5'
7640	20305	33414	0.81	1.5E-01	U46560.1	NT	Saccharomyces cerevisiae weak multicopy suppressor of los1-1 (SOL3) gene, complete cds
7957	20652	33775	0.96	1.5E-01	P21303	SWISSPROT	MEROZOITE RECEPTOR PK66 PRECURSOR (66 KD PROTECTIVE MINOR SURFACE ANTIGEN)

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8118	20812	33947	1.13	1.5E-01	AA970317.1	EST_HUMAN	oa85g12.s1 NCL CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1573030 3' similar to gb:M26062
8211	20905		0.95	1.5E-01	BE884799.1	EST_HUMAN	INTERLEUKIN-2 RECEPTOR BETA CHAIN PRECURSOR (HUMAN);
8299	20993		11.54	1.5E-01	C16800.1	EST_HUMAN	G01510523F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3912004 5'
8332	21025	34162	1.8	1.5E-01	L27835.1	NT	C16800 Clontech human aorta polyA+ mRNA (#8572) Homo sapiens cDNA clone GEN-529H09 5'
8491	21183	34325	1.85	1.5E-01	D84476.1	NT	Pangasinanodon gigas growth hormone (GH) mRNA, complete cds
8512	21204		0.71	1.5E-01	P43446	SWISSPROT	Homo sapiens mRNA for ASK1, complete cds
8737	21429	34575	1.18	1.5E-01	4501972	NT	WNT-10A PROTEIN PRECURSOR
9002	21692	34842	2.88	1.5E-01	N74226.1	EST_HUMAN	Homo sapiens adaptor-related protein complex 1, beta 1 subunit (ADTB1), mRNA
9092	21781	34945	1	1.5E-01	BF585465.1	EST_HUMAN	za59e06.s1 Scores fetal liver spleen 1N1LS Homo sapiens cDNA clone IMAGE:296866 3' similar to PIR:S44443 S44443 RAD23 protein homolog 2 - human ;
9100	21788		2.3	1.5E-01	AV754819.1	EST_HUMAN	GVO000404 Human Psoriasis Differential Display Homo sapiens cDNA
9305	21972		0.74	1.5E-01	AU130007.1	EST_HUMAN	AV754819 TP Homo sapiens cDNA clone TPAAHB12 5'
9353	20424	33543	7.32	1.5E-01	U00455.1	NT	AU130007 NT2RP3 Homo sapiens cDNA clone NT2RP3000080 5'
9717	22368	35566	0.53	1.5E-01	M77144.1	NT	Acipenser transmontano vitellogenin mRNA, partial cds
9821	22472	35674	7.51	1.5E-01	AF007570.1	NT	Human type II 3-beta hydroxysteroid dehydrogenase/ 5-delta - 4-delta isomerase gene, complete cds
9821	22472	35675	7.51	1.5E-01	AF007570.1	NT	Aplysia californica carboxypeptidase D mRNA, complete cds
10103	22751	35965	2.92	1.5E-01	X98852.1	NT	Aplysia californica carboxypeptidase D mRNA, complete cds
10207	22855	36070	2.16	1.5E-01	A1814046.1	EST_HUMAN	P. leniusculus mRNA for integrin beta subunit
10207	22855	36071	2.16	1.5E-01	A1814046.1	EST_HUMAN	wk53h12.x1 NCL CGAP_P122 Homo sapiens cDNA clone IMAGE:2419175 3' similar to gb:M27508 BETA
10285	22833	36148	2.01	1.5E-01	U40932.1	NT	GALACTOSIDASE-RELATED PROTEIN PRECURSOR (HUMAN);
10438	23084	36311	1.43	1.5E-01	AJ011964.1	NT	wk53h12.x1 NCL CGAP_P122 Homo sapiens cDNA clone IMAGE:2419175 3' similar to gb:M27508 BETA
10438	23084	36312	1.43	1.5E-01	AJ011964.1	NT	GALACTOSIDASE-RELATED PROTEIN PRECURSOR (HUMAN);
10595	23289	36526	1.62	1.5E-01	BE089492.1	EST_HUMAN	IL5-CN0024-030300-025-D04 CN0024 Homo sapiens cDNA
10595	23289	36527	1.62	1.5E-01	BE089492.1	EST_HUMAN	Claviceps purpurea ps1 gene
10726	23414	36654	7.31	1.5E-01	AL163280.2	NT	CM2-BT0688-210300-122-f11 BT0688 Homo sapiens cDNA
10726	23414	36655	7.31	1.5E-01	AL163280.2	NT	CM2-BT0688-210300-122-f11 BT0688 Homo sapiens cDNA
10896	23576		1.7	1.5E-01	AB042975.1	NT	Homo sapiens chromosome 21 segment HS21C080
11012	23684	36944	1.8	1.5E-01	AW841915.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C080
11057	23727	36999	1.95	1.5E-01	AA425488.1	EST_HUMAN	Sus scrofa CYP51 gene for lanosterol 14 alpha-demethylase, exon 1
							IL5-CN0024-030300-025-D04 CN0024 Homo sapiens cDNA
							zw46d02.r1 Scores total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:773091 5' similar to contains element MER22 repetitive element ;

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Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11119	19973	33051	1.56	1.5E-01	AI973157.1	EST_HUMAN	wf52c08.x1 NCI_CGAP_U11 Homo sapiens cDNA clone IMAGE:2491310 3'
11625	24222		1.56	1.5E-01	AI193704.1	EST_HUMAN	qs72e01.x1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:1744536 3' similar to gb:M17887.60S ACIDIC RIBOSOMAL PROTEIN P2 (HUMAN);
11959	25202		11.07	1.5E-01	BF700582.1	EST_HUMAN	602128753F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4285549 5'
12320	24739		1.37	1.5E-01	AF030358.2	NT	Rattus norvegicus chemokine CX3C mRNA, complete cds
12324	24743		1.77	1.5E-01	AJ238332.1	NT	Mus musculus mRNA for death inducer-obliteror-1 (Dio-1)
12369	24771		5.35	1.5E-01	AB026898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
12385	25220		9.97	1.5E-01	R83077.1	EST_HUMAN	yp87e04.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:194430 5'
12472	25241		2.53	1.5E-01	AV741272.1	EST_HUMAN	AV741272 CB Homo sapiens cDNA clone CBDAGD04 5'
12573	25150	30897	9.2	1.5E-01	AL139074.2	NT	Campylobacter jejuni NCTC11188 complete genome; segment 1/6
12783	25036	30965	1.89	1.5E-01	AJ276242.1	NT	Sus scrofa mRNA for sodium iodide symporter
292	13088		1.72	1.4E-01	AF009693.1	NT	Homo sapiens T cell receptor beta locus, TORBV85SP to TORBV21S2A2 region
890	13659		3.62	1.4E-01	D78638.1	NT	Xenopus laevis mRNA for DNA (cytosine-5)-methyltransferase, complete cds
1236	13985		2.48	1.4E-01	T91864.1	EST_HUMAN	yd54c01.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:112032 3'
1742	14484		1.5	1.4E-01	6679980	NT	Mus musculus growth differentiation factor 5 (Gdf5), mRNA
1745	14487	27186	1.71	1.4E-01	AE001710.1	NT	Thermotoga maritima section 22 of 136 of the complete genome
1898	14635		0.96	1.4E-01	AW135741.1	EST_HUMAN	UI-H-B1-acf-a-09-0-UI.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2714009 3'
1978	14714		9.33	1.4E-01	AA720615.1	EST_HUMAN	ny72d07.s1 NCI_CGAP_GGB1 Homo sapiens cDNA clone IMAGE:1283821 3'
2478	15196	27935	1.38	1.4E-01	P30706	SWISSPROT	GLYCEROL-3-PHOSPHATE ACYLTRANSFERASE PRECURSOR (GPAT)
2795	15500	28241	4.23	1.4E-01	AI933496.1	EST_HUMAN	wn74d01.x1 NCI_CGAP_U12 Homo sapiens cDNA clone IMAGE:2441665 3'
3879	16629	29267	0.96	1.4E-01	R59232.1	EST_HUMAN	yg97a03.r1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:41467 5'
3879	16829	29268	0.96	1.4E-01	R59232.1	EST_HUMAN	yg97a03.r1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:41467 5'
4153	16895	29524	8.69	1.4E-01	AI698094.1	EST_HUMAN	bx56c02.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2273570 3'
4153	16895	29525	8.69	1.4E-01	AI698094.1	EST_HUMAN	bx56c02.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2273570 3'
4212	16953	29577	3.73	1.4E-01	AE001710.1	NT	Thermotoga maritima section 22 of 136 of the complete genome
5014	17735	30342	0.94	1.4E-01	U12283.1	NT	Mus musculus transcription factor USF2 (USF2) gene, exons 8-10 and complete cds
5223	18030	30656	5.48	1.4E-01	T90677.1	EST_HUMAN	ye15c11.s1 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:117812 3'
5246	18052	30679	4.6	1.4E-01	AB004556.1	NT	Candida tropicalis DNA for mitochondrial NADP-linked isocitrate dehydrogenase, complete cds
5246	18052	30680	4.6	1.4E-01	AB004556.1	NT	Candida tropicalis DNA for mitochondrial NADP-linked isocitrate dehydrogenase, complete cds
6205	18980	31959	3	1.4E-01	BE326891.1	EST_HUMAN	hn67c02.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3133638 3'
6391	19160	32160	5.6	1.4E-01	AU117147.1	EST_HUMAN	AU117147 HEMBA1 Homo sapiens cDNA clone HEMBA1000769 5'
6391	19160	32161	5.6	1.4E-01	AU117147.1	EST_HUMAN	AU117147 HEMBA1 Homo sapiens cDNA clone HEMBA1000769 5'
6477	19244	32244	3.14	1.4E-01	AW082796.1	EST_HUMAN	xb71d12.x1 Soares_NFL_I_GBC_S1 Homo sapiens cDNA clone IMAGE:2581751 3'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6490	19257		1.64	1.4E-01	BE266536.1	EST_HUMAN	601193523F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3537581 5'
6509	19274	32275	2.45	1.4E-01	BF378633.1	EST_HUMAN	QV1-UM0036-080300-103-409 UM0036 Homo sapiens cDNA
7026	19718		0.66	1.4E-01	AL118568.1	EST_HUMAN	DKFZp761A0910.1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761A0910 5'
7284	19867		1.51	1.4E-01	AW015373.1	EST_HUMAN	UI-H-B10-aat-c-09-0-U1.s1 NC1_CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2710289 3'
7521	20192	33283	1.19	1.4E-01	U85845.1	NT	Oryctolagus cuniculus fructose 1,6-bisphosphate aldolase (AldB) gene, complete cds
7653	20317	33427	0.98	1.4E-01	AI305192.1	EST_HUMAN	q190b12.x1 Soares NIHMPu_S1 Homo sapiens cDNA clone IMAGE:1879563 3'
8373	21066		1.23	1.4E-01	AV659047.1	EST_HUMAN	AV659047 GLC Homo sapiens cDNA clone GLCFSH06 3'
8683	21376		0.57	1.4E-01	AI436093.1	EST_HUMAN	ih92b12.x1 Soares NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2126111 3' similar to TR:O02710 O02710 GAG POLYPROTEIN.
8811	21503	34650	4.18	1.4E-01	AA307073.1	EST_HUMAN	EST178192 Colon carcinoma (HCC) cell line Homo sapiens cDNA 5' end
8892	21583	34722	0.59	1.4E-01	AW023636.1	EST_HUMAN	df58b03.y1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:2487485 5'
9021	21711	34884	0.97	1.4E-01	R62746.1	EST_HUMAN	y10h05.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:138873 5'
9021	21711	34865	0.97	1.4E-01	R62746.1	EST_HUMAN	y10h05.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:138873 5'
9085	21774	34938	8.81	1.4E-01	BF310959.1	EST_HUMAN	601885465F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4124824 5'
9175	21845	35011	1.24	1.4E-01	W93411.1	EST_HUMAN	z194a04.r1 Soares fetal heart NbHH19W Homo sapiens cDNA clone IMAGE:357102 5' similar to contains element KER repetitive element:
9246	21925	35095	0.46	1.4E-01	X73293.1	NT	M.vannielii genes rpoH, rpoB and rpoA
9246	21925	35096	0.46	1.4E-01	X73293.1	NT	M.vannielii genes rpoH, rpoB and rpoA
9258	21937	35111	1.46	1.4E-01	Y10196.1	NT	Homo sapiens PHEX gene
9258	21937	35112	1.46	1.4E-01	Y10196.1	NT	Homo sapiens PHEX gene
9350	20421	33541	1.98	1.4E-01	AF121381.1	NT	Drosophila melanogaster signal transducing adaptor protein (STAM), serine threonine kinase 1a1 (IAL), and zinc finger protein (DNZ1) genes, complete cds
9704	22355	35551	0.97	1.4E-01	X66092.1	NT	C.perfringens ORF for putative membrane transport protein
9887	22537	35732	1.26	1.4E-01	AF023813.1	NT	Macronitrium levatum small ribosomal protein 4 (rps4) gene, chloroplast gene encoding chloroplast protein, partial cds
9988	22636	35846	0.56	1.4E-01	AW021908.1	EST_HUMAN	df29h08.y1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:2485094 5'
9988	22636	35847	0.56	1.4E-01	AW021908.1	EST_HUMAN	df29h08.y1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:2485094 5'
10157	22805	36022	0.81	1.4E-01	BF375285.1	EST_HUMAN	MR3-ST0218-211299-013-a08 ST0218 Homo sapiens cDNA
10157	22805	36023	0.81	1.4E-01	BF375285.1	EST_HUMAN	MR3-ST0218-211299-013-a08 ST0218 Homo sapiens cDNA
10360	23007		0.57	1.4E-01	T84293.1	EST_HUMAN	y447d03.r1 Soares fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:111395 5'
10499	23145	36372	0.62	1.4E-01	Z99117.1	NT	Bacillus subtilis complete genome (section 14 of 21): from 2599451 to 2812870
10607	23301		1.64	1.4E-01	AA811480.1	EST_HUMAN	ca99a03.s1 NC1_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1320364 3'
10746	23433	36676	3.24	1.4E-01	R53400.1	EST_HUMAN	y170c05.r1 Soares breast 2NbHBst Homo sapiens cDNA clone IMAGE:154088 5'
10954	23631	36879	1.31	1.4E-01	AW104982.1	EST_HUMAN	xt73e10.x1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2603274 3'

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11036	23707	36975	1.3	1.4E-01	T96102.1	EST_HUMAN	ye47g10.1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:120930 5'
11036	23707	36976	1.3	1.4E-01	T96102.1	EST_HUMAN	ye47g10.1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:120930 5'
11038	23709	36979	2.35	1.4E-01	P08648	SWISSPROT	INTEGRIN ALPHA-5 PRECURSOR (FIBRONECTIN RECEPTOR ALPHA SUBUNIT) (INTEGRIN ALPHA-F) (VLA-5) (CD49E)
11262	23924	37215	1.66	1.4E-01	X66092.1	NT	C. parvulus ORF for putative membrane transport protein
11301	19967		1.41	1.4E-01	AW015373.1	EST_HUMAN	UI-H-B10-aat-c-09-0-UI.s1 NCI_CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2710289 3'
11446	23213	36445	2.37	1.4E-01	U28760.1	NT	Borrelia burgdorferi glyceraldehyde-3-phosphate dehydrogenase (GAPDH), phosphoglycerate kinase (PGK), triosephosphate isomerase (TPI) genes, complete cds
11512	24112		1.82	1.4E-01	X52102.1	NT	M.musculus p16K gene for 16 kDa protein
11743	24335	37691	1.83	1.4E-01	AF146793.2	NT	Mus musculus neuromedin U precursor (Nmu) gene, partial cds; (Prlp) gene, partial cds; CLOCK (Clock) gene, complete cds; PFT27 (PFT27) gene, complete cds; and HBAR (H5ar) gene, complete cds
11827	24411	37747	1.31	1.4E-01	AW664572.1	EST_HUMAN	h14h08.x1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2972319 3'
11827	24411	37748	1.31	1.4E-01	AW664572.1	EST_HUMAN	h14h08.x1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2972319 3'
12213	25172	30904	1.98	1.4E-01	AB000690.1	NT	Ephydratia fluvialis mRNA for aldolase, partial cds
12261	24706	31049	2.03	1.4E-01	X74773.1	NT	P. salina plastid gene secY
12275	24714		2.2	1.4E-01	11968117	NT	Rattus norvegicus desmin (Des), mRNA
12318	25393		2.84	1.4E-01	BE513802.1	EST_HUMAN	601316638F1 NIH_MGC_3 Homo sapiens cDNA clone IMAGE:3634329 5'
12413	24794		1.35	1.4E-01	AF083221.1	NT	Fugu rubripes putative neurotransmitter receptors, YDR140w homolog, and glycylamide ribonucleotide transferase (GART) genes, complete cds
12425	24801		2.97	1.4E-01	D64004.1	NT	Synechocystis sp. PCC6803 complete genome, 23/27, 2668767-3002965
12500	26407		3.15	1.4E-01	P10447	SWISSPROT	TYROSINE-PROTEIN KINASE TRANSFORMING PROTEIN ABL
12708	25221		6.26	1.4E-01	D82983.1	NT	Mus musculus mRNA for prolidase, complete cds
12779	25033		2.37	1.4E-01	AW377998.1	EST_HUMAN	MRO-HT0208-221299-204-c08 HT0208 Homo sapiens cDNA
314	13118	25756	3.12	1.3E-01	4758467	NT	Homo sapiens G protein-coupled receptor 50 (GPR50) mRNA
314	13118	25757	3.12	1.3E-01	4758467	NT	Homo sapiens G protein-coupled receptor 50 (GPR50) mRNA
516	13300	25932	2.8	1.3E-01	AB013139.1	NT	Homo sapiens gene for NBS1, complete cds
621	13400	26035	1.05	1.3E-01	AJ277606.1	NT	Human calicivirus HUJNLV/Girlington/93/UK RNA for capsid protein (ORF2), strain HUJNLV/Girlington/93/UK
621	13400	26036	1.05	1.3E-01	AJ277606.1	NT	Human calicivirus HUJNLV/Girlington/93/UK RNA for capsid protein (ORF2), strain HUJNLV/Girlington/93/UK
824	13594	26264	0.92	1.3E-01	X63330.1	NT	P. dumerilii histone gene cluster for core histones H2A, H2B, H3 and H4
874	13643	26313	1.8	1.3E-01	AF139518.1	NT	Rattus norvegicus A-kinase anchor protein mRNA, complete cds
1005	13765	26425	1.31	1.3E-01	AL117078.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation

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Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1105	13862		2.6	1.3E-01	AL115285.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
1183	13945	26609	1.13	1.3E-01	AV712467.1	EST_HUMAN	AV712467 DCA Homo sapiens cDNA clone DCAAF05 5'
1425	14172		1.18	1.3E-01	AF146277.1	NT	Homo sapiens adapter protein CMS mRNA, complete cds
1850	14588	27303	0.97	1.3E-01	6880957	NT	Mus musculus procollagen, type XI, alpha 1 (Cd11a1), mRNA
1952	14887	27400	2.18	1.3E-01	AL117078.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
2167	14896		1.22	1.3E-01	AJ243578.1	NT	Rhodospirillum rubrum actinophila pucB5, pucA6, pucB6, pucB7, pucA8 and pucC genes and ORF151
2288	15013		1.2	1.3E-01	AW812104.1	EST_HUMAN	RC4-ST0173-191099-032-012 ST0173 Homo sapiens cDNA
2379	15101		3.34	1.3E-01	AE001016.1	NT	Archaeoglobus fulgidus section 91 of 172 of the complete genome
2592	15306	28042	4.76	1.3E-01	M86918.1	NT	Carassius auratus keratin type I mRNA, complete cds
3065	15831	28474	1.01	1.3E-01	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C007
3443	16199	28849	0.98	1.3E-01	M21572.1	NT	Bovine branched chain alpha-keto acid dihydrolipoyl transacylase mRNA, complete cds
3969	16718		1.43	1.3E-01	AL161581.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 77
4117	16859		1.27	1.3E-01	AF020713.1	NT	Bacteriophage SPB22 complete genome
4137	16879		4.24	1.3E-01	AW364941.1	EST_HUMAN	QV3-DT0018-081299-036-003 DT0018 Homo sapiens cDNA
4145	16987	29518	2.03	1.3E-01	AF026805.1	NT	Schistosoma mansoni fructose biphosphate aldolase mRNA, complete cds
4163	16903	29532	18.52	1.3E-01	AW273741.1	EST_HUMAN	xv23f10.x1 Scares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2813995 3'
4257	16998	29627	0.99	1.3E-01	AV752279.1	EST_HUMAN	AV752279 NPD Homo sapiens cDNA clone NPDAZE02 5'
4257	16998	29628	0.99	1.3E-01	AV752279.1	EST_HUMAN	AV752279 NPD Homo sapiens cDNA clone NPDAZE02 5'
4279	17018		12.76	1.3E-01	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
4445	17181	29806	0.77	1.3E-01	M21572.1	NT	Bovine branched chain alpha-keto acid dihydrolipoyl transacylase mRNA, complete cds
4497	17233	29883	2.68	1.3E-01	BE272339.1	EST_HUMAN	601126096F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:2990063 5'
4963	17688		0.74	1.3E-01	BF091980.1	EST_HUMAN	RC4-TN0077-180900-012-005 TN0077 Homo sapiens cDNA
5242	18048	30677	0.83	1.3E-01	AW466988.1	EST_HUMAN	ha07b06.x1 NCL_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2872979 3' similar to contains L1.b1 L1
5278	18083	30739	2.23	1.3E-01	AW804417.1	EST_HUMAN	QV0-UM0093-100400-189-a06 UM0093 Homo sapiens cDNA
5414	18213		0.77	1.3E-01	AF107793.1	NT	Emicella nidulans DNA-dependent RNA polymerase II RPB140 (RPB2) gene, partial cds
5487	18295		0.75	1.3E-01	AF056880.1	NT	Hepatitis C virus 88_C10 genome polyprotein gene, partial cds
5638	18433	31346	0.97	1.3E-01	BF210920.1	EST_HUMAN	601874591F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4101119 5'
5896	18681	31628	0.57	1.3E-01	BF527281.1	EST_HUMAN	602039337F2 NCL_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4177233 5'
5896	18681	31629	0.57	1.3E-01	BF527281.1	EST_HUMAN	602039337F2 NCL_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4177233 5'
6392	19161	32162	15.12	1.3E-01	AB031326.1	NT	Schizosaccharomyces pombe gene for Alp41, complete cds
6474	19241	32241	1.95	1.3E-01	X88891.1	NT	C. jacchus intron 4 of visual pigment gene (red allele)
6681	19608		0.75	1.3E-01	W26367.1	EST_HUMAN	2663 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA

Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6914	19651		0.99	1.3E-01	BF529560.1	EST_HUMAN	602044345F1 NCI_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4181866 5'
7162	19849		1.96	1.3E-01	H48664.1	EST_HUMAN	y33d02.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:207075 5'
7859	20554		0.88	1.3E-01	BE272339.1	EST_HUMAN	601126096F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:2980063 5'
7873	20568	33694	1.34	1.3E-01	11423294	NT	Homo sapiens PRO6811 protein (PRO6811), mRNA
7902	20597	33727	1.17	1.3E-01	BF690522.1	EST_HUMAN	602187015T1 NIH_MGC_49 Homo sapiens cDNA clone IMAGE:4298074 3'
8136	20830		0.51	1.3E-01	BE562528.1	EST_HUMAN	601335828F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3689934 5'
8172	20866	33998	0.54	1.3E-01	11421556	NT	Homo sapiens TED protein (TED), mRNA
8243	20937		4.47	1.3E-01	Z74102.1	NT	S.cerevisiae chromosome IV reading frame ORF YDL054c
8285	20979		4.44	1.3E-01	8923919	NT	Homo sapiens core histone macroH2A2.2 (MACROH2A2), mRNA
8426	21119	34258	1.02	1.3E-01	BF690522.1	EST_HUMAN	602187015T1 NIH_MGC_49 Homo sapiens cDNA clone IMAGE:4298074 3'
8847	21538	34683	0.58	1.3E-01	R11172.1	EST_HUMAN	y33g11.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:129284 5' similar to SP:RL2B_RAT P29316 60S RIBOSOMAL PROTEIN ;
8847	21538	34684	0.58	1.3E-01	R11172.1	EST_HUMAN	y33g11.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:129284 5' similar to SP:RL2B_RAT P29316 60S RIBOSOMAL PROTEIN ;
9119	21807	34873	0.61	1.3E-01	11068003	NT	Plutella xylostella granulovirus, complete genome
9119	21807	34874	0.61	1.3E-01	11068003	NT	Plutella xylostella granulovirus, complete genome
9372	21947	35120	3.71	1.3E-01	AF023129.1	NT	Oryctolagus cuniculus H+K+ATPase alpha 2c subunit mRNA, complete cds
9671	22323		0.56	1.3E-01	N86348.1	EST_HUMAN	J7837F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone J7837 5' similar to B-CELL RECEPTOR ASSOCIATED PROTEIN (BAP) 29
9951	22599		0.99	1.3E-01	8393940	NT	Rattus norvegicus peptidyl arginine deiminase, type IV (Pdi4), mRNA
10030	22678	35894	0.95	1.3E-01	AW851599.1	EST_HUMAN	MR2-CT0222-201099-001-e01 CT0222 Homo sapiens cDNA
10291	25128	36151	1.1	1.3E-01	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
10423	23069	36280	0.64	1.3E-01	AU121237.1	EST_HUMAN	AU121237 HEMBB1 Homo sapiens cDNA clone HEMBB1002387 5'
10471	23117	36347	0.52	1.3E-01	AW247836.1	EST_HUMAN	2820637.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2820837 3'
10528	23225		2.93	1.3E-01	BF330999.1	EST_HUMAN	MR4-BT0358-130700-010-H08 BT0358 Homo sapiens cDNA
10775	23458	36701	1.56	1.3E-01	H01883.1	EST_HUMAN	y32d09.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:150449 5'
11039	23710	36980	1.33	1.3E-01	AF119117.1	NT	Homo sapiens dopamine transporter (SLC6A3) gene, complete cds
11216	23879		3.28	1.3E-01	6671745	NT	Mus musculus cofilin 2, muscle (Cif2), mRNA
11304	23963	37263	1.42	1.3E-01	BF677328.1	EST_HUMAN	602087045F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4251346 5'
11304	23963	37264	1.42	1.3E-01	BF677328.1	EST_HUMAN	602087045F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4251346 5'
11589	24188	37504	4.26	1.3E-01	BE279449.1	EST_HUMAN	601158052F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3504804 5'
11723	24317	37640	1.94	1.3E-01	BE619364.1	EST_HUMAN	601473369F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3876208 5'
11755	24346	37676	1.44	1.3E-01	BF883555.1	EST_HUMAN	602139760F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4300863 5'
12114	24607	31088	1.37	1.3E-01	BE618346.1	EST_HUMAN	601462741F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3866003 5'

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12247	24895		4.43	1.3E-01	AJ242790.1	NT	Gallus gallus scyc1 gene for lympholactin, exons 1-3
12274	24713		1.51	1.3E-01	Z13994.1	NT	R. norvegicus crp2 gene for cystatin related protein 2
12806	24915		1.43	1.3E-01	AB028829.1	NT	Ephydratia flumilis mRNA for SALK-6, complete cds
12636	24936		2.26	1.3E-01	AW001114.1	EST_HUMAN	wu244d09.x1 Soares, Dieckgraefe, colon_NHCD Homo sapiens cDNA clone IMAGE:2520977 3' similar to TR:O60287 KIAA0539 PROTEIN ;
374	13199	25844	8.42	1.2E-01	AI421744.1	EST_HUMAN	if39b02.x1 NCI_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:2098539 3' similar to gb:U05760_mn1
416	12828		1.05	1.2E-01	U66912.1	NT	ANNEXIN V (HUMAN);
534	13317		4.33	1.2E-01	AF039442.1	NT	Dicystostellum discoideum ORF DG1016 gene, partial cds
1355	14103	26778	3.22	1.2E-01	AU149146.1	EST_HUMAN	Homo sapiens colon cancer antigen NY-CO-45 mRNA, partial cds
1355	14103	26779	3.22	1.2E-01	AU149146.1	EST_HUMAN	AU149146 NT2RM4 Homo sapiens cDNA clone NT2RM4001691 3'
1362	14110		4.36	1.2E-01	AV735249.1	EST_HUMAN	AU149146 NT2RM4 Homo sapiens cDNA clone NT2RM4001691 3'
1496	14243		1.23	1.2E-01	AA897474.1	EST_HUMAN	AV735249 cda Homo sapiens cDNA clone cdaAJB11 5'
1627	14373	27062	1.26	1.2E-01	Q14934	SWISSPROT	al48e09.s1 Soares, NFL_I_GBC_S1 Homo sapiens cDNA clone IMAGE:1460584 3' similar to TR:Q16871
1646	14392	27082	2.81	1.2E-01	AI285402.1	EST_HUMAN	Q16871 ANTH-MULLERIAN HORMONE TYPE II RECEPTOR PRECURSOR ;
1762	14504		20.17	1.2E-01	X89211.1	NT	NUCLEAR FACTOR OF ACTIVATED T-CELLS, CYTOPLASMIC 4 (T CELL TRANSCRIPTION FACTOR NFAT3) (NF-ATC4) (NF-AT3)
1913	14650		1.03	1.2E-01	AW449368.1	EST_HUMAN	q69709.x1 NCI_CGAP_Eso2 Homo sapiens cDNA clone IMAGE:1960553 3'
2181	14910	27842	1.75	1.2E-01	BF248490.1	EST_HUMAN	H. sapiens DNA for endogenous retroviral like element
2284	15009	27748	1.2	1.2E-01	AL163213.2	NT	U1-H-B13-akt-e-10-0-J1.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2734554 3'
2597	15311	28047	1.49	1.2E-01	AW696556.1	EST_HUMAN	601821567F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4046224 5'
							Homo sapiens chromosome 21 segment HS21C013
							QV3-BN0046-220300-128-f10 BN0046 Homo sapiens cDNA
							Is18g07.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2228988 3' similar to TR:Q14048 Q14048
2731	15438	28176	1.12	1.2E-01	AI623388.1	EST_HUMAN	COLLAGEN VI ALPHA-2 ALTERNATIVE C-TERMINAL DOMAIN, [1]: contains element PTR5 repetitive element ;
2847	15615	28262	1.3	1.2E-01	U18018.1	NT	Human E1A enhancer binding protein (E1A-F) mRNA, partial cds
2903	15669	28318	2.5	1.2E-01	AI720470.1	EST_HUMAN	as80c09.x1 Barslead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2335024 3' similar to gb:L05095
2935	15701	28350	2.92	1.2E-01	M16364.1	NT	60S RIBOSOMAL PROTEIN L30 (HUMAN);
3004	15770	28418	0.97	1.2E-01	X56882.1	NT	Human creatine kinase-B mRNA, complete cds
3224	15987	28641	1.39	1.2E-01	AW370668.1	EST_HUMAN	Wheat mRNA for a group 3 late embryogenesis abundant protein (LEA)
3252	16014		1.12	1.2E-01	U67600.1	NT	QV1-BT0259-261099-021-d05 BT0259 Homo sapiens cDNA
3472	16228		0.8	1.2E-01	Z99118.1	NT	Methanococcus jannaschii section 142 of 150 of the complete genome
3511	16267	28921	0.92	1.2E-01	X56882.1	NT	Bacillus subtilis complete genome (section 15 of 21): from 2785131 to 3013540
							Wheat mRNA for a group 3 late embryogenesis abundant protein (LEA)

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3511	16267	28922	0.82	1.2E-01	X66882.1	NT	Wheat mRNA for a group 3 late embryogenesis abundant protein (LEA)
3592	16228		1.46	1.2E-01	Z99118.1	NT	Bacillus subtilis complete genome (section 15 of 21): from 2795131 to 3013540
4160	16900	29528	1.97	1.2E-01	Z54255.1	NT	P.clarkii mRNA; repeat region (ID 2MR17)
4160	16900	29529	1.97	1.2E-01	Z54255.1	NT	P.clarkii mRNA; repeat region (ID 2MR17)
4672	17406	30041	1.1	1.2E-01	Z48183.1	NT	L.esculentum mRNA for glycylase-I
4739	17471		0.92	1.2E-01	AF221633.1	NT	Rana ridibunda pituitary adenylate cyclase-activating polypeptide variant 2 precursor, mRNA, complete cds, alternatively spliced
5170	17979	30492	0.81	1.2E-01	AA744369.1	EST_HUMAN	ny83c04.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1282950 3'
5217	18025	30649	1	1.2E-01	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
5227	18034	30659	2.59	1.2E-01	W33035.1	EST_HUMAN	zc08d02.r1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:321699 5'
5264	18089	30749	2.3	1.2E-01	Z98266.1	NT	Homo sapiens gene encoding plakophilin (exons 1-13)
5418	18217	30926	0.68	1.2E-01	Z48234.1	NT	M.domestica Borkh. Granny Smith adh mRNA for alcohol dehydrogenase
6107	18884	31853	1.93	1.2E-01	BE620945.1	EST_HUMAN	601493518F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3895613 5'
6153	18930	31888	1.36	1.2E-01	P10842	SWISSPROT	MATING-TYPE P-SPECIFIC POLYPEPTIDE P1
6206	19081	31960	2.35	1.2E-01	AW845275.1	EST_HUMAN	IL0-CT0031-221099-113-e04 CT0031 Homo sapiens cDNA
6270	19043	32020	1.54	1.2E-01	M26925.1	NT	Mouse galactosyltransferase mRNA, complete cds
6337	19107	32097	0.57	1.2E-01	AA747535.1	EST_HUMAN	nc85c01.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1269024 3'
6550	19315	32321	1.14	1.2E-01	BF347985.1	EST_HUMAN	602023112F1 NCI_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4158386 5'
6700	19616	32658	0.59	1.2E-01	AF296739.1	NT	JC virus agnoprotein, VP2, VP3, VP1, large T antigen, and small t antigen genes, complete cds
7793	20488		1.4	1.2E-01	BE007072.1	EST_HUMAN	PM3-BN0137-290300-002-009 BN0137 Homo sapiens cDNA
7862	20557	33683	4.36	1.2E-01	A1913753.1	EST_HUMAN	wc99g03.x1 NCI_CGAP_C03 Homo sapiens cDNA clone IMAGE:2326804 3' similar to SW:GST2_HUMAN
7906	20601	33731	0.67	1.2E-01	Q02369	SWISSPROT	Q99735 MICROSOMAL GLUTATHIONE S-TRANSFERASE II ;
8208	20902	34037	0.73	1.2E-01	A1832681.1	EST_HUMAN	NADH-UBIQUINONE OXIDOREDUCTASE B22 SUBUNIT (COMPLEX I-B22) (Cl-B22)
8295	20989		10.29	1.2E-01	AW083652.1	EST_HUMAN	at71b10.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2377435 3'
							xc49d07.x1 NCI_CGAP_Esc02 Homo sapiens cDNA clone IMAGE:2587597 3' similar to gb:IM13452 LAMIN A (HUMAN);
8315	21008		3.34	1.2E-01	AF053772.1	NT	Staphylococcus aureus plasmid pSK23 putative recombinase Sin (sin) gene, partial cds; and transcriptional regulator QacR (qacR)
8354	21047	34184	0.99	1.2E-01	J03956.1	NT	N.crassa vacuolar ATPase 57-Kd subunit (vma-2) gene, complete cds
8354	21047	34185	0.99	1.2E-01	J03956.1	NT	N.crassa vacuolar ATPase 67-Kd subunit (vma-2) gene, complete cds
8499	21191		1.09	1.2E-01	AJ271736.1	NT	Homo sapiens Xq pseudocautosomal region; segment 2/2
8569	21281		1.49	1.2E-01	U32714.1	NT	Haemophilus influenzae Rd section 29 of 163 of the complete genome

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8823	21315		0.62	1.2E-01	X15191.1	NT	M.musculus DNA fragment of Apolipoprotein B gene
9471	22060	35252	2.93	1.2E-01	X77961.1	NT	S.cerevisiae HXT5 gene
9606	22655	35750	1.59	1.2E-01	AV710857.1	EST_HUMAN	AV710857 Cu Homo sapiens cDNA clone CUAKE08 5'
10611	23305	36543	1.38	1.2E-01	BF314481.1	EST_HUMAN	601900763F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4130103 5'
10801	23494		2.17	1.2E-01	D26184.1	NT	Yeast MPT5 gene for suppressor protein, complete cds
10999	23672		3.18	1.2E-01	BE962324.2	EST_HUMAN	601655578R1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3846283 3'
11094	23764		1.58	1.2E-01	BF314481.1	EST_HUMAN	601900763F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4130103 5'
11220	23883	37168	2.61	1.2E-01	AF190493.1	NT	Homo sapiens dynein intermediate chain DNA11 (DNA11) gene, exon 17
11283	23944	37238	1.65	1.2E-01	R40249.1	EST_HUMAN	yf80c02.s1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:28880 3'
11492	24093		1.67	1.2E-01	M65109.1	NT	Rabbit glycogen-associated protein phosphatase regulatory subunit (RG1) mRNA, complete cds
11892	24462		2.53	1.2E-01	AV658033.1	EST_HUMAN	AV658033 GLC Homo sapiens cDNA clone GLC1B12 3'
12230	24683		3.52	1.2E-01	AJ271736.1	NT	Homo sapiens Xq pseudautosomal region; segment 2/2
12305	25351	30605	2.87	1.2E-01	Q04912	SWISSPROT	MACROPHAGE-STIMULATING PROTEIN RECEPTOR PRECURSOR (MSP RECEPTOR) (P185-RON) (CDW136) (CD136 ANTIGEN)
12417	24796		3.16	1.2E-01	AF18892.1	NT	Drosophila melanogaster strain Oregon R potential RNA-binding protein gene, complete cds; and syntactin gene, partial cds
12419	13317		3.19	1.2E-01	AF039442.1	NT	Homo sapiens colon cancer antigen NY-CO-45 mRNA, partial cds
12525	24872		2.11	1.2E-01	X53981.1	NT	R.norvegicus NF68 gene for 68kDa neurofilament
12586	25364	30611	1.44	1.2E-01	BE081418.1	EST_HUMAN	QV4-BT0234-111199-031-g10 BT0234 Homo sapiens cDNA
12610	24917	31007	5.86	1.2E-01	A1299903.1	EST_HUMAN	qr20g05.x1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1898840 3'
12632	24932		2.83	1.2E-01	L10187.1	NT	Xenopus laevis integrin alpha 3 subunit mRNA, partial cds
12638	25289		7.95	1.2E-01	O96433	SWISSPROT	CYCLIN T
12663	24962	30989	1.39	1.2E-01	AE004428.1	NT	Vibrio cholerae chromosome II, section 85 of 93 of the complete chromosome
12800	16228		1.91	1.2E-01	Z99118.1	NT	Bacillus subtilis complete genome (section 15 of 21); from 2795131 to 3013540
12812	25372	30614	1.38	1.2E-01	9845282	NT	Mus musculus protein (16kDa) similar to human SYK interacting protein (p16K), mRNA
551	13334	25964	0.8	1.1E-01	A1561003.1	EST_HUMAN	fr18d08.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2167983 3'
601	13379	28010	1.65	1.1E-01	AA569006.1	EST_HUMAN	nm08g11.s1 NCI_CGAP_Co10 Homo sapiens cDNA clone IMAGE:1059620 3' similar to gb:X06985_rna1
1032	13792	26452	2.03	1.1E-01	BF697308.1	EST_HUMAN	HEME OXYGENASE 1 (HUMAN);
1063	13821		1.3	1.1E-01	AL161560.2	NT	602129847F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4286771 5'
1136	15561	26552	4.62	1.1E-01	AW972158.1	EST_HUMAN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 60
1227	13977	26648	3.01	1.1E-01	D64004.1	NT	EST384142 IMAGE resequences, MAGL Homo sapiens cDNA
1511	14257	26943	2.52	1.1E-01	AU140363.1	EST_HUMAN	Synechocystis sp. PCC6803 complete genome, 23/27, 2868767-3002965
2312	15037		1.85	1.1E-01	6755215	NT	AU140363 PLACE2 Homo sapiens cDNA clone PLACE2000403 5'
						NT	Mus musculus pre T-cell antigen receptor alpha (P1cra), mRNA

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2540	15530		1	1.1E-01	6978676	NT	Rattus norvegicus Procollagen II alpha 1 (Col2a1), mRNA
2572	15268		1.17	1.1E-01	AW821909.1	EST_HUMAN	RC0-ST0379-210100-032-g04 ST0379 Homo sapiens cDNA
3030	15796	28442	0.82	1.1E-01	F03265.1	EST_HUMAN	HSC-TRF022 normalized Infant brain cDNA Homo sapiens cDNA clone c-1f02 3'
3336	16096		1.76	1.1E-01	6753231	NT	Mus musculus calcium channel, voltage-dependent, T type, alpha 1G subunit (Cacna1g), mRNA
3415	16173	28822	2.11	1.1E-01	BE393186.1	EST_HUMAN	601308679F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3627066 5'
3444	16200	28850	1.21	1.1E-01	X62135.1	NT	C.reithardti nuclear gene on linkage group XIX
3570	16325	28972	0.77	1.1E-01	Y07695.1	NT	A.immersus gene for transposase
3688	16441		0.74	1.1E-01	P97384	SWISSPROT	ANNEXIN XI (CALCYCLIN-ASSOCIATED ANNEXIN 50) (CAP-50)
3696	16450	29089	1.47	1.1E-01	X52708.1	NT	G.gallus gene encoding non-histone chromosomal protein HMG-14b, exons 4 and 5
4090	16833	29456	1.28	1.1E-01	AW819412.1	EST_HUMAN	MR3-ST0290-290100-025-g07 ST0290 Homo sapiens cDNA
4090	16833	29457	1.26	1.1E-01	AW819412.1	EST_HUMAN	MR3-ST0290-290100-025-g07 ST0290 Homo sapiens cDNA
4226	16967		8.78	1.1E-01	AF157086.1	NT	Drosophila melanogaster klarsicht protein (klar) mRNA, complete cds
4254	16995	28624	0.77	1.1E-01	AW602056.1	EST_HUMAN	IL5-UM0070-020500-068-a08 UM0070 Homo sapiens cDNA
4594	17329	29956	0.96	1.1E-01	S44957.1	NT	Tape-1 integral membrane protein TAPA-1 [mice, B cell lymphoma line 38C13, Genomic, 1973 nt, segment 1 of 7]
4780	17512	30134	1.2	1.1E-01	Y07695.1	NT	A.immersus gene for transposase
4957	18339						Mus musculus major histocompatibility locus class II region:butyrophilin-like protein gene, partial cds; Notch4, PBX2, RAGE, lysophosphatidic acid acyl transferase-alpha, palmitoyl-protein thioesterase 2 (PPT2), CREB-RP, and tenascin X (TNX) genes, complete>
5077	17796	30412	0.85	1.1E-01	AF030001.1	NT	SYNAPTONEMAL COMPLEX PROTEIN 3 (SCP-3 PROTEIN)
5584	18381		1	1.1E-01	P70281	SWISSPROT	nx76a03.s1 NCI_CGAP_Ew1 Homo sapiens cDNA clone IMAGE:1288140 similar to contains Alu repetitive element; contains element MER35 repetitive element;
5584	18381		1.4	1.1E-01	AA747216.1	EST_HUMAN	6 Homo sapiens diacylglycerol kinase 3 (DAGK3) gene, exon 6
5653	18448	31361	1.23	1.1E-01	AF020927.1	NT	Betvylis chirensa strain T4 cDNA library under conditions of nitrogen deprivation
5687	18480	31399	0.58	1.1E-01	AL110985.1	NT	S.pombe ste8 gene encoding protein kinase
5745	18537	31459	1.81	1.1E-01	X68851.1	NT	Providencia rettgeri penicillin G amidase gene
5781	18572	31500	5.31	1.1E-01	M86533.1	NT	Homo sapiens LGMD2B gene
5936	18718	31676	1.67	1.1E-01	AJ007973.1	NT	PM3-FT0024-130600-004-F12 FT0024 Homo sapiens cDNA
5955	18737	31696	1.75	1.1E-01	BE769152.1	EST_HUMAN	RC3-CT0254-280989-011-e01 CT0254 Homo sapiens cDNA
5975	18757	31719	9.4	1.1E-01	AW853699.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C082
6330	19100	32088	0.87	1.1E-01	AL163282.2	NT	AF035748 Human salivary gland cell line HSG Homo sapiens cDNA clone RL43
6338	19108	32098	1.25	1.1E-01	AF035746.1	EST_HUMAN	qg76d06.x1 Soares, NFL T_GBC_S1 Homo sapiens cDNA clone IMAGE:1841099 3'
6381	19150	32149	0.72	1.1E-01	AI216307.1	EST_HUMAN	ACETYL-COENZYME A SYNTHETASE (ACETATE-COA LIGASE) (ACYL-ACTIVATING ENZYME)
6512	19277	32278	3.71	1.1E-01	O69835	SWISSPROT	Homo sapiens syntaxin 4 binding protein UNC-18c (UNC-18c) mRNA, complete cds
6604	19367		3.03	1.1E-01	AF032922.1	NT	

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6897	19814	32855	2.81	1.1E-01	11432372	NT	Homo sapiens phosphatidylinositol glycan, class B (PIGB), mRNA
6948	19430	32445	0.7	1.1E-01	AE002155.1	NT	Ureaplasma urealyticum section 56 of 59 of the complete genome
6948	19430	32446	0.7	1.1E-01	AE002155.1	NT	Ureaplasma urealyticum section 56 of 59 of the complete genome
7087	25423		0.89	1.1E-01	BF382758.1	EST_HUMAN	601816524F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4050653 5'
7203	25107	32964	0.84	1.1E-01	AP000006.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 1166001-1485000 nt. position (617)
7435	20112	33189	7.16	1.1E-01	BF684628.1	EST_HUMAN	602140976F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4302019 5'
7435	20112	33200	7.16	1.1E-01	BF684628.1	EST_HUMAN	602140976F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4302019 5'
7555	20225	33329	1.93	1.1E-01	P41087	SWISSPROT	TRAB PROTEIN
7666	20263	33371	3.35	1.1E-01	AA788784.1	EST_HUMAN	at31606.s1 Soares_perathryoid_tumor_NbHPA Homo sapiens cDNA clone 1240403 3' similar to gb:J03483
7668	20563	33690	0.5	1.1E-01	U67482.1	NT	CHROMOGHRANIN A PRECURSOR (HUMAN);
8107	20801	33933	1.7	1.1E-01	AA493574.1	EST_HUMAN	Methanococcus jannaschii section 34 of 150 of the complete genome
8107	20801	33934	1.7	1.1E-01	AA493574.1	EST_HUMAN	nt04910.s1 NCI_CGAP_Thy1 Homo sapiens cDNA clone IMAGE:943362
8153	20847	33979	1.15	1.1E-01	X91233.1	NT	nt04910.s1 NCI_CGAP_Thy1 Homo sapiens cDNA clone IMAGE:943362
8193	20887		1.14	1.1E-01	AW817918.1	EST_HUMAN	H. sapiens IL15 gene
8249	20943	34081	1.45	1.1E-01	AL134349.1	EST_HUMAN	PM1-ST0270-080200-001-r09 ST0270 Homo sapiens cDNA
8717	21409	34552	2.08	1.1E-01	U02482.1	NT	DKFZp547P194_r1 547 (synonym: hbr1) Homo sapiens cDNA clone DKFZp547P194 5'
8810	21502	34649	0.86	1.1E-01	A1807474.1	EST_HUMAN	Pedilococcus acidilactici H plasmid pSMB74 pediocin ACh production (pap) gene cluster papA, papB, papC and papD genes, complete cds
8906	21597	34739	0.47	1.1E-01	AF050081.1	NT	wf48c01.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2358816 3' similar to contains Alu repetitive element
8941	21632	34776	2.04	1.1E-01	AA192153.1	EST_HUMAN	Homo sapiens C16orf3 large protein mRNA, complete cds
8941	21632	34776	2.04	1.1E-01	AA192153.1	EST_HUMAN	zp93b12.r1 Stratagene muscle 937209 Homo sapiens cDNA clone IMAGE:627743 5'
9033	21723	34877	0.74	1.1E-01	Y12727.1	NT	zp93b12.r1 Stratagene muscle 937209 Homo sapiens cDNA clone IMAGE:627743 5'
9063	21762	34912	2.04	1.1E-01	T72675.1	EST_HUMAN	P. furiosus partial dph5 gene and argF gene
9090	21779		0.6	1.1E-01	BE693260.1	EST_HUMAN	y418h03.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:108725 3' similar to
9322	21989		0.88	1.1E-01	BE142305.1	EST_HUMAN	gb:U8181 SODIUMPOTASSIUM-TRANSPORTING ATPASE BETA-2 (HUMAN);
9396	22058		2	1.1E-01	BF085149.1	EST_HUMAN	601436972F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3922048 5'
9810	22461		0.5	1.1E-01	AL161543.2	NT	OM3-HT0142-271096-026-g11 HT0142 Homo sapiens cDNA
10017	22665		0.45	1.1E-01	BE315509.1	EST_HUMAN	MR2-GN0027-040900-005-a08 GN0027 Homo sapiens cDNA
10106	22754		1.57	1.1E-01	R80560.1	EST_HUMAN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 43
10235	22883	36096	1.26	1.1E-01	U60529.1	NT	601140231F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3049543 5'
10708	15786	28442	2.05	1.1E-01	F03265.1	EST_HUMAN	y98a09.s1 Soares placenta NB2HP Homo sapiens cDNA clone IMAGE:147064 3'
							Ceratitis capitata jojo retrotransposon gag-like, pol-like and env-like genes, complete cds
							HSC:IRF022 normalized infant brain cDNA Homo sapiens cDNA clone c-1r02 3'

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10840	23622		2.75	1.1E-01	AF169032.1	NT	Carassius auratus actin beta A precursor, mRNA, complete cds
10974	23650	36903	3.91	1.1E-01	R23708.1	EST_HUMAN	y135f12.1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:131759 5' similar to contains Alu repetitive element; contains TAR1 repetitive element;
10983	23658	36911	1.39	1.1E-01	6981351	NT	Rattus norvegicus Phosphofructokinase, liver, B-type (PFK), mRNA
11002	18480	31399	1.31	1.1E-01	AL110985.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
11134	23802	37079	1.58	1.1E-01	X70058.1	NT	M.musculus cytokine gene
11168	23836	37117	3.21	1.1E-01	Z11910.1	NT	Z.mobilis tqt and lig genes encoding tRNA guanine transglycosylase and DNA ligase
11169	23836	37118	3.21	1.1E-01	Z11910.1	NT	Z.mobilis tqt and lig genes encoding tRNA guanine transglycosylase and DNA ligase
11277	23938	37230	2.81	1.1E-01	P17437	SWISSPROT	SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN)
11674	24289		1.65	1.1E-01	AL161511.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 23
11990	24529		1.36	1.1E-01	AA192153.1	EST_HUMAN	zp93b12.1 Stratagene muscle 937209 Homo sapiens cDNA clone IMAGE:627743 5'
12098	24598		3.92	1.1E-01	BE767023.1	EST_HUMAN	RC2-NT0112-120600-014-003 NT0112 Homo sapiens cDNA
12341	25160		1.97	1.1E-01	BE974556.1	EST_HUMAN	601680551R2 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3950604 3'
12750	25012	30977	3.15	1.1E-01	BF239753.1	EST_HUMAN	601906350F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4134086 5'
1179	13932		2.74	1.0E-01	O62855	SWISSPROT	DEOXYRIBONUCLEASE II PRECURSOR (DNASE II) (ACID DNASE) (LYSOSOMAL DNASE II)
1249	13998	26665	2.63	1.0E-01	A1985499.1	EST_HUMAN	ws08d01.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2496577 3' similar to contains MER7.13
1371	14119	26794	1.95	1.0E-01	AL161504.2	NT	MER7 repetitive element;
2493	15210	27952	1.11	1.0E-01	AW451365.1	EST_HUMAN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 16
3503	16259	28913	1.19	1.0E-01	BF033991.1	EST_HUMAN	U1-H-B13-alc-d-07-Q-UJ.st NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2736420 3'
3708	16461	29100	1.03	1.0E-01	BF239818.1	EST_HUMAN	601466301F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3859849 5'
3817	16569	29200	0.96	1.0E-01	AF297061.1	NT	601906489F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4134071 5'
3817	16569	29201	0.96	1.0E-01	AF297061.1	NT	Escherichia coli enterotoxin EspC (espC) gene, complete cds; and unknown genes
3935	16685	29328	2.53	1.0E-01	BF365703.1	EST_HUMAN	Escherichia coli enterotoxin EspC (espC) gene, complete cds; and unknown genes
4518	17253		0.95	1.0E-01	AF792349.1	EST_HUMAN	QV2-NT0048-160800-316-e05 NT0048 Homo sapiens cDNA
4664	17398	30032	1.19	1.0E-01	U50450.1	NT	an32c04.y6 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:1700358 5'
4966	17594	30217	2.95	1.0E-01	AW952344.1	EST_HUMAN	Drosophila melanogaster tyrosine kinase p45 isoform (fer) mRNA, complete cds
5238	18044		9.73	1.0E-01	W86490.1	EST_HUMAN	EST384414 IMAGE resequences, MAGB Homo sapiens cDNA
5789	18580		1.21	1.0E-01	AK024472.1	NT	zh62H04.s1 Soares fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:416695 3'
5934	18717	31675	14.15	1.0E-01	AF274875.1	NT	Homo sapiens mRNA for FLJ00065 protein, partial cds
6243	19017	31991	0.99	1.0E-01	AA481879.1	EST_HUMAN	Homo sapiens growth factor receptor-bound protein 7 (GRB7) gene, complete cds
6256	19030	32005	0.7	1.0E-01	AA406039.1	EST_HUMAN	z41g10.s1 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:756258 3' similar to contains L1.13 L1 repetitive element;
						EST_HUMAN	z167c12.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:743062 3'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6924	19660		1.81	1.0E-01	R23821.1	EST_HUMAN	y134h06.1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:131675 5' similar to contains Alu repetitive element;
7635	20300		2.67	1.0E-01	Y12488.1	NT	M. musculus wtn gene
7709	20373	33486	0.65	1.0E-01	AJ011400.1	NT	Bos taurus mRNA for b17.2 subunit of NADH:ubiquinone oxidoreductase complex (complex I)
7709	20373	33487	0.65	1.0E-01	AJ011400.1	NT	Bos taurus mRNA for b17.2 subunit of NADH:ubiquinone oxidoreductase complex (complex I)
7834	20529	33656	0.65	1.0E-01	AA861091.1	EST_HUMAN	ak32g01 s1 Soares testis NHT Homo sapiens cDNA clone IMAGE:1407696 3' similar to gb:M34182 CAMP-DEPENDENT PROTEIN KINASE, GAMMA-CATALYTIC SUBUNIT (HUMAN);
8066	20760		0.5	1.0E-01	4758365	NT	Homo sapiens fibroblast growth factor 13 (FGF13) mRNA
8390	21083		0.96	1.0E-01	AW189797.1	EST_HUMAN	X108h01.x1 NCL CGAP_U14 Homo sapiens cDNA clone IMAGE:2675689 3' similar to gb:X17206 40S RIBOSOMAL PROTEIN S4 (HUMAN); contains TAR1 t3 TAR1 repetitive element ;
9084	21773	34937	1.04	1.0E-01	AF102856.2	NT	Rattus norvegicus synaptic SAPAP-interacting protein Synapton mRNa, complete cds
9395	22057	35228	0.51	1.0E-01	R44993.1	EST_HUMAN	y333h04.s1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:34549 3'
9407	22069		1.6	1.0E-01	M76729.1	NT	Human pro-alpha-1 (V) collagen mRNA, complete cds
9450	22000		3.02	1.0E-01	AE001501.1	NT	Helicobacter pylori, strain J99 section 62 of 132 of the complete genome
9464	22074	35245	0.76	1.0E-01	W01955.1	EST_HUMAN	z666c10.s1 Soares fetal heart NbrH19W Homo sapiens cDNA clone IMAGE:327282 3'
9721	22372	35571	1.67	1.0E-01	BF240154.1	EST_HUMAN	601095661F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4133487 5'
9835	22486	35687	8.12	1.0E-01	AB046799.1	NT	Homo sapiens mRNA for KIAA1579 protein, partial cds
9835	22486	35688	8.12	1.0E-01	AB046799.1	NT	Homo sapiens mRNA for KIAA1579 protein, partial cds
10043	22691		0.97	1.0E-01	AW957425.1	EST_HUMAN	EST369615 MAGE resequences, MAGE Homo sapiens cDNA
10048	22696	35912					y529a06.s1 Stratagene fetal spleen (#837205) Homo sapiens cDNA clone IMAGE:72562 3' similar to contains Alu repetitive element
10229	22877	36089	0.51	1.0E-01	T51952.1	EST_HUMAN	601584604F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3839096 5'
10554	23250		0.89	1.0E-01	BE782750.1	EST_HUMAN	AU159127 THYRO1 Homo sapiens cDNA clone THYRO1000895 3'
10554	23250		1.85	1.0E-01	AU159127.1	EST_HUMAN	601877703F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4106089 5'
10958	23634	36884	2.35	1.0E-01	BF242946.1	EST_HUMAN	601877703F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4106089 5'
10958	23634	36885	2.35	1.0E-01	BF242946.1	EST_HUMAN	601877703F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4106089 5'
11376	23883	37283	5.22	1.0E-01	BE790543.1	EST_HUMAN	601582558F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3836734 5'
11510	24110		1.52	1.0E-01	AP000400.1	NT	Escherichia coli O157:H7 genomic DNA, prophage (Sakai-VT1) inserted region, substrain: RIMD 0609952
11594	24193	37511	1.46	1.0E-01	Z71446.1	NT	A. thaliana mRNA for GLC-b chloride channel protein
11594	24193	37512	1.46	1.0E-01	Z71446.1	NT	A. thaliana mRNA for GLC-b chloride channel protein
11832	24416	37755	1.89	1.0E-01	AV649035.1	EST_HUMAN	AV649035 GLC Homo sapiens cDNA clone GLCBPG01 3'
11832	24416	37756	1.89	1.0E-01	AV649035.1	EST_HUMAN	AV649035 GLC Homo sapiens cDNA clone GLCBPG01 3'
12083	24921		4.32	1.0E-01	BE537719.1	EST_HUMAN	601065554F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3451933 5'
12300	24725		1.71	1.0E-01	7662165	NT	Homo sapiens KIAA0514 gene product (KIAA0514), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12317	24738		2.22	1.0E-01	X00854.1	NT	Drosophila melanogaster tiz gene
12614	24921		2.74	1.0E-01	BE537719.1	EST_HUMAN	601065554F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3451933 5'
12677	25318		5.03	1.0E-01	U66834.1	NT	Saccharomyces cerevisiae suppressor of ABF1 (SAB2) gene, complete cds
12733	25002		9.8	1.0E-01	AF001507.1	NT	Bacillus halodurans genomic DNA, section 1/14
2781	15488	28224	1.27	9.9E-02	AF274008.1	NT	Drosophila melanogaster cAMP-dependent protein kinase type II regulatory subunit (pka-R11) mRNA, complete cds
2790	15495	28235	1.53	9.9E-02	BE545554.1	EST_HUMAN	601070219F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3456365 5'
2790	15495	28236	1.53	9.9E-02	BE545554.1	EST_HUMAN	601070219F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3456365 5'
3260	16022	28971	1.32	9.9E-02	AF098810.1	NT	Homo sapiens neuraxin III-alpha gene, partial cds
3933	16883	29324	0.75	9.9E-02	AI921837.1	EST_HUMAN	zu45c03.x5 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:740932 3'
4632	17367	30003	0.83	9.9E-02	BE674249.1	EST_HUMAN	7u77c12.x1 NCI CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3278998 3'
6875	17951	30547	9.17	9.9E-02	D83710.1	NT	Aspergillus terreus BSD mRNA for blasticidin S deaminase, complete cds
7815	20510	33634	0.93	9.9E-02	AW103088.1	EST_HUMAN	xd43c09.x1 NCI CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2596528 3' similar to contains Alu repetitive element; contains element MIR MIR repetitive element ;
7815	20510	33635	0.93	9.9E-02	AW103088.1	EST_HUMAN	xd43c09.x1 NCI CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2596528 3' similar to contains Alu repetitive element; contains element MIR MIR repetitive element ;
9156	21887	35055	0.98	9.9E-02	6755111	NT	Mus musculus phospholipid transfer protein (Pltp), mRNA
550	13333		1.43	9.8E-02	X56338.1	NT	O. sativa RAmY3C gene for alpha-amylase
3100	15865		0.9	9.8E-02	4504578	NT	(Homo sapiens I factor (complement) (IF) mRNA
3142	15906	28550	3.64	9.8E-02	AF184274.1	NT	Daucus carota leucoanthocyanidin dioxygenase 2 (LDOX) mRNA, LDOX-2 allele, complete cds
4198	19339	29564	6.24	9.8E-02	AF257329.1	NT	Leptosphaeria maculans beta-tubulin mRNA, complete cds
4198	19339	29565	6.24	9.8E-02	AF257329.1	NT	Leptosphaeria maculans beta-tubulin mRNA, complete cds
7381	20061		0.77	9.8E-02	X54133.1	NT	Human HP TP delta mRNA for protein tyrosine phosphatase delta
9153	21884		1.18	9.8E-02	M61943.1	NT	Human laminin B1 chain gene, exon 26
11437	23204	36436	2.05	9.8E-02	BF037421.1	EST_HUMAN	601460793F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3864287 5'
12052	24570		1.78	9.8E-02	8393751	NT	Rattus norvegicus microtubule-associated protein tau (Mapt), mRNA
1328	14077	26752	1.31	9.7E-02	AB005808.1	NT	Aloe arborescens mRNA for NADP-malic enzyme, complete cds
1580	14326		1.49	9.7E-02	4503710	NT	Homo sapiens fibroblast growth factor receptor 3 (achondroplasia, thanatophoric dwarfism) (FGFR3) mRNA
2257	14984	27724	2.08	9.7E-02	BE168660.1	EST_HUMAN	QV1-HT0516-070300-095-a04 HT0516 Homo sapiens cDNA
3965	16714		3.48	9.7E-02	Q98795	SWISSPROT	CELL SURFACE A33 ANTIGEN PRECURSOR (GLYCOPROTEIN A33)
5261	18067	30695	0.94	9.7E-02	AF069189.1	NT	Caulobacter crescentus thymidylate kinase (tnk) and DNA polymerase III delta prime subunit (dnaC) genes, complete cds

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5281	18067	30696	0.84	9.7E-02	AF099189.1	NT	Caulobacter crescentius thymidylate kinase (tnk) and DNA polymerase III delta prime subunit (dnaC) genes, complete cds
5924	18708	31682	1.43	9.7E-02	AW954476.1	EST_HUMAN	EST366546 IMAGE resequences, MAGC Homo sapiens cDNA
7198	19894	32958	3.24	9.7E-02	Z99119.1	NT	Bacillus subtilis complete genome (section 16 of 21), from 2897771 to 3213410
7882	20577	33705	1.28	9.7E-02	N22798.1	EST_HUMAN	yw41c03.s1 Weizmann Olfactory Epithelium Homo sapiens cDNA clone IMAGE:254788 3'
7882	20577	33706	1.28	9.7E-02	N22798.1	EST_HUMAN	yw41c03.s1 Weizmann Olfactory Epithelium Homo sapiens cDNA clone IMAGE:254788 3'
8748	21440	34587	1.49	9.7E-02	AI953984.1	EST_HUMAN	wx78506.x1 NCJ_CGAP_Ov38 Homo sapiens cDNA clone IMAGE:254788 3'
11152	23819		2.84	9.7E-02	U58337.1	NT	PEPTIDYL-PROLYL CIS-TRANS ISOMERASE A (HUMAN);
2009	14744	27470	1.11	9.6E-02	AI080721.1	EST_HUMAN	Mus musculus ligatin (Lgtin) mRNA, partial cds
2009	14744	27471	1.11	9.6E-02	AI080721.1	EST_HUMAN	oz47a11.x1 Soares_NhlMPu_S1 Homo sapiens cDNA clone IMAGE:1678485 3'
4311	17050	29675	5.8	9.6E-02	Z32886.2	NT	oz47a11.x1 Soares_NhlMPu_S1 Homo sapiens cDNA clone IMAGE:1678485 3'
4940	17668	30276	0.89	9.6E-02	AW966230.1	EST_HUMAN	Proteus mirabilis fibrinolytic operon, strain H4320
6014	18795		3.13	9.6E-02	BE910039.1	EST_HUMAN	EST1378303 IMAGE resequences, MAGI Homo sapiens cDNA
8274	20968		0.6	9.6E-02	AI137084.1	EST_HUMAN	601498088F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3900165 5'
9444	22121	35300	1.31	9.6E-02	AV687898.1	EST_HUMAN	AU137084 PLACE1 Homo sapiens cDNA clone IMAGE:1005740 5'
9772	22423		1.12	9.6E-02	BE894895.1	EST_HUMAN	AV687898 GKC Homo sapiens cDNA clone GKCAAH02 5'
9839	22687	35790	1.29	9.6E-02	AJ243211.1	NT	Homo sapiens DMBT1 candidate tumour suppressor gene, exons 1 to 55
9839	22687	35791	1.29	9.6E-02	AJ243211.1	NT	Homo sapiens DMBT1 candidate tumour suppressor gene, exons 1 to 55
10020	22668	35884	0.5	9.6E-02	BF072720.1	EST_HUMAN	602086769F1 NIH_MGC_B3 Homo sapiens cDNA clone IMAGE:4250969 5'
10051	22699	35915	1.54	9.6E-02	AB013985.1	NT	Antirrhinum majus transposon Tam3 pseudogene for transposase (in S-5 copy)
10051	22699	35916	1.54	9.6E-02	AB013985.1	NT	Antirrhinum majus transposon Tam3 pseudogene for transposase (in S-5 copy)
10158	22806	36024	3.35	9.6E-02	P08174	SWISSPROT	COMPLEMENT DECAY-ACCELERATING FACTOR PRECURSOR (CD55)
10643	23334	36572	7.22	9.6E-02	Z79702.1	NT	Mycobacterium tuberculosis H37Rv complete genome, segment 102/162
12652	24954		3.34	9.6E-02	H14599.1	EST_HUMAN	ym19h03.s1 Soares Infant brain 1NIB Homo sapiens cDNA clone IMAGE:48653 3'
4081	18825	29452	2.1	9.5E-02	AW992395.1	EST_HUMAN	CM2-BN0023-050200-087-f12 BN0023 Homo sapiens cDNA
5579	18376	31289	0.85	9.5E-02	P51854	SWISSPROT	TRANSKETOLASE 2 (TK 2) (TRANSKETOLASE RELATED PROTEIN)
6988	19881	32729	0.55	9.5E-02	AA780728.1	EST_HUMAN	TRANSKETOLASE 2 (TK 2) (TRANSKETOLASE RELATED PROTEIN)
7202	19888	32963	4.72	9.5E-02	AB003473.1	NT	ac88a09.s1 Stralagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:867736 3'
7467	20141	33234	7.68	9.5E-02	AL161538.2	NT	Trimeresurus flavoviridis DNA for phospholipase A2 inhibitor, complete cds
7597	18376	31289	0.84	9.5E-02	P51854	SWISSPROT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 38
7780	20475	33600	1.83	9.5E-02	BF035861.1	EST_HUMAN	TRANSKETOLASE 2 (TK 2) (TRANSKETOLASE RELATED PROTEIN)
7780	20475	33601	1.83	9.5E-02	BF035861.1	EST_HUMAN	601453642F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3857243 5'
10578	23273	36509	2.36	9.5E-02	BF035861.1	EST_HUMAN	601453642F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3857243 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10578	23273	36610	2.36	9.5E-02	BF035861.1	EST_HUMAN	601453642F1 NIH_MGC_86 Homo sapiens cDNA clone IMAGE:3857243 5'
1826	14584	27275	2.82	9.4E-02	BF671063.1	EST_HUMAN	602150882F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4281917 5'
1857	14595	27310	0.89	9.4E-02	U55944.1	NT	Cavia porcellus 3beta-hydroxysteroid sulfotransferase mRNA, complete cds
1857	14595	27311	0.89	9.4E-02	U55944.1	NT	Cavia porcellus 3beta-hydroxysteroid sulfotransferase mRNA, complete cds
3860	16810	28249	4.43	9.4E-02	Z33039.1	NT	M. capricollum DNA for CONTIG MC073
6225	18998	31976	0.63	9.4E-02	AF097363.1	NT	Triticum aestivum heat shock protein 101 (Hsp101a) mRNA, complete cds
8498	21180						
10851	20168	33258	2.46	9.4E-02	Z46863.1	NT	Acinetobacter sp. cysD, cobQ, sodM, lysS, rubA, rubB, eslB, oxyR, ppk, mfgA, ORF2 and ORF3 genes
11941	25255		2.44	9.4E-02	L78833.1	NT	Human BRCA1, Rho7 and vail genes, complete cds, and lpr35 gene, partial cds
12871	24965		1.78	9.4E-02	U31815.1	NT	Rattus norvegicus calcium channel alpha-1C subunit (ROB2) mRNA, partial cds
2888	15754		1.92	9.4E-02	AF198036.1	NT	Mycoplasma pulmonis hypothetical membrane protein P93 gene, complete cds
3026	15792		1.97	9.3E-02	4809280	NT	Homo sapiens BAI1-associated protein 3 (BAIAP3) mRNA
3251	16013	28685	6.32	9.3E-02	6912525	NT	Homo sapiens nasopharyngeal epithelium specific protein 1 (NESG1), mRNA
4132	16874	29502	1.85	9.3E-02	BF575511.1	EST_HUMAN	602133036F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4288269 5'
4132	16874	29503	3.51	9.3E-02	BE391943.1	EST_HUMAN	601286082F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3607653 5'
4885	17419		3.51	9.3E-02	BE391943.1	EST_HUMAN	601286082F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3607653 5'
5578	18373		2.04	9.3E-02	AV732224.1	EST_HUMAN	AV732224 HTF Homo sapiens cDNA clone HTFAUA06 5'
8148	20840	33972	0.67	9.3E-02	AF001507.1	NT	Bacillus halodurans genomic DNA, section 1/14
9810	22263	35449	0.82	9.3E-02	AW568007.1	EST_HUMAN	EST69 Human Fetal Brain MATCHMAKER cDNA Library Homo sapiens cDNA
10091	22739	35953	2.15	9.3E-02	BE962631.2	EST_HUMAN	601855988R1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3855981 3'
10091	22739	35954	3.67	9.3E-02	Q15034	SWISSPROT	HYPOTHETICAL PROTEIN KIAA0032
10218	22868		3.67	9.3E-02	Q15034	SWISSPROT	HYPOTHETICAL PROTEIN KIAA0032
12194	25181		3.5	9.3E-02	AW206117.1	EST_HUMAN	U1-H-B11-afk-h-05-0-U1.s1 NCL_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2723553 3'
12550	25209		2.51	9.3E-02	AJ249850.1	NT	Photobacterium damsela subsp. damsela partial gyrB gene for DNA gyrase B subunit
			8.43	9.3E-02	AW468850.1	EST_HUMAN	h228112.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2910887 3'
							Mus musculus major histocompatibility locus class II region; Fas-binding protein Daxx (DAXX) gene, partial cds, BING1 (BING1), tapasin (tapasin), RalGDS-like factor (RLF), KE2 (KE2), BING4 (BING4), beta1, 3-galactosyl transferase (beta1,3-galactosyl tr?)
12752	25254		2.1	9.3E-02	AF100956.1	NT	Molluscum contagiosum virus subtype 1, complete genome
222	13034	25668	8.37	9.2E-02	U60315.1	NT	Molluscum contagiosum virus subtype 1, complete genome
222	13034	25669	8.37	9.2E-02	U60315.1	NT	Molluscum contagiosum virus subtype 1, complete genome
222	13034	25670	8.37	9.2E-02	U60315.1	NT	Molluscum contagiosum virus subtype 1, complete genome
2224	14952		1.68	9.2E-02	R54156.1	EST_HUMAN	y99607.t1 Scores infant brain 1NIB Homo sapiens cDNA clone IMAGE:41618 5'
3175	15938	28587	3.28	9.2E-02	Q28631	SWISSPROT	MAJOR EPIDIDYMIS-SPECIFIC PROTEIN E4 (EPIDIDYMAL PROTEIN BE-20)
3289	16061	28709	0.85	9.2E-02	AA534354.1	EST_HUMAN	nt79e01.s1 NCL_CGAP_C63 Homo sapiens cDNA clone IMAGE:926136 3'

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3573	16328		1.28	9.2E-02	8756215	NT	Mus musculus pre T-cell antigen receptor alpha (Ptra), mRNA
4213	16954		0.99	9.2E-02	U92048.1	NT	Human herpesvirus 1 strain KOS-63, latency-associated transcript, promoter region
4274	17013		0.76	9.2E-02	BE29722.1	EST_HUMAN	600944365F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2860176 5'
7907	20602	33732	1.98	9.2E-02	T49920.1	EST_HUMAN	ya86c09.11 Stratagene placenta (#337225) Homo sapiens cDNA clone IMAGE:69808 5' similar to similar to gb:X56009 GUANINE NUCLEOTIDE-BINDING PROTEIN G(S), ALPHA SUBUNIT (HUMAN)
8076	20770	33899	2.2	9.2E-02	X95256.1	NT	H. vulgare xylose isomerase gene
11695	24290	37614	1.27	9.2E-02	AF026552.3	NT	Mesocricetus auratus oviductin precursor (OVI) gene, complete cds
12736	25412		1.4	9.2E-02	11466872	NT	Podospora anserina mitochondrion, complete genome
414	12825	25439	4.19	9.1E-02	X77695.1	NT	O. cuniculus K12 keratin gene
4451	17187	29812	1.33	9.1E-02	AL161554.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 54
5643	18438	31352	1.44	9.1E-02	AF129756.1	NT	Homo sapiens MSH55 gene, partial cds; and C11C1, DDAH, G6b, G6c, G5b, G6d, G6e, G6f, BAT5, G5b, CSK2B, BAT4, G4, Apo M, BAT3, BAT2, AIF-1, TC7, LST-1, LTB, TNF, and LTA genes, complete cds
7285	19968	33045	14.94	9.1E-02	AW150658.1	EST_HUMAN	au74405.1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2781968 5'
7575	20244	33349	0.79	9.1E-02	AP000061.1	NT	Aeropyrum pernix genomic DNA, section 47
7609	20275	33383	0.72	9.1E-02	U39073.1	NT	Mus musculus thymopoietin zeta mRNA, complete cds
8822	21514	34659	0.88	9.1E-02	Y14379.1	NT	Homo sapiens gamma adducin gene, exon 9
10327	22874		1.37	9.1E-02	T02964.1	EST_HUMAN	FB19F10 Fetal brain. Stratagene Homo sapiens cDNA clone FB19F10 3'end
10354	23001	36218	1.25	9.1E-02	S74059.1	NT	Tg816=Cyl actin [Tripneustes gratilis sea urchins, embryos, Genomic, 5275 nt]
10383	23029	36244	1.19	9.1E-02	Y11187.1	NT	A. thaliana RH1, TC1, G14587-5, G14587-6, and PRL1 genes
12110	25348		1.4	9.1E-02	AA179901.1	EST_HUMAN	zp38h12 s1 Stratagene muscle 937209 Homo sapiens cDNA clone IMAGE:611783 3' similar to SW:TRT3_HUMAN P45378 TROPONIN T, FAST SKELETAL MUSCLE, ISOFORM BETA ;
12181	24653		2.12	9.1E-02	AF052695.1	NT	Rattus norvegicus cell cycle protein p55CDC gene, complete cds
12637	25204		1.93	9.1E-02	AJ291390.1	NT	Homo sapiens partial MUC3B gene for MUC3B much, exons 1-11
727	13501	26155	4.3	9.0E-02	P15328	SWISSPROT	FOLATE RECEPTOR ALPHA PRECURSOR (FR-ALPHA) (FOLATE RECEPTOR 1) (FOLATE RECEPTOR, ADULT) (ADULT FOLATE-BINDING PROTEIN) (FBP) (OVARIAN TUMOR-ASSOCIATED ANTIGEN MOV18) (KB CELLS FBP)
1631	14377	27064	5.28	9.0E-02	BE220482.1	EST_HUMAN	h339g10.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3175842 3' similar to contains Alu repetitive element
2806	15511	28252	6.45	9.0E-02	AF138522.1	NT	HIV-1 p8c095-06 from USA envelope glycoprotein (env) gene, partial cds
2806	15511	28253	6.45	9.0E-02	AF138522.1	NT	HIV-1 p8c095-06 from USA envelope glycoprotein (env) gene, partial cds
3331	16091	28744	0.84	9.0E-02	AF279135.1	NT	Dichytellium discoideum spore coat structural protein SP65 (cotE) gene, complete cds
4619	17354	29889	3.27	9.0E-02	X65740.2	NT	Plasmodium falciparum P-type ATPase 3 gene

Table 4
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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5906	18691	31640	5.21	9.0E-02	W56037.1	EST_HUMAN	z668a12.r1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:297694 5' similar to PIR:S52171 S52171 small G protein - human ;
6619	19381		1.14	9.0E-02	BF062651.1	EST_HUMAN	7h63d03.x1 NCI_CGAP_Co16 Homo sapiens cDNA clone IMAGE:3320645 3' similar to contains Alu repetitive element
6668	19585	32619	0.72	9.0E-02	R62805.1	EST_HUMAN	y11b08.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:136903 3'
12486	24845		2.01	9.0E-02	AF022236.1	NT	Escherichia coli strain E2348/69 pathogenicity island, rOrf1 (rOrf1), rOrf2 (rOrf2), EscR (escR), EscS (escS), EscT (escT), EscU (escU), CesD (cesD), EscC (escC), EscJ (escJ), SepZ (sepZ), EscV (escV), EscN (escN), SepQ (sepQ), Tir (tir), OrfU (orfU), >
1418	14166	26849	1.99	8.9E-02	BF701593.1	EST_HUMAN	602129030F2 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4285851 5'
1418	14166	26850	1.99	8.9E-02	BF701593.1	EST_HUMAN	602129030F2 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4285851 5'
2386	15107	27846	1.22	8.9E-02	BE153572.1	EST_HUMAN	PV0-H70339-251199-003-001 HT0339 Homo sapiens cDNA
4175	16915		1.93	8.9E-02	AF286055.1	NT	Atrichum angustatum AtranFla2 protein (AtranFla2) gene, partial cds
5760	18552	31474	3.22	8.9E-02	AW452122.1	EST_HUMAN	UI-H-B13-ab-f08-0-U1.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:3068284 3'
5760	18552	31475	3.22	8.9E-02	AW452122.1	EST_HUMAN	UI-H-B13-ab-f08-0-U1.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:3068284 3'
5776	18567	31496	3.39	8.9E-02	11433478	NT	Homo sapiens similar to endoglycan (H_sapiens) (LOC63107), mRNA
7093	19782	32848	1.64	8.9E-02	P47259	SWISSPROT	FOLD BIFUNCTIONAL PROTEIN [INCLUDES: METHYLENETETRAHYDROFOLATE DEHYDROGENASE; METHENYL TETRAHYDROFOLATE CYCLOHYDROLASE]
7458	20132		2.06	8.9E-02	Z79021.1	NT	H_sapiens flow-sorted chromosome 6 HindIII fragment, SC6pA20F8
7949	20644	33768	1.08	8.9E-02	P29475	SWISSPROT	NITRIC-OXIDE SYNTHASE, BRAIN (NOS, TYPE I) (NEURONAL NOS) (N-NOS) (NNOS) (CONSTITUTIVE NOS) (NC-NOS) (BNOS)
8030	20725	33858	0.72	8.9E-02	BF701665.1	EST_HUMAN	602129111F2 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4285827 5'
8030	20725	33859	0.72	8.9E-02	BF701665.1	EST_HUMAN	602129111F2 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4285827 5'
8496	21188	34331	4.72	8.9E-02	AA308319.1	EST_HUMAN	EST180187 Liver, hepatocellular carcinoma Homo sapiens cDNA 5' end
9520	22173	35356	0.8	8.9E-02	A1285627.1	EST_HUMAN	qu55c05.x1 NCI_CGAP_Lym6 Homo sapiens cDNA clone IMAGE:1968680 3' similar to contains MER10.b1 MER10 repetitive element
9520	22173	35357	0.8	8.9E-02	A1285627.1	EST_HUMAN	qu55c05.x1 NCI_CGAP_Lym6 Homo sapiens cDNA clone IMAGE:1968680 3' similar to contains MER10.b1 MER10 repetitive element
9632	22284	35477	0.76	8.9E-02	AA339356.1	EST_HUMAN	EST44454 Fetal brain I Homo sapiens cDNA 5' end
11882	25173		1.49	8.9E-02	P30143	SWISSPROT	HYPOTHETICAL 51.7 KD PROTEIN IN THRC-TALB INTERGENIC REGION (ORF8)
11940	25207		1.48	8.9E-02	P19524	SWISSPROT	MYOSIN-2 ISOFORM
12085	24591		3.05	8.9E-02	BF696918.1	EST_HUMAN	602129682F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4286180 5'
12284	24716		1.61	8.9E-02	U29895.1	NT	Human 4-hydroxyphenylpyruvate-dioxygenase gene, complete cds
1352	14100	26775	1.59	8.9E-02	Q27474	SWISSPROT	PROBABLE DNA LIGASE (POLYDEOXYRIBONUCLEOTIDE SYNTHASE [ATP])
3883	16633	29272	1.03	8.8E-02	AA299128.1	EST_HUMAN	EST11595 Uterus Homo sapiens cDNA 5' end

Table 4

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4014	16760		3.55	8.8E-02	O00288	SWISSPROT	TRANSCRIPTION INITIATION FACTOR TFIIID 135 KDA SUBUNIT (TAFII-135) (TAFII-130) (TAFII130)
4214	16955		0.99	8.8E-02	4502804	NT	Homo sapiens chromogranin A (parathyroid secretory protein 1) (CHGA) mRNA
4269	17009		1.27	8.8E-02	4580423	NT	Homo sapiens paired box gene 8 (eniridia, keratitis) (PAX8), isoform b, mRNA
7444	20120		0.57	8.8E-02	D17520.1	NT	Sheep mRNA for angiotensinogen, complete cds
8886	21577	34719	1.07	8.8E-02	AA151872.1	EST_HUMAN	zn98a05.s1 Stragelene colon (#937204) Homo sapiens cDNA clone IMAGE:566288 3'
11062	23732	37003	2.7	8.8E-02	BE264455.1	EST_HUMAN	601191770F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3535648 5'
11062	23732	37004	2.7	8.8E-02	BE264455.1	EST_HUMAN	601191770F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3535648 5'
11228	23891	37178	6.92	8.8E-02	AL040128.1	EST_HUMAN	DKFZp434D1313_71 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434D1313 5'
11805	24395	37729	1.49	8.8E-02	P67803	SWISSPROT	CYTOKINE INDUCIBLE SH2-CONTAINING PROTEIN 3 (PROTEIN EF-10)
12155	24641	31098	2.66	8.8E-02	Z71561.1	NT	S.cerevisiae chromosome XIV, reading frame ORF YNL285w
1842	14388	27077	1.15	8.7E-02	AI167281.1	EST_HUMAN	ox65b01.s1 Soares_NthMPu_S1 Homo sapiens cDNA clone IMAGE:1861181 3'
3681	16434	29077	3.66	8.7E-02	U82895.2	NT	Homo sapiens zinc finger protein 92 (ZFP92), expressed-Xq28STS protein (XQ28ORF), and biglycan (BGN) genes, complete cds; and plasma membrane calcium ATPase isoform 3 (PMCA3) gene, partial cds
3681	16434	29078	3.66	8.7E-02	U82895.2	NT	Homo sapiens zinc finger protein 92 (ZFP92), expressed-Xq28STS protein (XQ28ORF), and biglycan (BGN) genes, complete cds; and plasma membrane calcium ATPase isoform 3 (PMCA3) gene, partial cds
4658	17392	30027	1.19	8.7E-02	AF178636.1	NT	Mus musculus JNK interacting protein-3a (Jip3) mRNA, complete cds
5231	18037	30863	5.88	8.7E-02	AA286875.1	EST_HUMAN	zs55g08.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:701438 3'
5231	18037	30864	5.88	8.7E-02	AA286875.1	EST_HUMAN	zs55g08.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:701438 3'
6745	19578	32612	0.77	8.7E-02	AJ271885.2	NT	Mus musculus partial Kcnq1 gene for potassium channel protein, exons 10-14
6745	19578	32613	0.77	8.7E-02	AJ271885.2	NT	Mus musculus partial Kcnq1 gene for potassium channel protein, exons 10-14
6943	19425	32440	0.71	8.7E-02	AF281342.1	NT	Oncorhynchus mykiss TAT-binding protein 1 mRNA, partial cds
7761	20457		0.45	8.7E-02	AA284632.1	EST_HUMAN	z120603.s1 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:713692 3'
8413	21106	34245	0.9	8.7E-02	AE004787.1	NT	Pseudomonas aeruginosa PAO1, section 348 of 529 of the complete genome
8413	21106	34246	0.9	8.7E-02	AE004787.1	NT	Pseudomonas aeruginosa PAO1, section 348 of 529 of the complete genome
10610	23304		2.46	8.7E-02	L04758.1	NT	Oryctolagus cuniculus cytochrome P-450 (CYP4A4) gene, 5' end
11282	23843	37237	2.55	8.7E-02	AJ007763.1	NT	Gluconobacter oxydans tRNA-Ile and tRNA-Ala genes
12145	24633		2.1	8.7E-02	X17116.1	NT	Human DNA for immunoglobulin alpha heavy chain from a case of alpha heavy chain disease
12340	24750		1.75	8.7E-02	6679057	NT	Mus musculus nidogen 2 (Nid2), mRNA
1230	13979	26649	7.02	8.6E-02	AJ271736.1	NT	Homo sapiens Xq pseudautosomal region; segment 2/2
2240	14868	27708	1.82	8.6E-02	BE408667.1	EST_HUMAN	601304016F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3638643 5'
3183	15946	28596	4.57	8.6E-02	L05488.1	NT	Trichomonas vaginalis beta-tubulin (btub1) gene, complete cds

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3635	18388		3.77	8.6E-02	AF153362.1	NT	Dictyostelium discoidium adenyl cyclase (acrA) gene, complete cds
5134	17852		0.86	8.6E-02	BF570296.1	EST_HUMAN	602185716T1 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:4310259 3'
6003	18784	31746	4.75	8.6E-02	Y10826.1	NT	Homo sapiens LCN1b gene
6281	19054	32033	1.56	8.6E-02	J00440.1	NT	Mouse germline IgM chain gene, D region; D-q82, mu switch region (part e)
6281	19054	32034	1.56	8.6E-02	J00440.1	NT	Mouse germline IgM chain gene, D region; D-q82, mu switch region (part a)
7481	20153	33248	1.34	8.6E-02	P14616	SWISSPROT	INSULIN RECEPTOR-RELATED PROTEIN PRECURSOR (IRR) (IR-RELATED RECEPTOR)
7831	20526	33651	1.25	8.6E-02	5730066	NT	Homo sapiens Snf2-related CBP activator protein (SRCAP) mRNA
7831	20526	33652	1.25	8.6E-02	5730066	NT	Homo sapiens Snf2-related CBP activator protein (SRCAP) mRNA
7969	20664	33788	0.62	8.6E-02	11427428	NT	Homo sapiens hypothetical protein FLJ11006 (FLJ11006), mRNA
8031	20726		0.81	8.6E-02	U60168.1	NT	Dictyostelium discoidium proteasome subunit C2 homolog PrtC (prtC) gene, complete cds
9637	22289	35482	1.76	8.6E-02	AF111170.3	NT	Homo sapiens 14q32 Jagged2 gene, complete cds; and unknown gene
9673	22326		0.58	8.6E-02	AW662153.1	EST_HUMAN	h20c08.x1 NCL CGAP_GU1 Homo sapiens cDNA clone IMAGE:2872846 3'
10053	22701	35918	0.81	8.6E-02	AF026504.1	NT	Rattus norvegicus SPA-1 like protein p1284 mRNA, complete cds
10865	23545	36792	1.8	8.6E-02	AF206551.1	NT	Lacerta media cytochrome c oxidase subunit 1 gene, partial cds; mitochondrial product
10865	23545	36793	1.8	8.6E-02	AF206551.1	NT	Lacerta media cytochrome c oxidase subunit 1 gene, partial cds; mitochondrial product
11214	23877	37163	4.64	8.6E-02	BF305606.1	EST_HUMAN	601893437F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4139216 5'
11214	23877	37164	4.64	8.6E-02	BF305606.1	EST_HUMAN	601893437F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4139216 5'
11417	23184	36414	5.97	8.6E-02	AE001079.1	NT	Archaeoglobus fulgidus section 34 of 172 of the complete genome
11568	24167	37481	2.11	8.6E-02	AF283660.1	NT	Bacillus stearothermophilus BsrFI methylase (FIM) and BsrFI restriction endonuclease (FIR) genes, complete cds
2395	15116	27853	3.3	8.5E-02	AE000652.1	NT	Helicobacter pylori 26695 section 130 of 134 of the complete genome
5583	18380	31292	0.75	8.5E-02	AA985491.1	EST_HUMAN	601893437F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:1592917 3' similar to gb:K01144 HLA CLASS II HISTOCOMPATIBILITY ANTIGEN, GAMMA CHAIN PRECURSOR (HUMAN);
5921	18417		1.29	8.5E-02	P08089	SWISSPROT	M PROTEIN, SEROTYPE 6 PRECURSOR
5921	18706	31658	6.95	8.5E-02	AF233885.1	NT	Mus musculus phospholipase C-like protein mRNA, partial cds
8504	21196	34340	1.65	8.5E-02	6754779	NT	Mus musculus myosin XV (Myo15), mRNA
9736	22387	35591	2.81	8.5E-02	BE833054.1	EST_HUMAN	RC4-OT0037-200700-014-e05 OT0037 Homo sapiens cDNA
9736	22387	35592	2.81	8.5E-02	BE833054.1	EST_HUMAN	RC4-OT0037-200700-014-e05 OT0037 Homo sapiens cDNA
10261	22909	36119	0.54	8.5E-02	X76731.1	NT	V armodyes gene for armodyoxin C
10382	23028	36243	0.87	8.5E-02	11418108	NT	Homo sapiens chromosome 22 open reading frame 5 (C22ORF5), mRNA
11105	23775		8.87	8.5E-02	AF155510.1	NT	Homo sapiens heparanase precursor, mRNA, complete cds
11125	23784	37070	4.43	8.5E-02	AB001562.1	NT	Streptococcus mutans gene for glucose-1-phosphate uridylyltransferase, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12700	24981		3.8	8.5E-02	AA362834.1	EST_HUMAN	EST272736 Ovary II Homo sapiens cDNA 5' end
2872	16602	28121	3.73	8.4E-02	W69330.1	EST_HUMAN	zfd44e11.11 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:343532 5'
3801	16553	28184	1	8.4E-02	A1827586.1	EST_HUMAN	wf10f11.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2350221 3' similar to contains element MSR1 repetitive element ;
4321	17060	28685	1.07	8.4E-02	AF257213.1	NT	Cavia porcellus glycoprotein alpha-subunit mRNA, complete cds
4321	17060	28686	1.07	8.4E-02	AF257213.1	NT	Cavia porcellus glycoprotein alpha-subunit mRNA, complete cds
5137	17855	30472	4.97	8.4E-02	AB042555.1	NT	Homo sapiens mRNA, similar to rat myonogalin, complete cds
5229	18035	30661	9.84	8.4E-02	BE267153.1	EST_HUMAN	601190436F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3534393 5'
6590	18353	32366	1.72	8.4E-02	AK024458.1	NT	Homo sapiens mRNA for FLJ00050 protein, partial cds
7928	20623	33751	7.18	8.4E-02	BE065074.1	EST_HUMAN	GM3-BT0790-260400-162-d05 BT0790 Homo sapiens cDNA
8741	21433	34578	1.01	8.4E-02	AF218890.1	NT	Homo sapiens attractin precursor (ATRIN) gene, exon 2
10260	22908	36118	1.83	8.4E-02	A1735184.1	EST_HUMAN	es88g10.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2335842 3' similar to TR:088312
12070	24584	31122	1.68	8.4E-02	R79408.1	EST_HUMAN	O88312 G0B-4. ;
2005	14741	27485	0.92	8.3E-02	5835680	NT	y83h12.11 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:145895 5'
2005	14741	27466	0.92	8.3E-02	5835680	NT	Ixodes hexagonus mitochondrion, complete genome
3580	16335	28980	6.91	8.3E-02	P75334	SWISSPROT	Ixodes hexagonus mitochondrion, complete genome
3607	16360	29001	0.83	8.3E-02	A1436797.1	EST_HUMAN	HYPOTHETICAL LIPOPROTEIN MG309 HOMOLOG PRECURSOR
3607	16360	29002	0.83	8.3E-02	A1436797.1	EST_HUMAN	fh82g06.x1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:2125210 3'
6166	18943	31914	1.05	8.3E-02	A1942338.1	EST_HUMAN	fh82g06.x1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:2125210 3'
6273	19046	32023	3.05	8.3E-02	AF052683.1	NT	wo79f11.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2461581 3'
7880	20575	33702	2.98	8.3E-02	AF195787.1	NT	Homo sapiens protocadherin 43 gene, exon 1
7911	20608		1.48	8.3E-02	A4865295.1	EST_HUMAN	Rattus norvegicus dystrophin-related protein 2 A-form splice variant (Dtp2) mRNA, complete cds
8198	20892		1.32	8.3E-02	A4887873.1	EST_HUMAN	og88g08.s1 NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1455422 3' similar to contains L1.11 L1 L1 repetitive element ;
9438	22116	35291	1.41	8.3E-02	AW883503.1	EST_HUMAN	og81f10.s1 NCI_CGAP_Kid6 Homo sapiens cDNA clone IMAGE:1592779 3'
9451	22001		1.88	8.3E-02	AL161595.2	NT	la05h10.x1 Human Pancreatic Islets Homo sapiens cDNA 3' similar to TR:Q15332 Q15332 GAMMA SUBUNIT OF SODIUM POTASSIUM ATPASE LIKE. ;
10240	22888		0.46	8.3E-02	AF020409.1	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 91
12158	25353		1.67	8.3E-02	BE989458.1	EST_HUMAN	Dictyostelium discoideum DocA (docA) mRNA, complete cds
1357	14105		7.15	8.2E-02	Y08170.2	NT	601644770F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:3928993 5'
1481	14228	26914	1.98	8.2E-02	AF167077.2	NT	Gallus gallus mRNA for for OBCAM protein gamma isoform
3071	15837		2.07	8.2E-02	AL163206.2	NT	Canis familiaris glutamate transporter (EAA174) mRNA, complete cds
3784	16536		1.35	8.2E-02	AL161488.2	NT	Homo sapiens chromosome 21 segment HS21C006
							Arabidopsis thaliana DNA chromosome 4, contig fragment No. 10

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3989	16737	29371	1.07	8.2E-02	AL163206.2	NT	Homo sapiens chromosome 21 segment HS21C008
4251	16992	29617	4.97	8.2E-02	P48960	SWISSPROT	LEUCOCYTE ANTIGEN CD97 PRECURSOR
4251	16992	29618	4.97	8.2E-02	P48960	SWISSPROT	LEUCOCYTE ANTIGEN CD97 PRECURSOR
4251	16992	29619	4.97	8.2E-02	P48960	SWISSPROT	LEUCOCYTE ANTIGEN CD97 PRECURSOR
5022	17743	30354	2.44	8.2E-02	U76009.1	NT	Mus musculus zinc transporter (Znt-3) gene, complete cds
5070	17789		2.39	8.2E-02	Z68693.1	NT	T. inflatum transposon Restless DNA
5252	18058	30687	1.49	8.2E-02	BE997030.1	EST_HUMAN	601439576F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3924523 5'
6925	19661	32707	3.09	8.2E-02	AF309555.1	NT	Bos taurus connective tissue growth factor precursor (CTGF) gene, complete cds
7632	20298		0.57	8.2E-02	AV743341.1	EST_HUMAN	AV743341 CB Homo sapiens cDNA clone CBLANF07 5'
8670	21382	34509	2.95	8.2E-02	AW875126.1	EST_HUMAN	RC2-PT0004-031269-011-405 PT0004 Homo sapiens cDNA
9499	22162	35332	5.36	8.2E-02	X04197.1	NT	Beet necrotic yellow vein virus RNA-2
9663	22315	35512	2.24	8.2E-02	BE254318.1	EST_HUMAN	601115055F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:33555596 5'
12164	24646	31102	4.03	8.2E-02	AE002246.2	NT	Chlamydomonas reinhardtii AFR39, section 73 of 84 of the complete genome
12554	25138		3.65	8.2E-02	AF275366.1	NT	Mus musculus epidermal growth factor receptor (Egfr) gene, exons 5 through 28, and complete cds, alternatively spliced
5668	18463	31378	0.79	8.1E-02	AE004006.1	NT	Xylella fastidiosa, section 152 of 229 of the complete genome
6286	19059	32040	1.19	8.1E-02	T11532.1	EST_HUMAN	A1484F Heart Homo sapiens cDNA clone A1484
7097	19786		0.66	8.1E-02	AL163279.2	NT	Homo sapiens chromosome 21 segment HS21C079
7482	20154		1.25	8.1E-02	A1692681.1	EST_HUMAN	wdb6f08.x1 NCL CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2338503 3'
8238	20932	34067	0.61	8.1E-02	11426974	NT	Homo sapiens hypothetical protein FLJ10060 (FLJ10060), mRNA
8238	20932	34068	0.61	8.1E-02	11426974	NT	Homo sapiens hypothetical protein FLJ10060 (FLJ10060), mRNA
9812	22463		1.64	8.1E-02	AY005150.1	NT	Homo sapiens extracellular glycoprotein lacritin precursor, gene, complete cds
11482	24083	37395	2.08	8.1E-02	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
5	15634	25447	5.03	8.0E-02	AW954653.1	EST_HUMAN	EST366723 MAGE resequences, MAGE Homo sapiens cDNA
915	13682	26344	0.79	8.0E-02	U60315.1	NT	Molluscum contagiosum virus subtype 1, complete genome
1694	15576	27134	9.85	8.0E-02	D26535.1	NT	Human gene for dihydrolipoamide succinyltransferase, complete cds (exon 1-16)
1694	15576	27135	9.85	8.0E-02	D26535.1	NT	Human gene for dihydrolipoamide succinyltransferase, complete cds (exon 1-16)
1698	14933	27343	3.27	8.0E-02	BE087219.1	EST_HUMAN	PM3-BT0347-170200-001-b08 BT0347 Homo sapiens cDNA
2374	15096	27835	1.09	8.0E-02	D90915.1	NT	Synechocystis sp. PCC6803 complete genome, 17/27, 2137259-2267259
2374	15096	27836	1.09	8.0E-02	D90915.1	NT	Synechocystis sp. PCC6803 complete genome, 17/27, 2137259-2267259
2473	15191		4.2	8.0E-02	BF246744.1	EST_HUMAN	801855548F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4075619 5'
2823	13827	28486	0.98	8.0E-02	M23449.1	NT	Dictyocaulum discoideum cyclic nucleotide phosphodiesterase gene, complete cds
2901	15667	28315	1.45	8.0E-02	AL445067.1	NT	Thermoplasma acidophilum complete genome, segment 5/6
3797	16549	29182	1.01	8.0E-02	AW968118.1	EST_HUMAN	EST3787191 MAGE resequences, MAGE Homo sapiens cDNA

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Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4725	17457	30093	1.43	8.0E-02	A1434202.1	EST_HUMAN	t31g02.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2132114 3'
4764	17496		6.33	8.0E-02	X72794.1	NT	M.musculus gene for gelatinase B
5108	17828	30443	0.87	8.0E-02	AW207037.1	EST_HUMAN	UI-H-B11-afid.f-10-0-J1 st NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2721547 3'
5801	18591	31516	3.15	8.0E-02	AF276948.1	NT	Homo sapiens ABCA1 (ABCA1) gene, complete cds
7080	18591	31516	1.82	8.0E-02	AF276948.1	NT	Homo sapiens ABCA1 (ABCA1) gene, complete cds
8027	20722	33854	3.79	8.0E-02	AL114993.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
9289	21956	35127	1.12	8.0E-02	X74208.1	NT	H.sapiens AGT gene, intron 4
9289	21956	35128	1.12	8.0E-02	X74208.1	NT	H.sapiens AGT gene, intron 4
10058	22706		0.55	8.0E-02	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
10692	23383	36823	2.27	8.0E-02	AF217796.1	NT	Homo sapiens SCG10 like-protein, helicase-like protein NHL, M88, and ADP-ribosylation factor related protein 1 (ARFRP1) genes, complete cds
12198	24665	31070	6.39	8.0E-02	AJ005375.1	NT	Drosophila arena hunchback region
12748	17903		2.21	8.0E-02	4503034	NT	Homo sapiens cAMP responsive element binding protein-like 2 (CREBL2) mRNA
2171	14900	27634	3.52	7.9E-02	BE250008.1	EST_HUMAN	600943191F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2859510 5'
2878	15744	28392	7.25	7.9E-02	AI582029.1	EST_HUMAN	60S RIBOSOMAL PROTEIN L38 (HUMAN); ar8c08.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2173848 3' similar to gb:Z28876
3777	16529	29168	0.97	7.9E-02	AF030694.2	NT	Plasmodium falciparum strain Dd2 heat shock protein 86 (HSP86), O1 (o1), O3 (o3), O2 (o2), CG8 (cg8), CG4 (cg4), CG3 (cg3), putative chloroquine resistance transporter (crt), CG9 (cg9), CG1 (cg1), CG8 (cg8), CG2 (cg2), and CG7 (cg7) genes, complete cds
3832	16583	29217	5.01	7.9E-02	6881044	NT	Mus musculus colony stimulating factor 1 receptor (Csf1r), mRNA
3832	16583	29218	5.01	7.9E-02	6881044	NT	Mus musculus colony stimulating factor 1 receptor (Csf1r), mRNA
4845	17379	30011	0.89	7.9E-02	BF348454.1	EST_HUMAN	602019770F1 NCI_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4155401 5'
4760	17492		1.31	7.9E-02	AB008019.1	NT	Arabidopsis thaliana RXW24L mRNA, partial cds
4851	17581	30204	1.02	7.9E-02	L24757.1	NT	Human bone sialoprotein (BSP) gene, exons 2, 3 and 4
6597	18360		1.16	7.9E-02	BF368016.1	EST_HUMAN	RC3-GN0042-310800-024-311 GN0042 Homo sapiens cDNA
7831	20628	33754	2.78	7.9E-02	U27832.1	NT	Saccharomyces cerevisiae suppressor of Mif2 Sm14p (SMT4) gene, complete cds
9927	22575	35773	4.21	7.9E-02	AI081644.1	EST_HUMAN	ou63b05.s1 NCI_CGAP_Br2 Homo sapiens cDNA clone IMAGE:1632465 3' similar to WP:C37A2.2 CE08811;
9927	22575	35774	4.21	7.9E-02	AI081644.1	EST_HUMAN	ou63b05.s1 NCI_CGAP_Br2 Homo sapiens cDNA clone IMAGE:1632465 3' similar to WP:C37A2.2 CE08811;
1188	13940	26604	1.77	7.8E-02	AI793275.1	EST_HUMAN	ou59d02.y5 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1570467 5' similar to contains L1.13 L1 repetitive element;
1188	13940	26605	1.77	7.8E-02	AI793275.1	EST_HUMAN	ou59d02.y5 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1570467 5' similar to contains L1.13 L1 repetitive element;

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Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5027	18484		2.47	7.8E-02	BE250048.1	EST_HUMAN	600943055F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2959693 5'
6976	19457	32479	0.88	7.8E-02	U82695.2	NT	Homo sapiens zinc finger protein 92 (ZFP92), expressed-Xq28STS protein (XQ28ORF), and biglycan (BGN) genes, complete cds; and plasma membrane calcium ATPase isoform 3 (PMCA3) gene, partial cds
6978	19457	32480	0.88	7.8E-02	U82695.2	NT	Homo sapiens zinc finger protein 92 (ZFP92), expressed-Xq28STS protein (XQ28ORF), and biglycan (BGN) genes, complete cds; and plasma membrane calcium ATPase isoform 3 (PMCA3) gene, partial cds
8894	21376	34520	0.71	7.8E-02	BE897947.1	EST_HUMAN	601440439F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3925449 5'
8779	21471	34616	0.66	7.8E-02	X78344.1	NT	S.cerevisiae CAT8 gene
8951	21642	34789	0.79	7.8E-02	AF233437.1	NT	Homo sapiens FYVE domain-containing dual specificity protein phosphatase FYVE-DSP1b mRNA, complete cds
8951	21642	34790	0.79	7.8E-02	AF233437.1	NT	Homo sapiens FYVE domain-containing dual specificity protein phosphatase FYVE-DSP1b mRNA, complete cds
9281	22016	35183	1.07	7.8E-02	AA469364.1	EST_HUMAN	nc88806.r1 NCL_CGAP_P1 Homo sapiens cDNA clone IMAGE:771731
9701	22352	35547	0.62	7.8E-02	Z99124.1	NT	Bacillus subtilis complete genome (section 21 of 21); from 3999281 to 4214814
10562	23258	36494	4.58	7.8E-02	U32323.1	NT	Human interleukin-11 receptor alpha chain gene, complete cds
12754	25016		3.92	7.8E-02	AF096349.1	NT	HIV-1 strain 97USNG30 from USA, envelope glycoprotein (env) gene, partial cds
1378	15568	26800	1.25	7.7E-02	AF181897.1	NT	Homo sapiens WRN (WRN) gene, complete cds
3574	19329		1.97	7.7E-02	AJ238093.1	NT	Homo sapiens partial AF-4 gene, exons 2 to 7 and Alu repeat elements
5458	18255	31145	0.59	7.7E-02	AF062836.1	NT	Gallus gallus collagen type XII alpha-1 (COL12A1) gene, promoter region and partial cds
7809	20504	33625	5.37	7.7E-02	AA402949.1	EST_HUMAN	TR:G1173905 G1173905 SPLICEOSOME ASSOCIATED PROTEIN ;
9735	22386	35590	3.94	7.7E-02	P38080	SWISSPROT	PROBABLE SERINE/THREONINE-PROTEIN KINASE YBR059C
10031	22679	35895	0.85	7.7E-02	AJ318662.1	EST_HUMAN	ta80b08.x1 NCL_CGAP_HSC2 Homo sapiens cDNA clone IMAGE:2050359 3' similar to gb:Z26876 60S
10031	22679	35896	0.85	7.7E-02	AJ318662.1	EST_HUMAN	RIBOSOMAL PROTEIN L38 (HUMAN);
10933	23613	36863	4.51	7.7E-02	11422757	NT	RIBOSOMAL PROTEIN L38 (HUMAN);
12889	25215		2.68	7.7E-02	11436859	NT	Homo sapiens interferon regulatory factor 7 (IRF7), mRNA
3382	16141	28798	1.97	7.6E-02	BE514432.1	EST_HUMAN	601316426F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3634903 5'
3403	16161	28812	1.14	7.6E-02	AA296447.1	EST_HUMAN	EST112214 Cerebellum II Homo sapiens cDNA 5' end similar to similar to protocadherin 43
3547	19302	28962	0.71	7.6E-02	AJ400877.1	NT	Homo sapiens ASCL3 gene, CEGP1 gene, C11orf14 gene, C11orf15 gene, C11orf16 gene and C11orf17 gene
6006	18787	31749	0.81	7.6E-02	AJ061275.1	EST_HUMAN	an25g02.x1 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:1699730 3'

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6263	19037	32012	0.92	7.6E-02	BE37828.1	EST_HUMAN	601236402F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3608401 5'
9270	22024	35194	1.47	7.6E-02	AL131016.1	NT	Homo sapiens SCL gene locus
9797	22448		1.63	7.6E-02	AL139078.2	NT	Campylobacter jejuni NCTC11168 complete genome; segment 5/6
10119	22767	35979	0.49	7.6E-02	BE708002.1	EST_HUMAN	RC1-H70545-020800-017-406 HT0545 Homo sapiens cDNA
10247	22895		0.75	7.6E-02	BE708002.1	EST_HUMAN	601654915R1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:3839810 3'
10487	23133	36359	0.71	7.6E-02	X92656.1	NT	L. esculentum mRNA for triose phosphate translocator
10487	23133	36360	0.71	7.6E-02	X92656.1	NT	L. esculentum mRNA for triose phosphate translocator
11678	24273	37595	2.45	7.6E-02	AW996845.1	EST_HUMAN	QV3-BN0048-150400-151-e04 BN0046 Homo sapiens cDNA
767	13540	26199	1.44	7.5E-02	5902093	NT	Homo sapiens solute carrier family 8 (neurotransmitter transporter, glycine), member 9 (SLC6A9), mRNA
767	13540	26200	1.44	7.5E-02	5902093	NT	Homo sapiens solute carrier family 8 (neurotransmitter transporter, glycine), member 9 (SLC6A9), mRNA
4472	17207	29833	1.17	7.5E-02	AB015861.1	NT	Homo sapiens IL-18 gene for interleukin-18, intron 1 and exon 2
5762	18553	31477	0.91	7.5E-02	AJ948714.1	EST_HUMAN	wq24h09.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2472257 3'
8236	20930	34066	1.05	7.5E-02	AJ864387.1	EST_HUMAN	w52b02.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2472257 3'
8405	21098	34234	1.17	7.5E-02	AU116913.1	EST_HUMAN	ENOLASE (HUMAN);
9932	22580		0.54	7.5E-02	BF221730.1	EST_HUMAN	AU116913 HEMBA1 Homo sapiens cDNA clone HEMBA1000284 5'
10390	23036	36252	0.7	7.5E-02	BF206809.1	EST_HUMAN	7061c05.x1 NCI_CGAP_P128 Homo sapiens cDNA clone IMAGE:3578504 3' similar to contains element
10498	23134	36361	0.72	7.5E-02	X79460.1	EST_HUMAN	MER27 repetitive element;
465	13250	25891	1.46	7.4E-02	AW838547.1	EST_HUMAN	601870205F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4100449 5'
1445	14192		0.82	7.4E-02	AF030027.1	NT	C.fiml DSM 20113 16S rDNA
2565	15299		1.32	7.4E-02	6755099	NT	RC5-LT0054-260100-011-H09 LT0054 Homo sapiens cDNA
3561	16336	28981	0.86	7.4E-02	AJ807885.1	EST_HUMAN	Equine herpesvirus 4 strain NS80567, complete genome
4658	17390	30024	2.03	7.4E-02	L78810.1	NT	Mus musculus paired-like homeodomain transcription factor 1 (Pitx1), mRNA
4741	17473	30108	2.94	7.4E-02		NT	wf43h01.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2358385 3'
4889	17616	30235	2.1	7.4E-02	6678492	NT	Homo sapiens ADP/ATP carrier protein (ANT-2) gene, complete cds
6403	19172		2.18	7.4E-02	R17477.1	EST_HUMAN	Rattus norvegicus Activin receptor like kinase 1 (Acvrl1), mRNA
7801	20486	33618	1.52	7.4E-02	BE680112.1	EST_HUMAN	Mus musculus ubiquitin c-terminal hydrolase related polypeptide (Uchrlp), mRNA
8399	21092	34228	1.03	7.4E-02	U56089.1	NT	x914g08.r1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:32339 5'
9064	21753	34913	1.12	7.4E-02	AW629605.1	EST_HUMAN	601493368F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3895264 5'
							Human peridic tryptophan protein 2 (PW2) gene, exons 15 to 21, and complete cds
							h167d11.y1 NCI_CGAP_GUT1 Homo sapiens cDNA clone IMAGE:2967861 5' similar to SW:SCA2_HUMAN
							O15127 SECRETORY CARRIER-ASSOCIATED MEMBRANE PROTEIN 2;

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9064	21753	34914	1.12	7.4E-02	AW629605.1	EST_HUMAN	hh67d11.y1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2887861 5' similar to SW:SCA2_HUMAN
9339	20410	33525	0.52	7.4E-02	A1672939.1	EST_HUMAN	O15127 SECRETORY CARRIER-ASSOCIATED MEMBRANE PROTEIN 2 ;
9339	20410	33526	0.52	7.4E-02	A1672939.1	EST_HUMAN	we74d02.x1 Soares_Dieckgraefe_cdon_NHCD Homo sapiens cDNA clone IMAGE:2346819 3'
9714	22365	35563	1.03	7.4E-02	U62283.1	NT	we74d02.x1 Soares_Dieckgraefe_cdon_NHCD Homo sapiens cDNA clone IMAGE:2346819 3'
9841	22492	35692	0.52	7.4E-02	BF512678.1	EST_HUMAN	Human LIM-kinase1 and alternatively spliced LIM-kinase1 (LIMK1) gene, complete cds
10939	23619	36869	1.26	7.4E-02	AA059167.1	EST_HUMAN	UI-H-BW1-ang-g-06-0-UJ.s1 NCI_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3069898 3'
12126	24618		1.53	7.4E-02	11525893	NT	z64e01.r1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:381720 5'
12381	25329		2.21	7.4E-02	AW379431.1	EST_HUMAN	Homo sapiens histone deacetylase 5 (NY-CO-9), mRNA
456	13242	25881	1.5	7.3E-02	BE964961.2	EST_HUMAN	CM4-HT0243-081199-037-d11 HT0243 Homo sapiens cDNA
456	13242	25882	1.5	7.3E-02	BE964961.2	EST_HUMAN	601668738R1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3886209 3'
969	13445	26085	3.9	7.3E-02	AE001789.1	NT	601668738R1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3886209 3'
1464	15670	26900	3.62	7.3E-02	AW900281.1	EST_HUMAN	Thermotoga maritima section 101 of 136 of the complete genome
1837	15580		12.41	7.3E-02	AL183302.2	NT	CM0-NN1004-130300-284-g08 NN1004 Homo sapiens cDNA
6361	19131	32126	1.32	7.3E-02	AA779977.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C102
7368	20048	33128	2.58	7.3E-02	P05143	SWISSPROT	z24a02.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:451178 3' similar to
7368	20048	33128	2.58	7.3E-02	P05143	SWISSPROT	gb:L02426 26S PROTEASE SUBUNIT 4 (HUMAN);
8068	20762		1.15	7.3E-02	7682107	NT	PROLINE-RICH PROTEIN MP-3
9110	21798		1.14	7.3E-02	AB011090.1	NT	PROLINE-RICH PROTEIN MP-3
11179	19131	32126	2.06	7.3E-02	AA779977.1	EST_HUMAN	Homo sapiens KIAA0424 protein (KIAA0424), mRNA
11844	24428		5.07	7.3E-02	11560138	NT	Homo sapiens mRNA for KIAA0518 protein, partial cds
117	12937	25577	1	7.2E-02	AE000882.1	NT	z24a02.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:451178 3' similar to
117	12937	25578	1	7.2E-02	AE000882.1	NT	gb:L02426 26S PROTEASE SUBUNIT 4 (HUMAN);
1458	14205	26890	2.72	7.2E-02	AL163301.2	NT	Rattus norvegicus caspase recruitment domain protein 9 (LOC64171), mRNA
1458	14205	26891	2.72	7.2E-02	AL163301.2	NT	Methanobacterium thermoautotrophicum from bases 1029155 to 1039934 (section 88 of 148) of the complete genome
2552	15267		2.83	7.2E-02	U14794.1	NT	Methanobacterium thermoautotrophicum from bases 1029155 to 1039934 (section 88 of 148) of the complete genome
3865	16615	29254	0.95	7.2E-02	AW288322.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C101
4312	17051	29676	4.65	7.2E-02	BF572307.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C101
4844	17378	30010	0.7	7.2E-02	11466563	NT	Human immunodeficiency virus type 1 isolate 28 reverse transcriptase (pol) gene, internal fragment, partial cds
							UI-H-BWO-qj1-a-05-QJ.s1 NCI_CGAP_Sub6 Homo sapiens cDNA clone IMAGE:2732049 3'
							602077757F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4251950 5'
							Rhodomonas salina mitochondrion, complete genome

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Single Exon Probes Expressed in Brain

Probe SEQ ID NO.	Exon ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5205	18013	30835	2.88	7.2E-02	U67531.1	NT	Methanococcus jannaschii section 73 of 150 of the complete genome
5206	18014	30636	10.1	7.2E-02	P11120	SWISSPROT	CALMODULIN
7068	19799	32824	1.58	7.2E-02	BF216086.1	EST_HUMAN	601883558F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4095710 5'
7085	19775	32840	0.64	7.2E-02	AF221126.1	NT	Streptococcus pneumoniae putative response regulator (zmpR), putative histidine kinase (zmpS), and putative zinc metalloprotease (zmpB) genes, complete cds
7109	19797		1.5	7.2E-02	5834897	NT	Strongylocentrotus purpuratus mitochondrion, complete genome
8087	20781	33910	0.8	7.2E-02	P05143	SWISSPROT	PROLINE-RICH PROTEIN MP-3
8087	20781	33911	0.8	7.2E-02	P05143	SWISSPROT	PROLINE-RICH PROTEIN MP-3
8962	21653		0.61	7.2E-02	Y17217.1	NT	Lactococcus lactis cepE gene
9474	22127		0.49	7.2E-02	X16349.1	NT	Human gene for sex hormone-binding globulin (SHBG)
9511	22164	35346	2.32	7.2E-02	AV712452.1	EST_HUMAN	AV712452 DCA Homo sapiens cDNA clone DCAAUG01 5'
9659	22311	35509	3.8	7.2E-02	L14561.1	NT	Homo sapiens plasma membrane calcium ATPase isoform 1 (ATP2B1) gene, alternative splice products, partial cds
9814	22465	35667	0.93	7.2E-02	BF125399.1	EST_HUMAN	601763523F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:4026436 5'
9903	22552	35747	2.53	7.2E-02	AW873187.1	EST_HUMAN	h924f11.x1 NCL CGAP_Adr1 Homo sapiens cDNA clone IMAGE:3120333 3' similar to TR:Q92340 Q92340
10092	22740	35955	0.82	7.2E-02	AA769204.1	EST_HUMAN	ATYPICAL PKC SPECIFIC BINDING PROTEIN. ; ca62c07.s1 NCL CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1316844 3'
10250	22898	36108	1.93	7.2E-02	U82695.2	NT	Homo sapiens zinc finger protein 92 (ZFP92), expressed-Xq28STS protein (XQ28ORF), and biglycan (BGN) genes, complete cds; and plasma membrane calcium ATPase isoform 3 (PMCA3) gene, partial cds
10372	23018	36234	5.54	7.2E-02	BE565003.1	EST_HUMAN	601343926F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3688951 5'
10395	23041		3.88	7.2E-02	BE539214.1	EST_HUMAN	601065194F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3451559 5'
10509	23155	36381	0.48	7.2E-02	AA706897.1	EST_HUMAN	z28h05.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:451641 3'
10830	23512	36753	3.3	7.2E-02	AF049874.1	NT	Rattus norvegicus bHLH transcription factor Mist1 (Mist1) gene, complete cds
11849	24433	37775	1.34	7.2E-02	AY009080.1	NT	Homo sapiens putative transmembrane protein declin-1 mRNA, complete cds
12035	24560	31113	1.57	7.2E-02	AA773696.1	EST_HUMAN	af81a04.r1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:1048398 5'
12069	24583		4.45	7.2E-02	AJ230796.1	EST_HUMAN	AJ230796 Homo sapiens library (Seranski P) Homo sapiens cDNA clone PS13D5 3'
12182	24654		1.73	7.2E-02	U82828.1	NT	Homo sapiens ataxia telangiectasia (ATM) gene, complete cds
12196	25185		8.19	7.2E-02	AW90962.1	EST_HUMAN	GM4-NN1009-200300-116-c11 NN1009 Homo sapiens cDNA
12599	25362		3.62	7.2E-02	AF020439.1	NT	Homo sapiens ATP-citrate lyase gene, intron 3
1897	14634	27344	2.01	7.1E-02	L02290.1	NT	Human immunodeficiency virus type 1 (D9) proviral structural capsid protein (gag) gene, partial cds
2290	15015	27751	5.07	7.1E-02	BF208902.1	EST_HUMAN	601872281F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:4092981 5'
7807	20502	33622	0.77	7.1E-02	AI125264.1	EST_HUMAN	qd92a10.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1736922 3'

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Single Exon Probes Expressed in Brain

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11922	24483		6.41	7.1E-02	BE304764.1	EST_HUMAN	601143974F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:3051234 5'
515	13289	25831	1	7.0E-02	Q07092	SWISSPROT	COLLAGEN ALPHA 1(XVI) CHAIN PRECURSOR
1486	14233		1.27	7.0E-02	X96677.1	NT	Martellia Mfuit-1 gene
1756	14498	27199	1.08	7.0E-02	AA056343.1	EST_HUMAN	z166104.s1 Stragene colon (#837204) Homo sapiens cDNA clone IMAGE:509599 3'
3027	15763	28440	2.1	7.0E-02	AW138152.1	EST_HUMAN	UI-H-B1-acy-c-07-0-UI.s1 NCL CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2716020 3'
3878	16628	29266	0.74	7.0E-02	AA161438.1	EST_HUMAN	ai65a12.s1 Soares_testis_NHT Homo sapiens cDNA clone 1375678 3' similar to gb:K03002 60S
4119	16861		1.28	7.0E-02	AW792962.1	EST_HUMAN	GM0-JM0001-060300-270-s12 UM0001 Homo sapiens cDNA
4189	16930	28560	1.06	7.0E-02	AF077821.1	NT	Canis familiaris inducible nitric oxide synthase mRNA, complete cds
4877	17604	30227	7.24	7.0E-02	BF381987.1	EST_HUMAN	601816291F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4050071 5'
5293	18098		0.57	7.0E-02	Y09143.2	NT	Lumbricus rubellus mRNA for cyclophilin B
7300	19883	33059	1.29	7.0E-02	AV689285.1	EST_HUMAN	AV689285 GKc Homo sapiens cDNA clone GKCCAE06 5'
7506	20177	33271	0.84	7.0E-02	Y19187.1	NT	Gallus gallus mRNA for parial azonin, XL spliced variant (acz gene)
8996	21686	34836	1.26	7.0E-02	9628113	NT	African swine fever virus, complete genome
9497	22150	35331	1.24	7.0E-02	K02901.1	NT	Rat Ig gamma epsilon H-chain gene C-region, 3' end
9852	22502	35702	0.51	7.0E-02	U27286.1	NT	Human myosin binding protein H (MyBP-H) gene, complete cds
11345	24035	37338	4.98	7.0E-02	AA724295.1	EST_HUMAN	ah99a05.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1327184 3' similar to gb:L14837
501	13285	25917	4.3	6.9E-02	AL163210.2	NT	TIGHT JUNCTION PROTEIN ZO-1 (HUMAN);
501	13285	25918	4.3	6.9E-02	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
1310	14058		1.2	6.9E-02	4507968	NT	Homo sapiens chromosome 21 segment HS21C010
3773	16525	28163	1.41	6.9E-02	Q06364	SWISSPROT	Homo sapiens regulator of Gz-selective protein signaling (ZGAP1) mRNA, and translated products
3773	16525	28164	1.41	6.9E-02	Q06364	SWISSPROT	26S PROTEASOME REGULATORY SUBUNIT S3 (NUCLEAR ANTIGEN 21D7)
5113	17831	30448	0.89	6.9E-02	AF121254.1	NT	26S PROTEASOME REGULATORY SUBUNIT S3 (NUCLEAR ANTIGEN 21D7)
5127	17845	30462	1.25	6.9E-02	BE284605.1	NT	Enterococcus faecium cysteine aminopeptidase (pepC) gene, partial cds; phospho-beta-glucosidase BglB (bglB), beta-glucosidase specific transport protein (bglS), transcription antiterminator (bglR), enterocin B precursor (entB), enterocin B immunity protease
7516	20187		0.61	6.9E-02	AF164967.1	EST_HUMAN	601192383F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3636253 5'
7951	20646		1.12	6.9E-02	U12022.1	NT	Canine distemper virus strain A7517, complete genome
8451	21143	34282	1.01	6.9E-02	BE567435.1	EST_HUMAN	Human calmodulin (CALM1) gene, exons 2,3,4,5 and 6, and complete cds
8451	21143	34283	1.01	6.9E-02	BE567435.1	EST_HUMAN	601340661F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3683030 5'
9018	21708	34860	0.7	6.9E-02	U22967.1	NT	601340661F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3683030 5'
12065	24580		1.82	6.9E-02	X74315.1	NT	Barbatie duck parvovirus REP protein (rep) and three capsid protein VP (vp) genes, complete cds
							Xlaevis XF02 mRNA for fork head protein

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12232	24885		1.69	6.9E-02	P44621	SWISSPROT	PROTEIN TRANSPORT PROTEIN HOFCHOMOLOG
12447	24817		1.46	6.9E-02	AF195953.1	NT	Homo sapiens membrane-bound aminopeptidase P (XNPEP2) gene, complete cds
1875	14613	27321	1.56	6.8E-02	AA496759.1	EST_HUMAN	ae30f02.r1 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:897339 5' similar to gb:M22382 MITOCHONDRIAL MATRIX PROTEIN P1 PRECURSOR (HUMAN);
1875	14613	27322	1.56	6.8E-02	AA496759.1	EST_HUMAN	ae30f02.r1 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:897339 5' similar to gb:M22382 MITOCHONDRIAL MATRIX PROTEIN P1 PRECURSOR (HUMAN);
1900	14637	27346	3.77	6.8E-02	AF156673.1	NT	Homo sapiens putative hepatic transcription factor (WBSOR14) gene, complete cds
3097	15862	28503	1.19	6.8E-02	AA781996.1	EST_HUMAN	ai75a06.s1 Soares_testis_NHT Homo sapiens cDNA clone 1376626 3'
3097	15862	28504	1.19	6.8E-02	AA781996.1	EST_HUMAN	ai75a06.s1 Soares_testis_NHT Homo sapiens cDNA clone 1376626 3'
3097	15862	28505	1.19	6.8E-02	AA781996.1	EST_HUMAN	ai75a06.s1 Soares_testis_NHT Homo sapiens cDNA clone 1376626 3'
4516	17251		0.86	6.8E-02	BE141076.1	EST_HUMAN	MR0-HT0069-071099-001-c05 HT0069 Homo sapiens cDNA CELL-SURFACE RECEPTOR DAF-1 PRECURSOR
6525	19291		0.6	6.8E-02	P20792	SWISSPROT	RC1-BT0254-060300-017-409 BT0254 Homo sapiens cDNA
6799	19460		1.09	6.8E-02	BE061890.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C088
7180	19668	32939	8.73	6.8E-02	AL163288.2	NT	Dicystotellum discoideum myosin heavy chain kinase A (MHCKA) mRNA, complete cds
7584	20252	33358	0.63	6.8E-02	U16866.1	NT	Pyrococcus abyssi complete genome; segment 5/6
8186	20880	34017	5.01	6.8E-02	AJ248287.1	NT	Pyrococcus abyssi complete genome; segment 5/6
8186	20880	34018	5.01	6.8E-02	AJ248287.1	NT	Pyrococcus abyssi complete genome; segment 5/6
11873	26379		2.3	6.8E-02	T03214.1	EST_HUMAN	FB4A8 Fetal brain, Striatogene Homo sapiens cDNA clone FB4A8 3'end similar to LINE-1
12001	24537		2.85	6.8E-02	AA758014.1	EST_HUMAN	ah67f05.s1 Soares_testis_NHT Homo sapiens cDNA clone 1320705 3'
12551	24888		1.65	6.8E-02	AW975639.1	EST_HUMAN	EST387848 IMAGE resequences, MAGN Homo sapiens cDNA
12613	24920		3.06	6.8E-02	9910585	NT	Mus musculus latent TGF beta binding protein (Tgfb), mRNA
1519	14266		1.93	6.7E-02	AF115536.1	NT	Oncorhynchus mykiss TAP1 protein (OnmyTAP1) mRNA, OnmyTAP1*01 allele, complete cds
1866	14623	27333	2.27	6.7E-02	AI220285.1	EST_HUMAN	qg79e04.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1841406 3'
3706	16459	28097	4.52	6.7E-02	P17278	SWISSPROT	HOMEOBOX PROTEIN HOXD4 (CHOX-A)
7749	20445	33567	0.55	6.7E-02	X62895.1	NT	H.sapiens DNA for cGMP phosphodiesterase (exons 4-22)
7749	20445	33568	0.55	6.7E-02	X62895.1	NT	H.sapiens DNA for cGMP phosphodiesterase (exons 4-22)
8337	21030	34167	0.47	6.7E-02	AW082688.1	EST_HUMAN	xb61c11.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2580788 3'
9500	22153	35333	0.69	6.7E-02	AW137359.1	EST_HUMAN	UI-H-B11-acr-g-01-Q-JI.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2715433 3'
9500	22153	35334	0.69	6.7E-02	AW137359.1	EST_HUMAN	UI-H-B11-acr-g-01-Q-JI.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2715433 3'
1348	14096	26771	1.07	6.6E-02	AF245116.1	NT	Drosophila melanogaster cactin mRNA, complete cds
2180	14909	27641	3.31	6.6E-02	AJ289241.1	NT	Mus musculus Capn12 gene for calpain 12, exons 1-21, three alternative transcripts
3456	16212	28665	10.57	6.6E-02	R64306.1	EST_HUMAN	y18b10.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:139579 3'
3471	16227	28881	2.59	6.6E-02	7108357	NT	Homo sapiens mesothelin (MSLN), transcript variant 1, mRNA
3471	16227	28882	2.59	6.6E-02	7108357	NT	Homo sapiens mesothelin (MSLN), transcript variant 1, mRNA

Table 4

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4080	16805	29436	1.29	6.6E-02	AF280225.1	NT	Homo sapiens TESTIN 2 and TESTIN 3 genes, complete cds, alternatively spliced
4921	17849	30281	7.03	6.6E-02	Q61703	SWISSPROT	INTER-ALPHA-TRYPsin INHIBITOR HEAVY CHAIN H2 PRECURSOR (ITI HEAVY CHAIN H2)
4921	17849	30282	7.03	6.6E-02	Q61703	SWISSPROT	INTER-ALPHA-TRYPsin INHIBITOR HEAVY CHAIN H2 PRECURSOR (ITI HEAVY CHAIN H2)
6489	19256	32258	3.44	6.6E-02	X06411.1	NT	P. vulgaris mRNA for chalcone synthase
6701	19283	32286	0.56	6.6E-02	P25159	SWISSPROT	MATERNAL EFFECT PROTEIN STAUFEN
6701	19283	32287	0.56	6.6E-02	P25159	SWISSPROT	MATERNAL EFFECT PROTEIN STAUFEN
7847	20642	33870	1.81	6.6E-02	AF052572.1	NT	Homo sapiens chemokine receptor CXCR4 gene, promoter region and complete cds
8372	21065	34206	0.84	6.6E-02	AF006055.1	NT	Dictyostelium discoideum darlin (dar) gene, complete cds
8878	21370		0.53	6.6E-02	O60673	SWISSPROT	DNA POLYMERASE ZETA CATALYTIC SUBUNIT (HREV3)
8878	21611	34654	0.58	6.6E-02	9629198	NT	Human respiratory syncytial virus, complete genome
8819	21611	34655	0.58	6.6E-02	9629198	NT	Human respiratory syncytial virus, complete genome
9851	22501	35701	0.65	6.6E-02	A1458752.1	EST_HUMAN	Human respiratory syncytial virus, complete genome
9887	22635	35845	1.68	6.6E-02	Y07848.1	NT	Homo sapiens EWS, ga22, rp22 and bam22 genes
10022	22870		0.63	6.6E-02	11430559	NT	Homo sapiens vinculin (VCL), mRNA
10883	23563	36811	6.88	6.6E-02	BF374248.1	EST_HUMAN	MR1-SN0064-010600-006-a12 SN0064 Homo sapiens cDNA
11867	24451	37793	1.46	6.6E-02	AF052572.1	NT	Homo sapiens chemokine receptor CXCR4 gene, promoter region and complete cds
12442	24812		2.66	6.6E-02	9937891	NT	Mus musculus DIPB gene (Dipb), mRNA
12740	25008		1.38	6.6E-02	AF167430.1	NT	Rattus norvegicus cytochrome P450 2E1 (CYP2E1) gene, 5' flanking region
568	13349	25977	2.49	6.5E-02	BF027639.1	EST_HUMAN	601671046F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3964178 5'
968	13732	26398	1.32	6.5E-02	U7706088	NT	Homo sapiens E2F-like protein (LOC51270), mRNA
1370	14118	26793	3.08	6.5E-02	U47624.1	NT	Xenopus laevis alpha(E)-catenin mRNA, complete cds
1728	14470	27169	1.77	6.5E-02	AE000764.1	NT	Aquifex aeolicus section 66 of 109 of the complete genome
5471	18270	31162	2.03	6.5E-02	AA443991.1	EST_HUMAN	z46h12.s1 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:756743 3' similar to gb:M26038
6877	17953	30549	0.95	6.5E-02	U22661.1	NT	HLA CLASS II HISTOCOMPATIBILITY ANTIGEN, DR-5 BETA CHAIN (HUMAN);
8842	22493	35693	0.55	6.5E-02	BE963200.2	EST_HUMAN	Azobacter vinelandii ATCC 9046 negative regulator MucB (mucB) gene, partial cds
9842	22493	35694	0.55	6.5E-02	BE963200.2	EST_HUMAN	601656817R1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3865637 3'
10363	23010	36225	0.48	6.5E-02	BF106300.1	EST_HUMAN	601656817R1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3865637 3'
10335	23232	36466	5.56	6.5E-02	AA195648.1	EST_HUMAN	601823511F1 NIH_MGC_77 Homo sapiens cDNA clone IMAGE:4043138 5'
11894	24463		3.73	6.5E-02	M21496.1	NT	z32g05.s1 Soares_NhhMPu_S1 Homo sapiens cDNA clone IMAGE:665144 3'
12240	24691		4.66	6.5E-02	AF102993.1	NT	Rabbit microsomal epoxide hydrolase
561	13343	25970	2.09	6.4E-02	X94549.1	NT	Nectria haematococca kinesis related protein 2 (KRP2) gene, complete cds
3014	15780	28429	0.96	6.4E-02	6966923	NT	A. carterae precursor of peridinin-chlorophyll-a-protein (PCP) gene
4839	15780	28429	1.18	6.4E-02	6966923	NT	Mus musculus histone deacetylase 5 (Hdac5), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5363	18165	30850	1.67	6.4E-02	AI191956.1	EST_HUMAN	qe07b01.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1738249 3' similar to contains LTR8.b3 LTR8 repetitive element;
5791	18582	31509	0.65	6.4E-02	7305186	NT	Mus musculus IFN-response element binding factor 1 (IREBF-1), mRNA
6022	18802	31763	4.21	6.4E-02	AF052733.1	NT	Heterodera glycines beta-1,4-endoglucanase-1 precursor (HG-eng-1) gene, complete cds
6022	18802	31764	4.21	6.4E-02	AF052733.1	NT	Heterodera glycines beta-1,4-endoglucanase-1 precursor (HG-eng-1) gene, complete cds
6308	19080	32065	0.62	6.4E-02	AF072898.1	EST_HUMAN	we73g12.x1 Soares_Dieckgrafe_colon_NHCD Homo sapiens cDNA clone IMAGE:2346790 3'
6719	19634	32677	6.43	6.4E-02	BE974448.1	EST_HUMAN	601680425R2 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3950503 3'
7360	20041	33119	0.64	6.4E-02	AL162757.2	NT	Neisseria meningitidis serogroup A strain Z2491 complete genome; segment 6/7
8234	20928		2.91	6.4E-02	6753323	NT	Mus musculus chaperonin subunit 6a (zeta) (Cct6a), mRNA
8563	21255	34392	3.42	6.4E-02	AA093305.1	EST_HUMAN	kl1419.seq.F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA 5'
9025	21715	34868	0.77	6.4E-02	AF150195.1	EST_HUMAN	AF150195 Human mRNA from cd34+ stem cells Homo sapiens cDNA clone CBDAIA10
9488	22139		0.55	6.4E-02	BE834083.1	EST_HUMAN	RC1-OT0083-150600-014-506 OT0083 Homo sapiens cDNA
9617	22270	35457	1.73	6.4E-02	AB011126.1	NT	Homo sapiens mRNA for KIAA0554 protein, partial cds
10161	22809	36027	0.59	6.4E-02	AF087150.1	NT	Homo sapiens DNA topoisomerase II beta (TOP2B) gene, exons 16, 17, and 18
10161	22809	36028	0.59	6.4E-02	AF087150.1	NT	Homo sapiens DNA topoisomerase II beta (TOP2B) gene, exons 16, 17, and 18
11709	24304	37629	1.47	6.4E-02	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
11709	24304	37630	1.47	6.4E-02	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
12141	25288		2.7	6.4E-02	AF107890.1	NT	Homo sapiens mucin 6B (MUC6B) gene, partial cds
12188	24659	31065	2.47	6.4E-02	AJ277174.1	NT	Drosophila melanogaster mRNA for mod(mdg4)51.4 protein
1749	14491	27191	2.57	6.3E-02	AF108905.1	NT	Mus musculus major histocompatibility locus class III regions Hsc70t gene, partial cds; smRNP, G7A, NG23, MutS homolog, CLCP, NG24, NG25, and NG26 genes, complete cds; and unknown genes
3590	16344		2.36	6.3E-02	P37092	SWISSPROT	HEAT SHOCK PROTEIN 70 HOMOLOG
6045	18825	31786	1.18	6.3E-02	BF210736.1	EST_HUMAN	601873316F1 NIH_MGC_64 Homo sapiens cDNA clone IMAGE:4087499 5'
7142	19829		0.82	6.3E-02	X97669.1	NT	H sapiens gene encoding La autoantigen
9191	21861	35026	1.04	6.3E-02	AJ243916.1	NT	Drosophila melanogaster Domina gene, exons 1-3
9913	22562	35758	2.84	6.3E-02	AB010192.1	NT	Hepatitis G virus RNA for polyprotein (NS5A region), partial cds, strain: CMR-152
10171	22819		0.85	6.3E-02	AV698070.1	EST_HUMAN	AV698070 GKC Homo sapiens cDNA clone GKCAHE01 5'
10815	18825	31786	2.96	6.3E-02	BF210736.1	EST_HUMAN	601873316F1 NIH_MGC_64 Homo sapiens cDNA clone IMAGE:4087499 5'
4224	18965	29590	2.81	6.2E-02	AL161572.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 68

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4304	17043		1.02	6.2E-02	AF271235.1	NT	Rattus norvegicus differentiation-associated Na-dependent inorganic phosphate cotransporter (DNPI) mRNA, complete cds
4542	17277		6.31	6.2E-02	Q62191	SWISSPROT	52 KD RO PROTEIN (SJOGREN SYNDROME TYPE A ANTIGEN (SS-A)) (RO(SS-A)) (RO52)
6698	19615	32656	0.65	6.2E-02	D49530.1	NT	Spirulina platensis DNA for adenylate cyclase, complete cds
7527	20198	33292	1.03	6.2E-02	U41453.1	NT	Rattus norvegicus PKC binding protein and substrate mRNA, complete cds
8846	25429		0.6	6.2E-02	M61101.1	NT	Porcine group C rotavirus (strain Cowden) outer membrane protein (VP7) mRNA, complete cds
9243	21922	35092	0.52	6.2E-02	AA778450.1	EST_HUMAN	af20a06.31 Soares, total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:1032178 3'
9380	22042	35214	1.65	6.2E-02		NT	Mus musculus stromal cell derived factor receptor 2 (Sdf2), mRNA
11095	23765	37039	1.56	6.2E-02	AF217490.1	NT	Homo sapiens fragile 16D oxido reductase (FOR) gene, exons 8, 9, and partial cds
11320	24011	37315	1.53	6.2E-02	AJ242735.1	NT	Metarhizium anisopliae mRNA for Chymotrypsin (chyt) gene
11865	24449	37791	1.74	6.2E-02	AF200359.1	NT	Rattus norvegicus UDP-glucose glycoprotein:glucosyltransferase precursor (Uggt) mRNA, complete cds
11869	25405		13.39	6.2E-02	AE000750.1	NT	Aquifex aeolicus section 82 of 109 of the complete genome
12394	24782	31037	2.5	6.2E-02	BF112039.1	EST_HUMAN	7137f08.x1 Soares, NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3523815 3' similar to
249	13058	25697	5.59	6.1E-02	D16471.1	NT	TR-Q9Y4S6 Q9Y4S6 HYPOTHETICAL_30.3 KD PROTEIN, [1]; Human mRNA, Xq terminal portion
3972	16721		2.29	6.1E-02	U73325.1	NT	Arabidopsis thaliana K+ inward rectifying channel protein (AKC1) gene, complete cds
6023	18803		1.4	6.1E-02	4507070	NT	Homo sapiens SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 3 (SMARCA3) mRNA
8161	20855	33986	3.75	6.1E-02	X99268.1	NT	H. sapiens mRNA for BHLH DNA binding protein
8559	21251	34388	0.57	6.1E-02	BE971853.1	EST_HUMAN	607651086RT NIH_MGC_81 Homo sapiens cDNA clone IMAGE:3934604 3'
8559	21251	34389	0.57	6.1E-02	BE971853.1	EST_HUMAN	607651086RT NIH_MGC_81 Homo sapiens cDNA clone IMAGE:3934604 3'
10630	23323	36560	4.91	6.1E-02	BE179543.1	EST_HUMAN	IL3-HT0618-110500-136-C06 HT0618 Homo sapiens cDNA
11862	24446	37767	1.27	6.1E-02	AB025333.1	NT	Epitretus burgeri mRNA for RNA polymerase III largest subunit, partial cds
11945	25323		2.27	6.1E-02	X70969.1	NT	S. japonicum mRNA for serine-enzyme
12933	24933		5.61	6.1E-02	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C007
96	12922	25559	0.76	6.0E-02	AA188730.1	EST_HUMAN	zp78c04.r1 Stratagene HeLa cell s3 937216 Homo sapiens cDNA clone IMAGE:626310 5'
96	12922	25560	0.76	6.0E-02	AA188730.1	EST_HUMAN	zp78c04.r1 Stratagene HeLa cell s3 937216 Homo sapiens cDNA clone IMAGE:626310 5'
1239	13988	26655	1.54	6.0E-02	AE001777.1	NT	Thermotoga maritima section 88 of 136 of the complete genome
2882	15391	28130	1.09	6.0E-02	AW968948.1	EST_HUMAN	EST380924 MAGC resequences, MAGJ Homo sapiens cDNA
2775	15480		1.82	6.0E-02	AB031289.1	NT	Mesocricetus cori mitochondrial DNA, NADH dehydrogenase subunit 4, tRNA-Gln, tRNA-Phe, tRNA-Met, ATPase subunit 6, and NADH dehydrogenase subunit 2
2937	12922	25559	0.9	6.0E-02	AA188730.1	EST_HUMAN	zp78c04.r1 Stratagene HeLa cell s3 937216 Homo sapiens cDNA clone IMAGE:626310 5'
2937	12922	25560	0.9	6.0E-02	AA188730.1	EST_HUMAN	zp78c04.r1 Stratagene HeLa cell s3 937216 Homo sapiens cDNA clone IMAGE:626310 5'

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Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3223	15986	28639	1.48	6.0E-02	AA372376.1	EST_HUMAN	EST84266 Cdon adenocarcinoma IV Homo sapiens cDNA 5' end similar to tissue-specific protein
3223	15986	28640	1.48	6.0E-02	AA372376.1	EST_HUMAN	EST84266 Cdon adenocarcinoma IV Homo sapiens cDNA 5' end similar to tissue-specific protein
3625	16378		0.72	6.0E-02	BE664443.2	EST_HUMAN	601658150R1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3876060 3'
5037	17756	30370	0.69	6.0E-02	AF148738.1	NT	Rattus norvegicus testis specific protein mRNA, complete cds
5313	18117		0.94	6.0E-02	AW370211.1	EST_HUMAN	RC3-BT0253-011199-013-b04 BT0253 Homo sapiens cDNA
6122	18900	31868	0.77	6.0E-02	AI807537.1	EST_HUMAN	wf48h05.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2358873 3' similar to contains L1.1 L1 L1 repetitive element;
6891	17987	30524	3.07	6.0E-02	5174698	NT	Homo sapiens stimulated trans-acting factor (50 kDa) (STAF50) mRNA
6891	17987	30525	3.07	6.0E-02	5174698	NT	Homo sapiens stimulated trans-acting factor (50 kDa) (STAF50) mRNA
7088	19777	32842	2.33	6.0E-02	BF382349.1	EST_HUMAN	601815274F2 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4049226 5'
7580	20249	33355	2.13	6.0E-02	AI204275.1	EST_HUMAN	qf5b008.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1754199 3'
8321	21014		0.54	6.0E-02	11468495	NT	Recinomonas americana mitochondrion, complete genome
9172	21842	35007	1.17	6.0E-02	AI623167.1	EST_HUMAN	ts78a06.x1 NCI_CGAP_G06 Homo sapiens cDNA clone IMAGE:2237362 3'
9172	21842	35008	1.17	6.0E-02	AI623167.1	EST_HUMAN	ts78a06.x1 NCI_CGAP_G06 Homo sapiens cDNA clone IMAGE:2237362 3'
9306	21973	35147	1.66	6.0E-02	AJ245365.1	NT	Acipenser baeri partial GLV gene for Immunoglobulin light chain variable region, exons 1-2
9306	21973	35148	1.66	6.0E-02	AJ245365.1	NT	Acipenser baeri partial GLV gene for Immunoglobulin light chain variable region, exons 1-2
9805	22456	35659	0.5	6.0E-02	AA309797.1	EST_HUMAN	EST180654 Jurkat T-cells V Homo sapiens cDNA 5' end similar to similar to heat shock protein 1, 60 kDa-like
9805	22456	35660	0.5	6.0E-02	AA309797.1	EST_HUMAN	EST180654 Jurkat T-cells V Homo sapiens cDNA 5' end similar to similar to heat shock protein 1, 60 kDa-like
11306	23965		1.69	6.0E-02	AA128386.1	EST_HUMAN	zn87c08.r1 Stragene lung carcinoma 937218 Homo sapiens cDNA clone IMAGE:565166 5' similar to gb:X89781.60S RIBOSOMAL PROTEIN L31 (HUMAN);
12187	24658	31064	2.19	6.0E-02	11431702	NT	Homo sapiens DNA-dependent protein kinase catalytic subunit-interacting protein 2 (KIP2), mRNA
12564	24894		2.31	6.0E-02	AI809273.1	EST_HUMAN	wf69h03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2360885 3' similar to TR:O60298
223	13035	25871	3.87	5.9E-02	AW934719.1	EST_HUMAN	O60298 KIAA0551 PROTEIN;
2982	15748	28396	2.89	5.9E-02	AF190269.1	NT	RC1-DT0001-290100-012-010 DT0001 Homo sapiens cDNA
4817	17548	30173	1	5.9E-02	AF006304.1	NT	Mus musculus p53 tumor suppressor gene, exon 10 and 11, partial cds; alternatively spliced
5123	17841	30457	0.73	5.9E-02	AW028748.1	EST_HUMAN	Saccharomyces cerevisiae protein tyrosine phosphatase (PTP3) gene, complete cds
5123	17841	30458	0.73	5.9E-02	AW028748.1	EST_HUMAN	wv34e02.x1 NCI_CGAP_Ov18 Homo sapiens cDNA clone IMAGE:2531450 3' similar to TR:O65386
8515	21207	34350	1.68	5.9E-02	9055249	NT	O65386 F12F1.20 PROTEIN;
9351	20422		0.8	5.9E-02	BF242748.1	EST_HUMAN	wv34e02.x1 NCI_CGAP_Ov18 Homo sapiens cDNA clone IMAGE:2531450 3' similar to TR:O65386
							O65386 F12F1.20 PROTEIN;
							Mus musculus trophoblast related homeobox 5 (Drosophila) (hx5), mRNA
							Mus musculus trophoblast related homeobox 5 (Drosophila) (hx5), mRNA
							601877608F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4105894 5'

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Table 4

Single Exon Probes Expressed In Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10885	23376		3.2	5.9E-02	6679870	NT	Mus musculus follistatin-like (Fstl), mRNA
10844	23623	36872	1.44	5.9E-02	11433356	NT	Homo sapiens nirein (LOC51199), mRNA
11544	24144		1.59	5.9E-02	AJ240733.1	NT	Gallus gallus HKO9 telomere junction
912	13679		5.18	5.8E-02	D90110.1	NT	Thiobacillus ferrooxidans merC, merA genes and URF-1
2864	15632		0.96	5.8E-02	AJ223621.1	NT	Populus trichocarpa CCoAOMT1 gene, exon 1 to exon 5
4322	17061	29687	4.9	5.8E-02	AW051927.1	EST_HUMAN	wx24c02.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2544578 3'
4322	17061	29688	4.9	5.8E-02	AW051927.1	EST_HUMAN	wx24c02.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2544578 3'
4510	17245	29879	4.95	5.8E-02	AI247505.1	EST_HUMAN	qh56f01.x1 Soares_fetal_liver_spleen_1NLS_S1 Homo sapiens cDNA clone IMAGE:1848697 3' similar to gb:U13142 COAGULATION FACTOR XI PRECURSOR (HUMAN);
4510	17245	29880	4.95	5.8E-02	AI247505.1	EST_HUMAN	qh56f01.x1 Soares_fetal_liver_spleen_1NLS_S1 Homo sapiens cDNA clone IMAGE:1848697 3' similar to gb:U13142 COAGULATION FACTOR XI PRECURSOR (HUMAN);
4535	17270		2.62	5.8E-02	AF096284.1	NT	Gallus gallus tyrosine kinase JAK1 (JAK1) mRNA, complete cds
7578	20247	33352	2.99	5.8E-02	M99150.1	NT	Human polymorphic microsatellite DNA
7578	20247	33353	2.99	5.8E-02	M99150.1	NT	Human polymorphic microsatellite DNA
8565	21257	34394	0.87	5.8E-02	AL163283.2	NT	Homo sapiens chromosome 21 segment HS21C083
12084	24590		1.79	5.8E-02	AF220177.1	NT	Drosophila melanogaster male fruitless type-A (fru) mRNA, complete cds
12373	25396		7.06	5.8E-02	AA604289.1	EST_HUMAN	nc75e11.s1 NCI_CGAP_AA1 Homo sapiens cDNA clone IMAGE:1112684 3'
3053	15819	28463	1.36	5.7E-02	AI081644.1	EST_HUMAN	ou63b05.s1 NCI_CGAP_B2 Homo sapiens cDNA clone IMAGE:1632465 3' similar to WP:C37A2.2 CE08611
3068	15834	28478	1.29	5.7E-02	AF119117.1	NT	Homo sapiens dopamine transporter (SLC6A3) gene, complete cds
3694	18448		0.97	5.7E-02	AF001292.1	NT	Chironomus thummi thummi globin VIIA.1 (ctt-7A.1), globin 9.1 (ctt-9.1), globin II-beta (ctt-2beta), non-functional globin XIII (ctt-13R1), globin XII (ctt-12) and globin XI (ctt-11) genes, complete cds
3783	16535	29173	2.45	5.7E-02	AW968791.1	EST_HUMAN	EST378865 MAGE resequences, MAGI Homo sapiens cDNA
4637	17371		1.01	5.7E-02	M95099.1	NT	Bos taurus lysozyme gene (cow 3), complete cds
7438	20115	33203	0.69	5.7E-02	D78003.1	NT	Xenopus laevis mRNA for fourth component of complement, complete cds
7438	20115	33204	0.69	5.7E-02	D78003.1	NT	Xenopus laevis mRNA for fourth component of complement, complete cds
8055	20749	33880	1.42	5.7E-02	AJ286090.1	NT	Rattus norvegicus mRNA for potassium channel, alpha subunit (kv9.2 gene)
9750	22401	35606	0.64	5.7E-02	6681260	NT	Mus musculus ec2 oncogene (Ec2), mRNA
11143	23810	37090	4.42	5.7E-02	AI752685.1	EST_HUMAN	cn18b09.y1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC_cn18b09 random
11143	23810	37091	4.42	5.7E-02	AI752685.1	EST_HUMAN	cn18b09.y1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC_cn18b09 random
11321	24012		1.59	5.7E-02	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
12285	25213		7.24	5.7E-02	D50320.1	NT	Pig DNA for SPAI-2, complete cds

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Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12515	25283		3.18	5.7E-02	AF217490.1	NT	Homo sapiens fragile 18D oxido reductase (FOR) gene, exons 8, 9, and partial cds
12650	25387		2.61	5.7E-02	AF281280.1	NT	Pan troglodytes apolipoprotein-E gene, complete cds
1518	14265	28951	1.57	5.6E-02	AF094455.1	NT	Hydrocotyle rotundifolia ribosomal protein L16 (rpl16) gene, intron; chloroplast gene for chloroplast product
4595	17330	29957	1.12	5.6E-02	AB013100.1	NT	Lycopersicon esculentum LE-ACS6 mRNA for 1-aminocyclopropane-1-carboxylate synthase, complete cds
4648	17382	30014	1.46	5.6E-02	AA290599.1	EST_HUMAN	Zs45c01.s1 NCI CGAP_GCB1 Homo sapiens cDNA clone IMAGE:700476 3'
6562	19327	32334	6.57	5.6E-02	AW172708.1	EST_HUMAN	xi02c10.x1 NCI CGAP_U12 Homo sapiens cDNA clone IMAGE:2660050 3' similar to TR:O94979 O94979 KIAA0905 PROTEIN. ;
6791	19535	32563	1.25	5.6E-02	AA866182.1	EST_HUMAN	od47f1.2.s1 NCI CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1371119 3' similar to contains Alu repetitive element; contains element L1 repetitive element ;
7051	19742	32804	3.05	5.6E-02	BE008001.1	EST_HUMAN	QV0-BN0147-290400-214-g07 BN0147 Homo sapiens cDNA
7063	19754	32819	0.69	5.6E-02	A1983738.1	EST_HUMAN	w234f05.x1 NCI CGAP_Bn53 Homo sapiens cDNA clone IMAGE:2559969 3' similar to gb:X08409 RAF PROTO-ONCOGENE SERINE/THREONINE-PROTEIN KINASE (HUMAN);
7725	20388	33502	0.66	5.6E-02	A1153583.1	EST_HUMAN	qd64g1.1.x1 Scarsa testis_NHT Homo sapiens cDNA clone IMAGE:1734308 3'
8701	21393	34539	2.88	5.6E-02	BE542663.1	EST_HUMAN	601067158F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3453279 5'
8701	21393	34540	2.88	5.6E-02	BE542663.1	EST_HUMAN	601067158F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3453279 5'
9712	22363	35561	1.09	5.6E-02	AA482864.1	EST_HUMAN	rf49d07.s1 NCI CGAP_Alv1 Homo sapiens cDNA clone IMAGE:923245 similar to TR:G769859 G769859 LAMINA ASSOCIATED POLYPEPTIDE 1C. ;
11556	24155		2.35	5.6E-02	AF260225.1	NT	Homo sapiens TESTIN 2 and TESTIN 3 genes, complete cds, alternatively spliced
2660	15370	28108	6.8	5.5E-02	X97869.1	NT	H.sapiens gene encoding La autoantigen
3209	15972	28625	3.93	5.5E-02	6755501	NT	Mus musculus SH3 domain protein 1B (Sh3d1B), mRNA
4191	16932	29561	1	5.5E-02	L41561.1	NT	Gallid herpesvirus mRNA fragment
5573	18370	31281	3.05	5.5E-02	Q01174	SWISSPROT	TROPOMYOSIN ALPHA CHAIN, NON MUSCLE
5935	18370	31281	3.58	5.5E-02	Q01174	SWISSPROT	TROPOMYOSIN ALPHA CHAIN, NON MUSCLE
7277	19961	33038	2	5.5E-02	6755902	NT	Mus musculus tufelin 1 (Tuf1), mRNA
8019	20714	33845	0.63	5.5E-02	AF170911.1	NT	Homo sapiens sodium-dependent vitamin C transporter 1 (SVCT1), mRNA, complete cds
8019	20714	33846	0.63	5.5E-02	AF170911.1	NT	Homo sapiens sodium-dependent vitamin C transporter 1 (SVCT1), mRNA, complete cds
9555	22208	35392	0.6	5.5E-02	10947034	NT	Homo sapiens eIF4E-transpore (4E-T), mRNA
9555	22208	35393	0.6	5.5E-02	10947034	NT	Homo sapiens eIF4E-transpore (4E-T), mRNA
9650	22302	35497	1.32	5.5E-02	U69492.1	NT	Mus musculus second L11 receptor alpha chain (L11Ra2) gene, exons 1 and 2
10943	23622	36871	7.26	5.5E-02	U09771.1	NT	Citrobacter freundii DSM 30040 cyclopropane fatty acid synthase (cfa) gene, partial cds, dihydroxyacetone kinase (dhak), glycerol dehydrogenase (dhad), transcriptional activator (dhaR), 1,3-propanediol dehydrogenase (dhaT), glycerol dehydratase (dhaB), >

Table 4

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12797	25349	30604	1.49	5.5E-02	11421332	NT	Homo sapiens hypothetical protein SIRP-b2 (SIRP-b2), mRNA
3019	15785		0.91	5.4E-02	AJ277488.1	NT	Onyza sativa rib3-1 gene for putative Bowman Birk trypsin inhibitor
3416	17885		5.78	5.4E-02	BE073468.1	EST_HUMAN	RC5-BT0559-140200-012-C03 BT0559 Homo sapiens cDNA
3891	16641	29281	0.76	5.4E-02	U85806.1	NT	Hirudo medicinalis SNAP-25 homolog mRNA, complete cds
8024	20719		0.88	5.4E-02	Z99116.1	NT	Bacillus subtilis complete genome (section 13 of 21); from 2395281 to 2613730
8969	21659	34809	0.55	5.4E-02	AF260225.1	NT	Homo sapiens TESTIN 2 and TESTIN 3 genes, complete cds, alternatively spliced
10537	23234	36467	1.62	5.4E-02	AU120889.1	EST_HUMAN	AU120889 HEMBB1 Homo sapiens cDNA clone HEMBB1001630 5'
10598	23292	36530	2.01	5.4E-02	U20790.1	NT	Neurospora crassa ubiquinol-cytochrome c oxidoreductase subunit VIII (QCR8) mRNA, complete cds
11132	23800	37076	1.32	5.4E-02	BF371289.1	EST_HUMAN	RC6-FN0112-190700-021-D06 FN0112 Homo sapiens cDNA
11132	23800	37077	1.32	5.4E-02	BF371289.1	EST_HUMAN	RC6-FN0112-190700-021-D06 FN0112 Homo sapiens cDNA
1031	13791	26450	1.28	5.3E-02	AW391248.1	EST_HUMAN	QV0-ST0213-021239-062-409 ST0213 Homo sapiens cDNA
1031	13791	26451	1.28	5.3E-02	AW391248.1	EST_HUMAN	QV0-ST0213-021239-062-409 ST0213 Homo sapiens cDNA
1495	14242	26929	14.72	5.3E-02	T94759.1	EST_HUMAN	y63712.11 Stratagene lung (#637210) Homo sapiens cDNA clone IMAGE:119861 5' similar to gb:K01506
2501	15218	27961	2.47	5.3E-02	AJ276408.1	NT	HLA CLASS II HISTOCOMPATIBILITY ANTIGEN, DP(1) ALPHA CHAIN (HUMAN);
2943	15709	28360	0.95	5.3E-02	M58417.1	NT	Pseudomonas putida tlgS gene
2943	15709	28361	0.95	5.3E-02	M58417.1	NT	Drosophila melanogaster laminin B2 gene, complete cds
3150	15913	28558	5.51	5.3E-02	AJ276408.1	NT	Drosophila melanogaster laminin B2 gene, complete cds
5029	17749	30361	6.34	5.3E-02	M80483.1	NT	Pseudomonas putida tlgS gene
5236	18042	30670	1.98	5.3E-02	AE000527.1	NT	Mus musculus caudal type homeobox-1 (Cdx-1) gene, complete cds
5236	18042	30671	1.98	5.3E-02	AE000527.1	NT	Helicobacter pylori 26695 section 5 of 134 of the complete genome
6785	19529	32556	5.01	5.3E-02	9695413	NT	Helicobacter pylori 26695 section 5 of 134 of the complete genome
6992	19885	32733	1	5.3E-02	U32832.1	NT	Lymphocystis disease virus 1, complete genome
7260	19944		2.06	5.3E-02	S78221.1	NT	Haemophilus influenzae Rd section 147 of 163 of the complete genome
7777	20399	33514	0.65	5.3E-02	P38742	SWISSPROT	nuclear protein TIF1 isoform [mice, mRNA, 4053 nt]
8304	20998		0.7	5.3E-02	U10098.1	NT	HYPOTHETICAL 130.0 KD PROTEIN IN SNF5-SPO11 INTERGENIC REGION
9023	21713	34867	1.56	5.3E-02	X03127.1	NT	Mus musculus 129/Sv cystatin C (csf3) gene, complete cds
10032	22880	35897	0.62	5.3E-02	AB022605.1	NT	Podospora anserina mitochondrial epsilon-sen DNA
10032	22880	35898	0.62	5.3E-02	AB022605.1	NT	Homo sapiens hCMT1b mRNA for mRNA (guanine-7-methyltransferase, complete cds
10156	22804		0.63	5.3E-02	Y07907.1	NT	Homo sapiens hCMT1b mRNA for mRNA (guanine-7-methyltransferase, complete cds
10230	22878	36090	0.7	5.3E-02	X68432.1	NT	D. rerio mRNA for zp-23 POU gene, splice variant (neurula, 9-16 hpf and postmitogenesis, 20-28 hpf)
						NT	B. rerio pou3c mRNA for transcription factor

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12778	25030	30984	1.43	5.3E-02	AF276815.1	NT	Branchiostoma floridae homeodomain-containing protein Hox13 (Hox13) gene, exon 2 and partial cds
2283	15008		180.56	5.2E-02	5031908	NT	Homo sapiens meprin A, alpha (PABA peptide hydrolase) (MEP1A) mRNA
3112	15877	28518	2.34	5.2E-02	AJ277661.1	NT	Homo sapiens partial LMO1 gene for LIM domain only 1 protein, exon 1
3112	15877	28517	2.34	5.2E-02	AJ277661.1	NT	Homo sapiens partial LMO1 gene for LIM domain only 1 protein, exon 1
3919	16669	29310	1.23	5.2E-02	AF236101.1	NT	Arabidopsis thaliana putative dicarboxylate diiron protein (Crd1) mRNA, complete cds
3921	16671		1.19	5.2E-02	6871757	NT	Mus musculus cytokine inducible SH2-containing protein 3 (Cish3), mRNA
4245	16998	29609	3.02	5.2E-02	U07132.1	NT	Human steroid hormone receptor Ner-1 mRNA, complete cds
6053	17772		0.9	5.2E-02	AA297940.1	EST_HUMAN	EST11352 Uterus Homo sapiens cDNA 5' and
5828	18617	31548	0.61	5.2E-02	U14731.1	NT	Saccharomyces cerevisiae Cdc54p (CDC54) gene, complete cds
6016	18797		0.96	5.2E-02	AI830985.1	EST_HUMAN	wj80s04.x1 NCI_CGAP_Lym12 Homo sapiens cDNA clone IMAGE:2409150 3' similar to contains MER15.b1 MER15 repetitive element:
7174	19880	32932	3.13	5.2E-02	P36322	SWISSPROT	DNA POLYMERASE PROCESSIVITY FACTOR (POLYMERASE ACCESSORY PROTEIN) (PAP) (DNA-BINDING GENE 18 PROTEIN)
8095	20789		2.19	5.2E-02	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
9629	22282	35472	1.87	5.2E-02	D10927.1	NT	Turnip mosaic virus genomic RNA for Capsid protein, complete cds
9629	22282	35473	1.87	5.2E-02	D10927.1	NT	Turnip mosaic virus genomic RNA for Capsid protein, complete cds
12414	24795		1.93	5.2E-02	D03030	SWISSPROT	OXALOACETATE DECARBOXYLASE ALPHA CHAIN
2364	15086		1.17	5.1E-02	AL134071.1	EST_HUMAN	DKFZp547D073 t1 547 (synonym: hibr1) Homo sapiens cDNA clone DKFZp547D073 5'
4179	16918	29547	1.03	5.1E-02	AE001301.1	NT	Chlamydia trachomatis section 28 of 87 of the complete genome
4690	17685		49.38	5.1E-02	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
6575	19339	32350	0.72	5.1E-02	AF280369.1	NT	HIV-1 patient 98 from Italy protease (pol) gene, complete cds
6760	17929	30564	1.44	5.1E-02	BF378625.1	EST_HUMAN	QV0-UM0051-250800-350-b08 UM0051 Homo sapiens cDNA
8151	20845	33975	0.84	5.1E-02	M26434.1	NT	Human hypoxanthine phosphoribosyltransferase (HPRT) gene, complete cds
8151	20845	33978	0.84	5.1E-02	M26434.1	NT	Human hypoxanthine phosphoribosyltransferase (HPRT) gene, complete cds
8245	20839	34078	1.48	5.1E-02	AJ131988.1	NT	Spodoptera littoralis mRNA for 3-dehydrodysone 3beta-reductase
8783	21475	34622	0.98	5.1E-02	P02533	SWISSPROT	KERATIN, TYPE I CYTOSKELETAL 14 (CYTOKERATIN 14) (K14) (CK 14)
8783	21475	34623	0.98	5.1E-02	P02533	SWISSPROT	KERATIN, TYPE I CYTOSKELETAL 14 (CYTOKERATIN 14) (K14) (CK 14)
9709	22360	35558	6.2	5.1E-02	AF012898.1	NT	Candida albicans protein phosphatase Ssd1 homolog (SSD1) gene, complete cds
10082	22730	35945	1.89	5.1E-02	AF012898.1	SWISSPROT	ANTER-SPECIFIC PROLINE-RICH PROTEIN APG (PROTEIN CEX)
10733	23420	36661	2.44	5.1E-02	AF083930.1	NT	Homo sapiens ES18 mRNA, partial cds
10733	23420	36662	2.44	5.1E-02	AF083930.1	NT	Homo sapiens ES18 mRNA, partial cds
11620	24217	37540	1.3	5.1E-02	AL139078.2	NT	Campylobacter jejuni NCTC11168 complete genome; segment 3/6
12421	24797		2.96	5.1E-02	AF062467.1	NT	Cucumis melo polygalacturonase precursor (MPC3) mRNA, complete cds

Table 4

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12879	24968		1.41	5.1E-02	AA534104.1	EST_HUMAN	n73102.s1 NCL CGAP_P110 Homo sapiens cDNA clone IMAGE:898139
470	13258	25884	1.84	5.0E-02	AF098004.1	NT	Mus musculus fatty acid amide hydrolase gene, exon 10
1182	13834	26699	6.54	5.0E-02	Z99104.1	NT	Bacillus subtilis complete genome (section 1 of 21): from 1 to 213080
1983	14719	27438	3.91	5.0E-02	P02810	SWISSPROT	SALIVARY ACIDIC PROLINE-RICH PHOSPHOPROTEIN 1/2 PRECURSOR (PRP-1/PRP-3) (PRP-2/PRP-4) (PIF-F/PIF-S) (PROTEIN APROTEIN C) [CONTAINS: PEPTIDE P-C]
2821	13731	26397	1.28	5.0E-02	U72742.1	NT	Oryctolagus cuniculus UDP-glucuronosyltransferase (UGT2B13) mRNA, complete cds
3332	16092		1.42	5.0E-02	7305610	NT	Mus musculus Ubc-51 like kinase 2 (C. elegans) (Ulk2), mRNA
3582	16337		1.04	5.0E-02	U32782.1	NT	Haemophilus influenzae Rd section 97 of 163 of the complete genome
3672	16425	28068	5.83	5.0E-02	U12769.2	NT	Anthrax pernyi period clock protein homolog mRNA, complete cds
4770	17502		0.99	5.0E-02	P40232	SWISSPROT	CASEIN KINASE II BETA CHAIN (CK II)
6039	18819	31780	0.95	5.0E-02	AF068264.1	NT	Gallus gallus tyrosine kinase JAK1 (JAK1) mRNA, complete cds
6216	18990		1.3	5.0E-02	AJ242625.1	NT	Mus musculus Dmp-1 gene, exons 1-6
7437	20114	33202	12.48	5.0E-02	P35616	SWISSPROT	NEUROFILAMENT TRIPLET L PROTEIN (NEUROFILAMENT LIGHT POLYPEPTIDE) (NFL)
10100	22748	35963	1.28	5.0E-02	AF305238.1	NT	Mus musculus Fas-interacting serine/threonine kinase 3 (Fist3) mRNA, complete cds
10521	23167		0.45	5.0E-02	BF213260.1	EST_HUMAN	601844753F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4070101 5'
11473	24074	37383	2.5	5.0E-02	U67600.1	NT	Methanococcus jannaschii section 142 of 150 of the complete genome
11956	25246		3.5	5.0E-02	Q04047	SWISSPROT	NO-ON-TRANSIENT A PROTEIN
217	13028		24.03	4.9E-02	M14230.1	NT	Chicken 28-kDa vitamin D-dependent calcium-binding protein (CaBP-28) mRNA, complete cds
360	13158	25800	2.66	4.9E-02	AF275948.1	NT	Homo sapiens ABCA1 (ABCA1) gene, complete cds
360	13158	25801	2.66	4.9E-02	AF275948.1	NT	Homo sapiens ABCA1 (ABCA1) gene, complete cds
3282	16043	28692	2.53	4.9E-02	P54258	SWISSPROT	ATROPHIN-1 (DENTATORUBRAL-PALLIDOLYSIAN ATROPHY PROTEIN)
3556	16311		0.69	4.9E-02	AA189940.1	EST_HUMAN	zq48a12.s1 Stratagene hNT neuron (#937233) Homo sapiens cDNA clone IMAGE:632928 3' similar to contains: Alu repetitive element/contains element MSR1 repetitive element
3579	16334	28978	0.99	4.9E-02	AA400914.1	EST_HUMAN	z78a03.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:728428 3'
3576	16334	28979	0.99	4.9E-02	AA400914.1	EST_HUMAN	z78a03.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:728428 3'
4788	17519	30141	1.91	4.9E-02	AW167821.1	EST_HUMAN	xg56g10.x1 NCL CGAP_U14 Homo sapiens cDNA clone IMAGE:2632386 3'
4788	17519	30142	1.91	4.9E-02	AW167821.1	EST_HUMAN	xg56g10.x1 NCL CGAP_U14 Homo sapiens cDNA clone IMAGE:2632386 3'
5286	18091	30751	1.9	4.9E-02	L00122.1	NT	Rat elastase II gene, exon 6
5286	18091	30752	1.9	4.9E-02	L00122.1	NT	Rat elastase II gene, exon 6
7042	19733	32793	0.91	4.9E-02	AE000980.1	NT	Archaeoglobus fulgidus section 127 of 172 of the complete genome
8513	21205		0.8	4.9E-02	AE002309.1	NT	Chlamydia muridarum, section 40 of 85 of the complete genome
8652	21344	34489	0.71	4.9E-02	AL161559.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 59
10191	22839	36054	0.48	4.9E-02	P19532	SWISSPROT	TRANSCRIPTION FACTOR E3
10494	23140	36366	0.46	4.9E-02	AL163218.2	NT	Homo sapiens chromosome 21 segment HS21C018

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Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLASTE Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11378	23985	37285	3.22	4.9E-02	AF008303.1	NT	Homo sapiens prepro placental TGF-beta gene, complete cds
12345	24752		1.77	4.9E-02	8923880	NT	Homo sapiens CS box-containing WD protein (LOC55884), mRNA
12598	24912		3.41	4.9E-02	M18364.1	NT	Human gamma-B-crystallin (gamma 1-2) and gamma-C-crystallin (gamma 2-1) genes, complete cds
321	13123	25760	1.54	4.8E-02	D16471.1	NT	Human mRNA, Xq terminal portion
322	13123	25760	3.94	4.8E-02	D16471.1	NT	Human mRNA, Xq terminal portion
476	13262	25899	9.96	4.8E-02	AF003100.1	NT	Arabidopsis thaliana AP2 domain containing protein RAP2.7 mRNA, partial cds
2271	14997	27735	1.82	4.8E-02	W51983.1	EST_HUMAN	zc49b02.s1 Soares, senescent, fibroblasts NBHSF Homo sapiens cDNA clone IMAGE:325811 3' similar to
3203	15966	28620	2.1	4.8E-02	X17144.1	NT	gb-M30938 LUPUS KU AUTOANTIGEN PROTEIN P86 (HUMAN);
4623	17358		1.15	4.8E-02	Z64280.1	NT	Tetrahymena rosstrata histone H3II and histone H4II intergenic DNA
5144	17863	30478	1.03	4.8E-02	11693131	NT	S. scrofa gene for skeletal muscle ryanodine receptor
5144	17863	30479	1.03	4.8E-02	11693131	NT	Homo sapiens DKFZP434D222 protein (RENT2), mRNA
8037	20732	33864	1.32	4.8E-02	AW388497.1	EST_HUMAN	Homo sapiens DKFZP434D222 protein (RENT2), mRNA
9027	21717	34870	0.95	4.8E-02	AJ001398.1	NT	MR2-ST0128-221098-012-b02 ST0128 Homo sapiens cDNA
9027	21717	34871	0.95	4.8E-02	AJ001398.1	NT	Fugu rubripes rps24 gene
6731	19565	32597	3.83	4.7E-02	W01153.1	EST_HUMAN	Fugu rubripes rps24 gene
6819	19480	32503	2.02	4.7E-02	M62752.1	NT	yz97f08.r1 Soares melanocyte 2NBHM Homo sapiens cDNA clone IMAGE:291017 5' similar to contains Alu
8149	20843	33973	8.24	4.7E-02	X15543.1	NT	Rat statin-related protein (s1) gene, complete CDS
8852	21543	34690	0.96	4.7E-02	X89211.1	NT	B. taurus mRNA for RF-36-DNA-binding protein
8875	21566		2.68	4.7E-02	A8026678.1	NT	H sapiens DNA for endogenous retroviral like element
9127	21815	34981	6.89	4.7E-02	X15543.1	NT	Gallus gallus Wpkl-8 gene, complete cds
9547	22200	35382	0.67	4.7E-02	BF305237.1	EST_HUMAN	B. taurus mRNA for RF-36-DNA-binding protein
9635	22287		0.57	4.7E-02	AI873042.1	EST_HUMAN	601892892F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4138414 5'
10654	23345	36582	1.4	4.7E-02	6754565	NT	w678c10.x1 Soares NFL_T_GBC S1 Homo sapiens cDNA clone IMAGE:2347314 3'
11545	24145	37453	1.39	4.7E-02	U73621.1	NT	Mus musculus ligand of numb-protein X (Lnx), mRNA
11545	24145	37454	1.39	4.7E-02	U73621.1	NT	Bos taurus paired box protein (pax-6) gene, partial cds
264	13072	25712	0.83	4.6E-02	BE153583.1	EST_HUMAN	Bos taurus paired box protein (pax-6) gene, partial cds
722	13496	26149	2.91	4.6E-02	AE000445.1	NT	PMD-HT0339-251169-003-g05 HT0339 Homo sapiens cDNA
1269	14018		0.99	4.6E-02	AI014255.1	EST_HUMAN	Escherichia coli K-12 MG1655 section 335 of 400 of the complete genome
1338	14086	28762	3.47	4.6E-02	AV727059.1	EST_HUMAN	am50d02.s1 Johnston frontal cortex Homo sapiens cDNA clone IMAGE:1638979 3' similar to TR:P90533
							P90533 LIMA, contains element LTR1 repetitive element;
							AV727059 HTC Homo sapiens cDNA clone HTC8WC01 5'

Table 4

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2492	15209	27951	2.31	4.6E-02	AW296023.1	EST_HUMAN	xn24f03.x1 NCL CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2694653 3' similar to SW:GRF1_HUMAN
2811	13072	25712	1.9	4.6E-02	BE153583.1	EST_HUMAN	Q12849 G-RICH SEQUENCE FACTOR-1
3325	15774	28423	0.74	4.6E-02	BE153583.1	EST_HUMAN	PMO-HT0339-251199-003-g05 HT0339 Homo sapiens cDNA
3487	15774	28423	0.73	4.6E-02	BE153583.1	EST_HUMAN	PMO-HT0339-251199-003-g05 HT0339 Homo sapiens cDNA
4103	16846		1.35	4.6E-02	AF220365.1	NT	PMO-HT0339-251199-003-g05 HT0339 Homo sapiens cDNA
							Mus musculus nucleolar RNA helicase I/Gu (ddx21) gene, complete cds
5121	17839	30455	0.99	4.6E-02	AA079157.1	EST_HUMAN	zm92c10.s1 Stralagene ovarian cancer (#937219) Homo sapiens cDNA clone IMAGE:545394 3' similar to gb:X03212 KERTIN, TYPE II CYTOSKELETAL 7 (HUMAN);
5847	18442	31355	1.57	4.6E-02	AF078962.1	NT	Heplochromis burtoni gonadotropin-releasing hormone and GnRH-associated peptide precursor (GnRH2)
6136	18914	31883	3.51	4.6E-02	X61624.1	NT	gene, complete cds
6136	18914	31884	3.51	4.6E-02	X61624.1	NT	C.reinhardtii atp2 (atpB) mRNA
6702	19617	32659	1.47	4.6E-02	AI149574.1	EST_HUMAN	C.reinhardtii atp2 (atpB) mRNA
8554	21246	34386	2.69	4.6E-02	BE154006.1	EST_HUMAN	qc60b06.x1 Scores_placenta_80cweeks_2NbhHP80cW Homo sapiens cDNA clone IMAGE:1713971 3' similar to contains L1.13 L1 repetitive element;
11379	23986	37286	4.94	4.6E-02	AA913328.1	EST_HUMAN	PMO-HT0339-060400-005-G12 HT0339 Homo sapiens cDNA
12325	24744		1.88	4.6E-02	AV712871.1	EST_HUMAN	o127h09.s1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1524737 3'
12705	24985		3.98	4.6E-02	X57808.1	NT	AV712871 DCA Homo sapiens cDNA clone DCAAZF07 5'
434	13220	25866	1.72	4.5E-02	P22448	SWISSPROT	Human germline immunoglobulin lambda light chain gene
1196	13948	26612	1.11	4.5E-02	AF005730.1	NT	RETINOIC ACID RECEPTOR BETA (RAR-BETA)
1196	13948	26613	1.11	4.5E-02	AF005730.1	NT	Marburg virus strain M/S.Africa/Johannesburg/1975/Ozolin VP35 gene, complete cds
1797	14537	27247	4.57	4.5E-02	P32182	SWISSPROT	Marburg virus strain M/S.Africa/Johannesburg/1975/Ozolin VP35 gene, complete cds
2103	14834	27568	3.76	4.5E-02	AE003964.1	NT	HEPATOCYTE NUCLEAR FACTOR 3-BETA (HNF-3B)
3710	16463	29102	3.86	4.5E-02	AL163278.2	NT	Xyella fastidiosa, section 110 of 229 of the complete genome
							Homo sapiens chromosome 21 segment HS21C078
6137	18915	31885	1.61	4.5E-02	AJ400877.1	NT	Homo sapiens ASCL3 gene, CEGP1 gene, C11orf14 gene, C11orf15 gene, C11orf16 gene and C11orf17 gene
6415	19183	32182	0.77	4.5E-02	AL163280.2	NT	gene
							Homo sapiens chromosome 21 segment HS21C080
6779	19523	32550	0.61	4.5E-02	L26487.1	NT	Methanosarcina frisia carbon monoxide dehydrogenase large subunit (cdh1A) gene; carbon monoxide dehydrogenase small subunit (cdh1B) gene, complete cds
6779	19523	32551	0.61	4.5E-02	L26487.1	NT	Methanosarcina frisia carbon monoxide dehydrogenase large subunit (cdh1A) gene; carbon monoxide dehydrogenase small subunit (cdh1B) gene, complete cds
8292	20986	34125	1.96	4.5E-02	AF036864.1	NT	dehydrogenase small subunit (cdh1B) gene, complete cds
9849	22499	35689	4.57	4.5E-02	AA325216.1	EST_HUMAN	Arabidopsis thaliana CCAAT-box binding factor HAP3 homolog gene, complete cds
10000	22648	35860	0.48	4.5E-02	X95508.1	NT	EST28167 Cerebellum II Homo sapiens cDNA 5' end similar to neuro-D4 protein
							A.europaeum mRNA for legumin-like protein

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
876	13645	26315	1.35	4.2E-02	AW003645.1	EST_HUMAN	wx34q01.x1 NCI_CGAP_P11 Homo sapiens cDNA clone IMAGE:2545684 3' similar to TR:Q63291 Q63291
1714	14457		1.02	4.2E-02	AL445066.1	NT	L1 RETROPOSON, ORF2 MRNA, contains L1.3 L1 L1 repetitive element;
1771	14513	27213	1.01	4.2E-02	P23091	SWISSPROT	Thermoplasma acidophilum complete genome, segment 4/5
3655	16408	29047	2.43	4.2E-02	P23091	SWISSPROT	TRANSFORMING PROTEIN MAF
4100	16843	29471	0.7	4.2E-02	BE262605.1	EST_HUMAN	TRANSFORMING PROTEIN MAF
4284	17023	29648	1.83	4.2E-02	U26674.1	NT	601150933F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3503505 5'
4284	17023	29649	1.83	4.2E-02	U26674.1	NT	Saccharomyces cerevisiae general sporulation (GSG1) gene, complete cds
4695	17429	30060	2.32	4.2E-02	BF342995.1	EST_HUMAN	Saccharomyces cerevisiae general sporulation (GSG1) gene, complete cds
							602017105F1 NCI_CGAP_Bm64 Homo sapiens cDNA clone IMAGE:4152672 5'
5530	18328	31231	0.68	4.2E-02	AF280107.1	NT	Homo sapiens cytochrome P450 polypeptide 43 (CYP3A43) gene, partial cds; cytochrome P450 polypeptide 4 (CYP3A4) and cytochrome P450 polypeptide 7 (CYP3A7) genes, complete cds; and cytochrome P450 polypeptide 5 (CYP3A5) gene, partial cds
5530	18328	31232	0.68	4.2E-02	AF280107.1	NT	Homo sapiens cytochrome P450 polypeptide 43 (CYP3A43) gene, partial cds; cytochrome P450 polypeptide 4 (CYP3A4) and cytochrome P450 polypeptide 7 (CYP3A7) genes, complete cds; and cytochrome P450 polypeptide 5 (CYP3A5) gene, partial cds
6886	17962	30517	0.56	4.2E-02	BE268286.1	EST_HUMAN	601124596F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:2889319 5'
7426	20103	33190	4.7	4.2E-02	AF276752.1	NT	Legionella pneumophila catalase-peroxidase (katA) gene, complete cds
8710	21402	34547	3.96	4.2E-02	P05095	SWISSPROT	ALPHA-ACTININ 3, NON MUSCULAR (F-ACTIN CROSS LINKING PROTEIN)
10064	22712	35630	1.22	4.2E-02	Q16650	SWISSPROT	T-BRAIN-1 PROTEIN (T-BOX BRAIN PROTEIN 1) (TBR-1) (TES-56)
10969	23645	36898	2.82	4.2E-02	AA976118.1	EST_HUMAN	on33b11.s1 NCI_CGAP_Lu6 Homo sapiens cDNA clone IMAGE:1568461 3' similar to gb:M65280
11278	23839	37231	2.54	4.2E-02	BE815822.1	EST_HUMAN	INTERLEUKIN-12 BETA CHAIN PRECURSOR (HUMAN);
11278	23839	37232	2.54	4.2E-02	BE815822.1	EST_HUMAN	PM3-BN0174-250500-009-d10 BN0174 Homo sapiens cDNA
11489	24090	37402	1.68	4.2E-02	AF176458.1	NT	PM3-BN0174-250500-009-d10 BN0174 Homo sapiens cDNA
12415	25335		3.43	4.2E-02	AF883494.1	EST_HUMAN	PRRS isolate PRRSV36 envelope glycoprotein gene, complete cds
497	13281	25016	1.24	4.1E-02	AF200629.1	NT	wf49g10.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2510850 3'
2083	15392	28131	1.04	4.1E-02	AE002330.2	NT	Homo sapiens HPS1 gene, intron 5
4439	17175		7.52	4.1E-02	AE002330.2	NT	Chlamydia muridarum, section 60 of 85 of the complete genome
5556	18353	31262	0.82	4.1E-02	AW893484.1	EST_HUMAN	QV1-NN0012-180400-164-006 NN0012 Homo sapiens cDNA
5556	18353	31263	0.82	4.1E-02	BE251894.1	EST_HUMAN	601107535F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3343856 5'
6783	19527		0.67	4.1E-02	BE251894.1	EST_HUMAN	601107535F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3343856 5'
6999	19691	32742	1.25	4.1E-02	X76881.1	NT	A.thaliana mRNA for plasma membrane intrinsic protein 1a
7413	20090	33174	2.09	4.1E-02	AE002132.1	NT	Ureaplasma urealyticum section 33 of 59 of the complete genome
					7662347	NT	Homo sapiens KIAA0867 protein (KIAA0867), mRNA

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7502	20173	33285	0.66	4.1E-02	L02110.1	NT	Mus musculus proviral retroviral insertion in the cGMP-phosphodiesterase (rd beta PDE) gene, intron 1, with the proviral insert encompassing the env pseudogene (3' end) and 3' LTR
7665	20329	33439	3.12	4.1E-02	AF028198.1	NT	Fugu rubripes neural cell adhesion molecule L1 homolog (L1-CAM) gene, complete cds; putative protein 1 (PUT1) gene, partial cds; mitosis-specific chromosome segregation protein SMC1 homolog (SMC1) gene, complete cds; and calcium channel alpha-1 subunit>
8541	21233	34376	0.68	4.1E-02	P34687	SWISSPROT	CUTICLE COLLAGEN 34
9052	21741	34899	0.81	4.1E-02	AA372398.1	EST_HUMAN	EST84291 Colon adenocarcinoma IV Homo sapiens cDNA 5' end
12728	25336	30715	4.07	4.1E-02	AJ271909.1	NT	Brassica napus glh gene for plastid glutamine synthetase, exons 1-12
3238	19000	28850	3.26	4.0E-02	AB040904.1	NT	Homo sapiens mRNA for KIAA1471 protein, partial cds
3780	16532	29170	1.27	4.0E-02	L11910.1	NT	Human retinoblastoma susceptibility gene exons 1-27, complete cds
5285	18100	30759	5.4	4.0E-02	AF280107.1	NT	Homo sapiens cytochrome P450 polypeptide 43 (CYP3A43) gene, partial cds; cytochrome P450 polypeptide 4 (CYP3A4) and cytochrome P450 polypeptide 7 (CYP3A7) genes, complete cds; and cytochrome P450 polypeptide 5 (CYP3A5) gene, partial cds
6120	18898	31866	0.93	4.0E-02	BF110434.1	EST_HUMAN	Tn52h07 x1 NCL CGAG_Lu24 Homo sapiens cDNA clone IMAGE:3568380 3' similar to TR:O76286 O75298 R29124.1;
7590	20258	33366	6.57	4.0E-02	L23838.1	NT	Strongylocentrotus purpuratus homolog of human bone morphogenetic protein 1 (submp) mRNA, complete cds
7650	20314		0.86	4.0E-02	AL161535.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 35
7666	20330	33440	0.7	4.0E-02	AB000381.1	NT	Homo sapiens DNA for GPI-anchored molecule-like protein, complete cds
7666	20330	33441	0.7	4.0E-02	AB000381.1	NT	Homo sapiens DNA for GPI-anchored molecule-like protein, complete cds
8617	21309	34451	2.22	4.0E-02	P08640	SWISSPROT	GLUCOAMYLASE S1/S2 PRECURSOR (GLUCAN 1,4-ALPHA-GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE)
9544	22197		0.78	4.0E-02	BF679376.1	EST_HUMAN	602153884F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4294724 5'
9567	22220	35408	4.01	4.0E-02	AJ000941.1	NT	Methanobacterium thermoautotrophicum strain Marburg, Thiol:fumarate reductase subunit A
9884	22534		1.21	4.0E-02	D43949.1	NT	Human mRNA for KIAA0082 gene, partial cds
11778	24369		1.54	4.0E-02	AJ001018.1	NT	Kluyveromyces fragilis gene for Cst+ ATPase
12053	25158	30898	3.31	4.0E-02	AJ001058.1	NT	Ovis aries mRNA for acetyl-coA carboxylase
1098	13858	26516	2.75	3.9E-02	BF516149.1	EST_HUMAN	U-H-BW7-ant-h-08-0-JJ st NCL CGAG_Sub7 Homo sapiens cDNA clone IMAGE:3084134 3'
1323	14072	26745	2.45	3.9E-02	P41047	SWISSPROT	FAS ANTIGEN LIGAND
1954	14689	27402	2.4	3.9E-02	AJ403386.1	NT	M.musculus DNA for desmin-binding fragment DesD7
2708	15415		1.69	3.9E-02		NT	Homo sapiens succinate dehydrogenase complex, subunit C, integral membrane protein, 15kD (SDHC) mRNA
4118	18860	29487	0.93	3.9E-02	8924019	NT	Homo sapiens hypothetical protein PRO1163 (PRO1163), mRNA
4118	18860	29488	0.93	3.9E-02	8924019	NT	Homo sapiens hypothetical protein PRO1163 (PRO1163), mRNA

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5408	18207	30913	0.55	3.9E-02	D50608.1	NT	Rat gene for cholecystokinin type-A receptor (CCKAR), complete cds
5408	18207	30914	0.55	3.9E-02	D50608.1	NT	Rat gene for cholecystokinin type-A receptor (CCKAR), complete cds
5644	18439	31353	1.04	3.9E-02	BE68841.1	EST_HUMAN	601849874F1 NIH_MGC_74 Homo sapiens cDNA clone IMAGE:3933642 5'
5766	18557	31484	0.95	3.9E-02	BF675203.1	EST_HUMAN	602138132F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4274910 5'
6957	19439	32454	1.18	3.9E-02	BE271437.1	EST_HUMAN	601140729F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3049830 5'
7739	20435	33557	1.14	3.9E-02	BF239613.1	EST_HUMAN	601808848F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4134779 5'
7959	20654	33778	0.79	3.9E-02	AJ228041.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3
7959	20654	33779	0.79	3.9E-02	AJ228041.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3
11386	20396	33511	2	3.9E-02	P48778	SWISSPROT	ANTIGEN GOR
11913	25288		15.38	3.9E-02	AB042553.1	NT	Felis catus G-CSF gene for granulocyte colony-stimulating factor, complete cds
12543	24883		1.83	3.9E-02	U66061.1	NT	Human gemline T-cell receptor beta chain TCRBV17S1A1T, TCRBV2S1, TCRBV10S1P, TCRBV28S1P, TCRBV14S1P, TCRBV14S1, TCRBV11S1A1T, HVB relic, TCRBV28S1P, TCRBV34S1, TCRBV14S1, TCRBV3S1, TCRBV4S1A1T, TRY4, TRY5, TRY6, TRY7, TRY8, TCRBD1, TCRBJ1S1, TCRBJ1S2, >
12668	25223		5.31	3.9E-02	AL049868.2	NT	Mus musculus chromosome X contigB; X-linked lymphocyte regulated 5 gene, Zinc finger protein 275, Zinc finger protein 92, mrxq28orf
1945	14680	27394	1.16	3.8E-02	BE885137.1	EST_HUMAN	601510891F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3912215 5'
2114	14845		1.77	3.8E-02	AJ261973.1	NT	Homo sapiens partial steath-1 gene
4876	17603	30226	1.1	3.8E-02	AU124122.1	EST_HUMAN	AU124122 NT2RM2 Homo sapiens cDNA clone NT2RM2001688 5'
5354	18157	30840	1	3.8E-02	M11228.1	NT	Human protein C gene, complete cds
5986	18777	31739	1.32	3.8E-02	P10284	SWISSPROT	HOMEOBOX PROTEIN HOX-B4 (HOX-2.6)
7218	19903	32976	1.66	3.8E-02	6005700	NT	Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 8 (ABCA8), mRNA
8562	21254		1.33	3.8E-02	M60675.1	NT	Human von Willebrand factor gene, exons 23 through 34
10549	23245	36481	2.62	3.8E-02	AF143962.2	NT	Homo sapiens PELOTA (PELOTA) gene, complete cds
971	13736	26401	4.94	3.7E-02	P19137	SWISSPROT	LAMININ ALPHA-1 CHAIN PRECURSOR (LAMININ A CHAIN)
1367	14115	26790	0.91	3.7E-02	L14561.1	NT	Homo sapiens plasma membrane calcium ATPase isoform 1 (ATP2B1) gene, alternative splice products, partial cds
2230	14958	27698	3.84	3.7E-02	A1984808.1	EST_HUMAN	wf85a08.x1 NCL_OGAP_Kid11 Homo sapiens cDNA clone IMAGE:2494502 3'
2582	15296	28034	0.92	3.7E-02	AB018261.1	NT	Homo sapiens mRNA for KIAA0718 protein, partial cds
3045	15811	28457	0.9	3.7E-02	P79944	SWISSPROT	ECMESODERMIN
3047	15813	28458	2.99	3.7E-02	BF312963.1	EST_HUMAN	601896233F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4125584 5'
3447	16203		1.17	3.7E-02	6680541	NT	Mus musculus potassium large conductance pH-sensitive channel, subfamily M, alpha member 3 (Kcnma3), mRNA
6978	25422		0.83	3.7E-02	AP000063.1	NT	Aeropyrum pernix genomic DNA, section 617

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Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7592	20260	33368	0.56	3.7E-02	AE003975.1	NT	Xylella fastidiosa, section 121 of 229 of the complete genome
9914	22563		1	3.7E-02	AA782516.1	EST_HUMAN	ai55609.s1 Soares_parrathyroid_tumor_NHHPA Homo sapiens cDNA clone 1360912 3'
11954	24506	37811	3.86	3.7E-02	BF124974.1	EST_HUMAN	601762117F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:4024973 5'
12803	25193	30813	1.94	3.7E-02	11418392	NT	Homo sapiens solute carrier family 22 (organic cation transporter), member 1 (SLC22A1), mRNA
3846	16389	29039	1.38	3.6E-02	X73221.1	NT	H. vulgare Sst1 gene for sucrose synthase
3654	16407	29046	0.88	3.6E-02	AL098806.1	NT	Homo sapiens genomic region containing hypervariable minisatellites chromosome 10(10q26.3) of Homo sapiens
5341	18144	30806	0.58	3.6E-02	X59403.1	NT	C. glutamicum gap, pgk and tpi genes for glyceraldehyde-3-phosphate, phosphoglycerate kinase and triosephosphate isomerase
5341	18144	30823	0.58	3.6E-02	X59403.1	NT	C. glutamicum gap, pgk and tpi genes for glyceraldehyde-3-phosphate, phosphoglycerate kinase and triosephosphate isomerase
5413	18212	30921	0.64	3.6E-02	AF181722.1	NT	Homo sapiens RU2A5 (RU2) mRNA, complete cds
6607	19370	32382	5.47	3.6E-02	AW945516.1	EST_HUMAN	CM2-EN0013-110500-192-510 EN0013 Homo sapiens cDNA
6607	19370	32383	5.47	3.6E-02	AW945516.1	EST_HUMAN	CM2-EN0013-110500-192-510 EN0013 Homo sapiens cDNA
6985	19678	32725	2.5	3.6E-02	AF029952.1	NT	Chromatium vinosum sulfur globule protein Cv2 precursor (sgp2) gene, complete cds
7206	19891	32967	2.76	3.6E-02	AA714521.1	EST_HUMAN	rw20a05.s1 NCL_CGAP_GC50 Homo sapiens cDNA clone IMAGE:1241024 3' similar to gb.J00314_rna2
7533	20203	33298	1.03	3.6E-02	BE143078.1	EST_HUMAN	TUBULIN BETA-1 CHAIN (HUMAN);
9291	21958	35130	1.72	3.6E-02	U20608.1	NT	Dictyostelium discoideum unknown spore germination-specific protein-like protein, orf1, orf2 and orf3 genes, complete cds
9291	21958	35131	1.72	3.6E-02	U20608.1	NT	Dictyostelium discoideum unknown spore germination-specific protein-like protein, orf1, orf2 and orf3 genes, complete cds
9512	22165	35347	0.83	3.6E-02	BF347596.1	EST_HUMAN	602020463F1 NCL_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4156116 5'
11135	23803	37080	1.4	3.6E-02	BF131609.1	EST_HUMAN	601820416F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4052570 5'
11135	23803	37081	1.4	3.6E-02	BF131609.1	EST_HUMAN	601820416F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4052570 5'
11852	24436		1.46	3.6E-02	AI280986.1	EST_HUMAN	qk49b09.x1 NCL_CGAP_Co8 Homo sapiens cDNA clone IMAGE:1872185 3'
875	13644	26314	1.08	3.5E-02	U08506.1	NT	Drosophila melanogaster tigrh mRNA, complete cds
988	13751	26413	1.39	3.5E-02	AF253417.1	NT	Homo sapiens microsomal epoxide hydrolase (EPHX1) gene, complete cds
1556	14303	26991	1.55	3.5E-02	BF678085.1	EST_HUMAN	602085136F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4249377 5'
1556	14303	26992	1.55	3.5E-02	BF678085.1	EST_HUMAN	602085136F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4249377 5'
4188	18629	29559	1.83	3.5E-02	AE001773.1	NT	Thermoboga maritima section 85 of 136 of the complete genome
4281	17020	29647	1.27	3.5E-02	P53780	SWISSPROT	CYSTATHIONINE BETA-LYASE PRECURSOR (GBL) (BETA-CYSTATHIONASE) (CYSTEINE LYASE)
6127	18905	31873	1.77	3.5E-02	J01238.1	NT	Maize actin 1 gene (MACT1), complete cds

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Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7877	20572		0.78	3.5E-02	H29951.1	EST_HUMAN	yp44a05.r1 Soares retina N2b5HR Homo sapiens cDNA clone IMAGE:180256 5' similar to contains Alu repetitive element;
8521	21213	34357	2.7	3.5E-02	BE958970.1	EST_HUMAN	601644701R2 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:3829737 3'
9917	22566	35762	1.45	3.5E-02	X76642.1	NT	Lladis MG1363 grpe and dnak genes
9965	22613	35817	0.5	3.5E-02	BE961042.1	EST_HUMAN	601344661F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3677654 5'
11477	24078	37388	1.82	3.5E-02	AW861641.1	EST_HUMAN	PM1-CT0326-291289-002-h03 CT0326 Homo sapiens cDNA
11477	24078	37389	1.82	3.5E-02	AW861641.1	EST_HUMAN	PM1-CT0326-291289-002-h03 CT0326 Homo sapiens cDNA
12596	25234		5.69	3.5E-02	BE276948.1	EST_HUMAN	601178765F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3543833 5'
564	13346	25973	1.14	3.4E-02	AK024424.1	NT	Homo sapiens mRNA for FLJ00013 protein, partial cds
564	13346	25974	1.14	3.4E-02	AK024424.1	NT	Homo sapiens mRNA for FLJ00013 protein, partial cds
565	13346	25973	6.47	3.4E-02	AK024424.1	NT	Homo sapiens mRNA for FLJ00013 protein, partial cds
565	13346	25974	6.47	3.4E-02	AK024424.1	NT	Homo sapiens mRNA for FLJ00013 protein, partial cds
1029	13789	26448	2.92	3.4E-02	AW274020.1	EST_HUMAN	xv26d07.x1 Soares NFL T_GBC_S1 Homo sapiens cDNA clone IMAGE:2814253 3' similar to SW:C211_HUMAN P53801 PUTATIVE SURFACE GLYCOPROTEIN C21ORF1 PRECURSOR ;
1184	13936		7.14	3.4E-02	11345459	NT	Homo sapiens hypothetical protein FLJ13220 (FLJ13220), mRNA
2391	15112	27849	2.06	3.4E-02	T57160.1	EST_HUMAN	yc20e06.r1 Strategene lung (#837210) Homo sapiens cDNA clone IMAGE:81250 5' similar to contains MER29 repetitive element
3424	16181	28831	1.4	3.4E-02	AL163208.2	NT	Homo sapiens chromosome 21 segment HS2TC008
3757	16509	29145	0.7	3.4E-02	BE839514.1	EST_HUMAN	RC3-FN0155-060700-011-d10 FN0155 Homo sapiens cDNA
3900	16650	29291	3.19	3.4E-02	AW794952.1	EST_HUMAN	RC8-UM0015-210200-021-A10 UM0015 Homo sapiens cDNA
4559	17294	29922	2.41	3.4E-02	X59799.1	NT	M.musculus S-antigen gene promoter region
5000	17723		3.59	3.4E-02	Q26457	SWISSPROT	LA PROTEIN HOMOLOG (LA RIBONUCLEOPROTEIN) (LA AUTOANTIGEN HOMOLOG)
5019	17740	30349	1.2	3.4E-02	AJ012469.1	NT	Caenorhabditis elegans mRNA for DYS-1 protein, partial
6754	17923	30558	4.73	3.4E-02	U24393.1	NT	Human lysyl oxidase-like protein gene, exon 3
8159	20853		3.25	3.4E-02	AI869629.1	EST_HUMAN	wf89d04.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2433031 3'
8946	21338	34482	1.36	3.4E-02	AA664896.1	EST_HUMAN	nu70f08.s1 NCI_CGAP_Alv1 Homo sapiens cDNA clone IMAGE:1216071 similar to contains Alu repetitive element/contains element MER25 MER25 repetitive element ;
							zq04f11.s1 Strategene muscle 937209 Homo sapiens cDNA clone IMAGE:628749 3' similar to TR:G1017425 G1017425
8814	21506		5.97	3.4E-02	AA194306.1	EST_HUMAN	IPISGKPLPKVTLSDRGVPLKATMRNFTEITAEULINLKESVTADAGRYEITAANSSGTTKAFINIVLDRPG
9678	22330		0.63	3.4E-02	AI092719.1	EST_HUMAN	PPT GPVVISDITEESVTWKWEPKYDGGSQVTKYLLKRETSSTAVWTEYSATVARTMKVMKL ... ;
363	13161		9.61	3.3E-02	AA398735.1	EST_HUMAN	oz99h08.x1 Soares parathyroid tumor_NbHPA Homo sapiens cDNA clone IMAGE:1683519 3'
1143	13898	26559	17.88	3.3E-02	AB035867.1	NT	z175e08.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:728198 3'
							Cricetus griseus CYP2A17 mRNA for cytochrome P450 2A17, complete cds

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1489	14236	26923	1.16	3.3E-02	L16870.1	NT	Homo sapiens cytochrome P450C18 (CYP2C18) gene, exons 2 and 3
1635	14381	27088	1.47	3.3E-02	AF110763.1	NT	Homo sapiens skeletal muscle LIM-protein 1 (FHL1) gene, complete cds
1732	14474		1.29	3.3E-02	AE000700.1	NT	Aquifex aeolicus section 32 of 109 of the complete genome
2077	14809		2.46	3.3E-02	R09112.1	EST_HUMAN	Y25609.1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:127888 5'
2453	15171	27910	1.31	3.3E-02	6755892	NT	Mus musculus tumor rejection antigen gp96 (Tra1), mRNA
4156	14381	27088	2.44	3.3E-02	AF110763.1	NT	Homo sapiens skeletal muscle LIM-protein 1 (FHL1) gene, complete cds
4435	17171	29800	1.78	3.3E-02	6755862	NT	Mus musculus tumor rejection antigen gp96 (Tra1), mRNA
6336	19106	32095	27.36	3.3E-02	BF245995.1	EST_HUMAN	601853910F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4073787 5'
6336	19106	32096	27.36	3.3E-02	BF245995.1	EST_HUMAN	601853910F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4073787 5'
7408	20085	33169	0.63	3.3E-02	AF124182.1	NT	Nicotiana plumbaginifolia molybdopterin synthase sulphurylase (cys5) gene, partial cds
9222	21901	35071	0.74	3.3E-02	BF115621.1	EST_HUMAN	7m92404.x1 NCI CGAP Bm23 Homo sapiens cDNA clone IMAGE:3562423 3'
9222	21901	35072	0.74	3.3E-02	BF115621.1	EST_HUMAN	7m92404.x1 NCI CGAP Bm23 Homo sapiens cDNA clone IMAGE:3562423 3'
9324	21991	35162	0.66	3.3E-02	AA488202.1	EST_HUMAN	ad08f09.s1 Soares NIHFB Homo sapiens cDNA clone IMAGE:877673 3' similar to gb:X70944_cds1
9324	21991	35163	0.66	3.3E-02	AA488202.1	EST_HUMAN	ad08f09.s1 Soares NIHFB Homo sapiens cDNA clone IMAGE:877673 3' similar to gb:X70944_cds1
11065	23735	37008	3.63	3.3E-02	BF691107.1	EST_HUMAN	MYOBLAST CELL SURFACE ANTIGEN 24.1D5 (HUMAN);
12142	24630		3.24	3.3E-02	T96545.1	EST_HUMAN	60224717F1 NIH_MGC_82 Homo sapiens cDNA clone IMAGE:4332497 5'
12259	24704		1.52	3.3E-02	AF289665.1	NT	ye49f11.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:121101 5'
12288	24718		2.92	3.3E-02	M81890.1	NT	Mus musculus EIF4H gene, partial cds; LIMK1 gene, complete cds; and ELN gene, partial cds
129	12944	25588	0.74	3.2E-02	AJ002005.1	NT	Human Interleukin 11 (IL11) gene, complete mRNA
1104	13861	26520	7.01	3.2E-02	AF096275.1	NT	Oryctolagus cuniculus gene encoding ileal sodium-dependent bile acid transporter
1104	13861	26521	7.01	3.2E-02	AF096275.1	NT	Drosophila melanogaster heat shock protein 68 (hsp68) gene, hsp68d allele, complete cds
2112	14843		3.01	3.2E-02	P28955	SWISSPROT	Drosophila melanogaster heat shock protein 68 (hsp68) gene, hsp68d allele, complete cds
3131	15898	28540	10.06	3.2E-02	BE867353.1	EST_HUMAN	LARGE TEGUMENT PROTEIN
3701	16454	29094	0.92	3.2E-02	AL163203.2	NT	601442431F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3846727 5'
3842	16692	28330	1.64	3.2E-02	Z74103.1	NT	Homo sapiens chromosome 21 segment HS21C003
3942	16692	28331	1.64	3.2E-02	Z74103.1	NT	S.cerevisiae chromosome IV reading frame ORF YDL055c
4193	16934		14.21	3.2E-02	X94788.1	NT	S.cerevisiae chromosome IV reading frame ORF YDL055c
							H.sapiens RP3 gene (XLRP gene 3)
4716	17448	30081	3.42	3.2E-02	AF114182.1	NT	
4894	17821		1.09	3.2E-02	AF109606.1	NT	Saxifraga nidifica maturase (matK) gene, chloroplast gene encoding chloroplast protein, partial cds
5448	18247	31135	1.83	3.2E-02	X68709.1	NT	Mus musculus MHC class III region RD gene, partial cds; Bf, C2, G9A, NG22, G9, HSP70, HSC70, and smRNP genes, complete cds; GTA gene, partial cds; and unknown genes
							S.griseocaneum whiG-Stv gene

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5448	18247	31136	1.83	3.2E-02	X68709.1	NT	S.griseacamelum wtiG-Siv gene
6431	19189	32196	3.13	3.2E-02	M32437.1	NT	Rat/polyomavirus left junction in cell line W98.14
6432	19200		33.46	3.2E-02	T89367.1	EST_HUMAN	yc33h12.s1 Soares fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:110087 3' similar to contains Alu repetitive element; contains LTR1 repetitive element ;
6513	19278	32279	4.14	3.2E-02	AF173845.1	NT	Saguinus oedipus tissue kallikrein gene, complete cds
7662	20328	33436	0.64	3.2E-02		NT	Homo sapiens cytochrome P450, subfamily 11B (phenobarbital-inducible) (CYP2B), mRNA
8199	20893	34030	4.84	3.2E-02	11424049	NT	Mus musculus kinesin family member 3c (Kif3c), mRNA
8839	21531		0.73	3.2E-02	6680565	NT	Homo sapiens chromosome 3 subtelomeric region
9125	21813	34978	1.21	3.2E-02	AF109718.1	EST_HUMAN	qm17b04.x1 NCJ_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1882063 3'
9125	21813	34979	1.21	3.2E-02	A1278971.1	EST_HUMAN	qm17b04.x1 NCJ_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1882063 3'
9957	22605		4.07	3.2E-02	AA719785.1	EST_HUMAN	zg54b12.s1 Soares pineal_gland_N3HPG Homo sapiens cDNA clone IMAGE:397151 3' similar to gbL08441 CYTOCHROME C OXIDASE POLYPEPTIDE III (HUMAN);
10256	22904	36114	0.95	3.2E-02	U96762.1	NT	Macaca mulatta chemokine receptor CCR5 mRNA, complete cds
1237	13986		2.14	3.1E-02	4503416	NT	Homo sapiens dual specificity phosphatase 4 (DUSP4) mRNA
1282	14032	26702	1.72	3.1E-02	P18845	SWISSPROT	NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN, ALPHA-3 CHAIN PRECURSOR (GF-ALPHA-3)
1885	14622	27332	1.09	3.1E-02	6671564	NT	Mus musculus adaptor-related protein complex AP-3, delta subunit (Ap3d), mRNA
1967	14703		1.34	3.1E-02	Z50097.1	NT	Drosophila melanogaster mRNA for headcase protein
5182	17990	30506	1.13	3.1E-02	U78104.1	NT	Human leukemia inhibitory factor receptor (LIFR) gene, promoter and partial exon 1
5276	18081		2.12	3.1E-02	AA278478.1	EST_HUMAN	zs81a06.r1 NCJ_CGAP_GOB1 Homo sapiens cDNA clone IMAGE:703858 5'
5561	18358	31268	0.74	3.1E-02	BF68742.1	EST_HUMAN	602066783F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4065789 5'
5628	25072	31338					Neisseria meningitidis DNA for region 2 (flaB- and flacC-homologs, unknown genes) and flanking genes, strain FAM18
8840	21532	34677	0.59	3.1E-02	AJ391284.1	NT	601688878R1 NIH_MGC_99 Homo sapiens cDNA clone IMAGE:3886291 3'
9931	22579	35778	0.46	3.1E-02	BE965092.2	EST_HUMAN	Enterococcus faecalis surface protein precursor, gene, complete cds
11765	24356	37689	2.93	3.1E-02	AF034779.1	NT	Mus musculus histidine rich calcium binding protein (Hrc), mRNA
1619	14388		1.78	3.1E-02	6754241	NT	
2590	15304	28040	1.98	3.0E-02	AF187125.1	NT	Pityoktelus minutus cytochrome oxidase I gene, partial cds; mitochondrial gene for mitochondrial product
3645	16398	26038	0.97	3.0E-02	AA402242.1	EST_HUMAN	z65h03.r1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:727253 5'
3728	16480		2.78	3.0E-02	AF247844.1	NT	Pseudomonas fluorescens family II aminotransferase gene, complete cds
3928	16679		0.74	3.0E-02	AW820223.1	EST_HUMAN	QV2-ST0296-150200-040-e09 ST0296 Homo sapiens cDNA
4991	17714	30318	1.42	3.0E-02	AA384003.1	EST_HUMAN	EST174530 Pineal gland II Homo sapiens cDNA 5' end
4991	17714	30319	5.83	3.0E-02	AF281074.1	NT	Homo sapiens neuropilin 2 (NRP2) gene, complete cds, alternatively spliced
4991	17714	30319	5.83	3.0E-02	AF281074.1	NT	Homo sapiens neuropilin 2 (NRP2) gene, complete cds, alternatively spliced
5307	18112		3.43	3.0E-02	AB046793.1	NT	Homo sapiens mRNA for KIAA1573 protein, partial cds

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Table 4
Single Exon Probes Expressed In Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6160	18937	31905	1.4	3.0E-02	N99615.1	EST_HUMAN	z339a10.1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:284906 5' similar to contains element TAR1 repetitive element ;
6160	18937	31906	1.4	3.0E-02	N99615.1	EST_HUMAN	z339a10.1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:284906 5' similar to contains element TAR1 repetitive element ;
6692	19609	32648	3.32	3.0E-02	AJ242906.1	NT	Cyprinus carpio mRNA for inducible nitric oxide synthase (iNOS gene)
6806	19487	32488	2.84	3.0E-02	BE889948.1	EST_HUMAN	601512206F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3913848 5'
6806	19487	32489	2.84	3.0E-02	BE889948.1	EST_HUMAN	601512206F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3913848 5'
6971	19453	32472	2.15	3.0E-02	AF213884.1	NT	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cds
6971	19453	32473	2.15	3.0E-02	AF213884.1	NT	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cds
7132	19819	32885	1.4	3.0E-02	M86624.1	NT	Human dystrophin gene
7483	20155		0.59	3.0E-02	BF246361.1	EST_HUMAN	60185498F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4074548 5'
8025	20720		0.48	3.0E-02	BF879708.1	EST_HUMAN	602154364F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4285654 5'
8539	21231	34373	0.66	3.0E-02	BF353889.1	EST_HUMAN	IL5-HT0704-290600-108-c04 HT0704 Homo sapiens cDNA
8692	21384		1.8	3.0E-02	AF275654.1	NT	Omithorhynchus anatinus coagulation factor X mRNA, complete cds
10357	23004	38221	1.49	3.0E-02	AE001797.1	NT	Thermotoga maritima section 109 of 136 of the complete genome
10446	23092	36322	0.49	3.0E-02	Z271211.1	EST_HUMAN	HSAAADTHS TEST1, Human adult Testis tissue Homo sapiens cDNA clone cam test244 (b)
11197	23882	37148	2.73	3.0E-02	M81357.1	NT	Human coagulation factor VII (F7) gene exon 1 and factor X (F10) gene, exon 1
11690	24285	37607	7.75	3.0E-02	AA483216.1	EST_HUMAN	ne8704.s1 NCI_OGAP_Kid1 Homo sapiens cDNA clone IMAGE:911263
12243	25389	30618	2	3.0E-02	R32019.1	EST_HUMAN	yt63d04.s1 Soares placenta NB2HP Homo sapiens cDNA clone IMAGE:134407 3'
12687	24909		2.46	3.0E-02	AW895565.1	EST_HUMAN	QV4-NN0038-270400-187-h05 NN0038 Homo sapiens cDNA
12629	25383		2.06	3.0E-02	AF048687.1	NT	Rattus norvegicus UDP-Gal:glucosylceramide beta-1,4-galactosyltransferase mRNA, complete cds
2436	15504	27891	1.27	2.9E-02	AF228703.1	NT	Homo sapiens mitochondrial glutathione reductase and cytosolic glutathione reductase (GRD1) gene, complete cds, alternatively spliced
2690	15756	28402	1.04	2.9E-02	BE565644.1	EST_HUMAN	601338428F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3680695 5'
2860	15756	28403	1.04	2.9E-02	BE565644.1	EST_HUMAN	601338428F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3680695 5'
3908	16658	29299	0.89	2.9E-02	H72805.1	EST_HUMAN	yu07e10.1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:233130 5'
5972	18784	31715	0.97	2.9E-02	AF060221.1	NT	Sus scrofa deoxyribonuclease II mRNA, complete cds
6199	18975	31853	7.39	2.9E-02	BF032233.1	EST_HUMAN	601452961F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3856598 5'
6855	19555	32585	0.56	2.9E-02	AJ391284.1	NT	Neisseria meningitidis DNA for region 2 (flaB- and flacC-homologs, unknown genes) and flanking genes, strain FAM18
7148	19835	32904	12.03	2.9E-02	BE271437.1	EST_HUMAN	601140729F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3049830 5'

Single Exon Probes Expressed in Brain

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7897	20592	33723	0.87	2.9E-02	AF129279.1	NT	Buchnera aphidicola natural-host Schlectendalia chinensis gluconate-6-phosphate dehydrogenase (gnd) gene, partial cds
7897	20592	33724	0.87	2.9E-02	AF129279.1	NT	Buchnera aphidicola natural-host Schlectendalia chinensis gluconate-6-phosphate dehydrogenase (gnd) gene, partial cds
9558	22211	35396	2.49	2.9E-02	AW875978.1	EST_HUMAN	CM3-PT0014-071299-051-c04 PT0014 Homo sapiens cDNA
9558	22211	35397	2.49	2.9E-02	AW875978.1	EST_HUMAN	CM3-PT0014-071299-051-c04 PT0014 Homo sapiens cDNA
9774	22425		0.75	2.9E-02	AW976597.1	EST_HUMAN	EST388706 MAGE resequences, MAGN Homo sapiens cDNA
10243	22891	36103	1.25	2.9E-02	AP000064.1	NT	Aeropyrum pernix genomic DNA, section 777
10977	17902	30580	1.97	2.9E-02	X55284.1	NT	Sheep gene for ultra high-sulphur keratin protein
552	13335		0.96	2.8E-02	AW970153.1	EST_HUMAN	EST382234 MAGE resequences, MAGK Homo sapiens cDNA
3360	16119	28775	1.3	2.8E-02	AF066063.1	NT	Homo sapiens retinal fascic (FSCN2) gene, exon 2
3360	16119	28776	1.3	2.8E-02	AF066063.1	NT	Homo sapiens retinal fascic (FSCN2) gene, exon 2
5400	18200	30905	11.62	2.8E-02	BE741083.1	EST_HUMAN	801594078F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3948087 5'
6711	19628	32670	1.15	2.8E-02	T78860.1	EST_HUMAN	Yd21b08.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:108855 5'
8226	20820	34058	1.61	2.8E-02	AJ005820.1	NT	Craterostigma plantagineum mRNA for homeodomain leucine zipper protein (hb-1)
8915	21808	34749	0.85	2.8E-02	AA280782.1	EST_HUMAN	zs96c06.r1 NCJ_CGAP_GCBT Homo sapiens cDNA clone IMAGE:711466 5'
9108	21798	34960	1	2.8E-02	AF187872.1	NT	Cavia porcellus inwardly-rectifying potassium channel Kir2.1 (KCNJ2) gene, complete cds
9212	21891	35058	0.89	2.8E-02	AE001092.1	NT	Archaeoglobus fulgidus section 15 of 172 of the complete genome
12528	25229		1.5	2.8E-02	R06966.1	EST_HUMAN	Yf12h02.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:126675 5'
12630	24878		1.48	2.8E-02	X06322.1	NT	Yeast CN31C chromosome III RAHS DNA (right arm transcription hot-spot)
1472	14219	26905					Human germline T-cell receptor beta chain Dopamine-beta-hydroxylase-like, TRY1, TRY2, TRY3, TCRBV27S1P, TCRBV22S1A2N1T, TCRBV9S1A1T, TCRBV7S1A1N2T, TCRBV6S1A1T, TCRBV13S3, TCRBV6S7P, TCRBV7S3A2T, TCRBV13S2A1T, TCRBV9S2A2PT, TCRBV7S2A1N4T, TCRBV13S9/13S2
3425	16182	28832	1.23	2.7E-02	U66059.1	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 6
4178	18918	28545	1.74	2.7E-02	AL161494.2	NT	Y66h12.r1 Soares_multiple_sclerosis_2NblHMSP Homo sapiens cDNA clone IMAGE:280487 5'
4178	18918	28546	1.92	2.7E-02	N47268.1	EST_HUMAN	Y66h12.r1 Soares_multiple_sclerosis_2NblHMSP Homo sapiens cDNA clone IMAGE:280487 5'
5355	18158	30841	1.2	2.7E-02	R12245.1	EST_HUMAN	Y33a09.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:128657 5' similar to SP-JC2264, JC2264 TISSUE FACTOR PATHWAY INHIBITOR - RHESUS
5812	18601	31529	0.86	2.7E-02	X61670.1	NT	T.aestivum pTTH20 mRNA for wheat type V thionin
5885	18671	31612	0.64	2.7E-02	AB004799.1	NT	Oryza sativa mRNA for ascorbate oxidase, partial cds
6505	19270		0.93	2.7E-02	X97580.1	NT	A.bisporus pdkA gene
6967	19449	32467	2.28	2.7E-02	AA993571.1	EST_HUMAN	cd96h03.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:1624661 3'

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Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8252	20946		1.06	2.7E-02	AI377036.1	EST_HUMAN	tc28g08.x1 Soares_t0tal_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:2065982 3' similar to
8514	21206	34349	0.49	2.7E-02	SI3442.1	NT	contains Alu repetitive element;
558	13340	25988	1.12	2.6E-02	AL163282.2	NT	transmembrane secretory component [human, leukocytes, Genomic, 657 nt, segment 4 of 11]
2368	15088	27825	3.29	2.6E-02	AA490021.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C082
2368	15090	27827	4.49	2.6E-02	6754241	NT	ab02b02.s1 Stralagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:839595 3'
2368	15090	27828	4.49	2.6E-02	6754241	NT	Mus musculus histidine rich calcium binding protein (Hrc), mRNA
2816	15682		1.86	2.6E-02	AF109906.1	NT	Mus musculus histidine rich calcium binding protein (Hrc), mRNA
4847	17577	30200	2.25	2.6E-02	L12032.1	NT	Mus musculus MHC class III region RD gene, partial cds; Bf, C2, G9A, NG22, G9, HSP70, HSP70, HSC70,
5005	17728	30332	1.56	2.6E-02	AE002014.1	NT	and smRNP genes, complete cds; G7A, gene, partial cds; and unknown genes
5032	17752	30364	2.35	2.6E-02	AW241154.1	EST_HUMAN	Chicken dorealin-1 mRNA, complete cds
5754	18546		0.7	2.6E-02	AL161563.2	NT	Deinococcus radiodurans R1 section 151 of 229 of the complete chromosome 1
5800	18590		0.59	2.6E-02	AL161563.2	NT	xa52b04.x1 NCI CGAP_Sar4 Homo sapiens cDNA clone IMAGE:2570383 3' similar to SW:Y069_HUMAN
6125	19033		7.34	2.6E-02	AI206030.1	EST_HUMAN	Q15041 HYPOTHETICAL PROTEIN KIAA00069 ;
6331	19101	32089	1.9	2.6E-02	BE821748.1	EST_HUMAN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 63
6728	19582	32593	0.9	2.6E-02	Z99084.1	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 63
6728	19562	32594	0.9	2.6E-02	Z99084.1	NT	gg27f11.x1 NCI CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1762317 3'
6810	19471	32494	7.11	2.6E-02	6981271	NT	601493473T1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3895578 3'
8403	21096	34232	0.71	2.6E-02	AA860946.1	EST_HUMAN	Vaccinia virus ORF1L, strain W yeth
9260	22014	35182	1.15	2.6E-02	11432020	NT	Vaccinia virus ORF1L, strain W yeth
9614	22267	35453	0.75	2.6E-02	AF114952.1	NT	Rattus norvegicus Nerve growth factor receptor, fast (Ngfr), mRNA
9614	22267	35454	0.75	2.6E-02	AF114952.1	NT	ak22f04.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1406719 3'
10303	22850	36165	4.39	2.6E-02	AL163303.2	NT	Homo sapiens KIAA1070 protein (KIAA1070), mRNA
11191	23856		1.67	2.6E-02	4506466	NT	Saccharomyces cerevisiae NRRL Y-12639(T) ATP synthase subunit 9 (ATP9) gene, mitochondrial gene
11361	24049		2.33	2.6E-02	AA279351.1	EST_HUMAN	encoding mitochondrial protein, complete cds
11553	24152	37465	2.2	2.6E-02	AW500547.1	EST_HUMAN	encoding mitochondrial protein, complete cds
12170	25375	30615	2.09	2.6E-02	BF343827.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C103
519	13303	25935	1.75	2.5E-02	AI793130.1	EST_HUMAN	Homo sapiens radixin (RDX) mRNA
519	13303	25936	1.75	2.5E-02	AI793130.1	EST_HUMAN	zs84c02.1 NCI CGAP_GCB1 Homo sapiens cDNA clone IMAGE:704162 5'
791	13563	26224	15.9	2.5E-02	BE974314.1	EST_HUMAN	UI-HF-BN0-akj-e-10-0-UJ.1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3077466 5'
							602015501F1 NCI CGAP_Bn04 Homo sapiens cDNA clone IMAGE:4150944 5'
							on26f06.y5 NCI CGAP_Lu6 Homo sapiens cDNA clone IMAGE:1557827 5'
							on26f06.y5 NCI CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1557827 5'
							601880305R2 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3950665 3'

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Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
849	13619	26289	7.2	2.5E-02	BE974314.1	EST_HUMAN	601680305R2 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3950665 3'
2766	15471		2.24	2.5E-02	U12671.1	NT	Rattus norvegicus rabphilin-3A mRNA, complete cds
2856	16722	28371	4.35	2.5E-02	X99697.1	NT	H. carterae mRNA for fucoxanthin chlorophyll a/c binding protein, Fcp1
2856	16722	28372	4.35	2.5E-02	X99697.1	NT	H. carterae mRNA for fucoxanthin chlorophyll a/c binding protein, Fcp1
4023	17879	28369	1	2.5E-02	BE701165.1	EST_HUMAN	PM2-NN0128-080700-001-a12 NN0128 Homo sapiens cDNA
4023	17879	29400	1	2.5E-02	BE701165.1	EST_HUMAN	PM2-NN0128-080700-001-a12 NN0128 Homo sapiens cDNA
4182	16922	29550	4.23	2.5E-02	AW592114.1	EST_HUMAN	H36h08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2934015 3'
5625	18422	31335	0.61	2.5E-02	A792776.1	EST_HUMAN	z83c10.x5 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:810354 3'
6100	18878		5.01	2.5E-02	BE670128.1	EST_HUMAN	7e30d09.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3284008 3' similar to contains L1, L1 L1 repetitive element
6115	18993		4.1	2.5E-02	BE746888.1	EST_HUMAN	601679935F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3926054 5'
6244	19018	31992	1.04	2.5E-02	L29029.1	NT	Chlamydomonas reinhardtii VSP-3 mRNA, complete cds
7563	20233	33336	1.7	2.5E-02	BF526722.1	EST_HUMAN	602070562F1 NCI_CGAP_Bm64 Homo sapiens cDNA clone IMAGE:4213406 5'
7563	20233	33337	1.7	2.5E-02	BF526722.1	EST_HUMAN	602070562F1 NCI_CGAP_Bm64 Homo sapiens cDNA clone IMAGE:4213406 5'
8724	21416	34560	0.81	2.5E-02	Q91713	SWISSPROT	CHORDIN PRECURSOR (ORGANIZER-SPECIFIC SECRETED DORSALIZING FACTOR)
8863	21554	34699	0.47	2.5E-02	AW025821.1	EST_HUMAN	wu08c10.x1 NCI_CGAP_G08 Homo sapiens cDNA clone IMAGE:2516370 3'
9966	22614		0.55	2.5E-02	X71303.1	NT	D. radiatum 28S ribosomal RNA, D2 domain
10482	23128	36356	0.65	2.5E-02	A1147615.1	EST_HUMAN	q022a08.x1 Soares_pregnant uterus_NbHPU Homo sapiens cDNA clone IMAGE:1696982 3'
10712	23401	36640	2.01	2.5E-02	Q10335	SWISSPROT	HYPOTHETICAL 46.7 KD PROTEIN C19G10.05 IN CHROMOSOME 1
10712	23401	36641	2.01	2.5E-02	Q10335	SWISSPROT	HYPOTHETICAL 46.7 KD PROTEIN C19G10.05 IN CHROMOSOME 1
10773	23456	36700	2.32	2.5E-02	AJ237936.1	NT	Bos taurus partial stat5B gene, exons 17-19
10795	23478		3.46	2.5E-02	AF050157.1	NT	Mus musculus major histocompatibility locus class II region: major histocompatibility protein class II alpha chain (Aalpha) and major histocompatibility protein class II beta chain (Ebeta) genes, complete cds; butyrophilin-like (NG9), butyrophilin-li>
11770	24381		2.55	2.5E-02	AB007546.1	NT	Homo sapiens gene for LECT2, complete cds
12134	25311		2.89	2.5E-02	11420078	NT	Homo sapiens similar to ALEX3 protein (H. sapiens) (LOC88634), mRNA
12311	25182		1.76	2.5E-02	11433220	NT	Homo sapiens mitogen-activated protein kinase kinase 13 (MAP3K13), mRNA
12432	24804	31043	1.94	2.5E-02	BE973927.1	EST_HUMAN	601652365R2 NIH_MGC_82 Homo sapiens cDNA clone IMAGE:3935513 3'
1593	14339	27028	1.7	2.4E-02	H65884.1	EST_HUMAN	y75f11.1 Soares fetal liver spleen tNfLS Homo sapiens cDNA clone IMAGE:211149 5'
2037	15584	27501	1.92	2.4E-02	P01901	SWISSPROT	H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN, K-B ALPHA CHAIN PRECURSOR (H-2K(B))
2037	15584	27502	1.92	2.4E-02	P01901	SWISSPROT	H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN, K-B ALPHA CHAIN PRECURSOR (H-2K(B))
4335	17074	29702	1.65	2.4E-02	J05110.1	NT	T.themophila calcium-binding 25 kDa (TCBP 25) protein mRNA, complete cds
4485	17220	29847	1.58	2.4E-02	P01901	SWISSPROT	H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN, K-B ALPHA CHAIN PRECURSOR (H-2K(B))
4485	17220	29848	1.58	2.4E-02	P01901	SWISSPROT	H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN, K-B ALPHA CHAIN PRECURSOR (H-2K(B))

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Single Exon Probes Expressed in Brain

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5068	17787	30403	0.95	2.4E-02	8922702	NT	Homo sapiens hypothetical protein FLJ10844 (FLJ10844), mRNA
6121	18898	31867	0.9	2.4E-02	W86680.1	EST_HUMAN	zh63h04.s1 Soares fetal liver spleen 1NFLS_S1 Homo sapiens cDNA clone IMAGE:416791 3'
6267	19040	32018	0.58	2.4E-02	M31650.1	NT	Chicken myristoylated alanine-rich C kinase substrate (MARCKS) mRNA, complete cds
6267	19040	32017	0.58	2.4E-02	M31650.1	NT	Chicken myristoylated alanine-rich C kinase substrate (MARCKS) mRNA, complete cds
7121	19809	32875	0.8	2.4E-02	Z20573.1	EST_HUMAN	HSAAACKVX T, Human adult Rhabdomyosarcoma cell-line Homo sapiens cDNA
7138	19825	32892	0.9	2.4E-02	X12925.1	NT	Rat gene for uncoupling protein (UCP)
7138	19825	32893	0.9	2.4E-02	X12925.1	NT	Rat gene for uncoupling protein (UCP)
7791	20486		0.72	2.4E-02	AW813007.1	EST_HUMAN	RC3-ST0186-230300-019-H08 ST0186 Homo sapiens cDNA
7844	20539		0.5	2.4E-02	M16780.1	NT	Human retrotransposon 3' long terminal repeat
8340	21033		0.69	2.4E-02	H78376.1	EST_HUMAN	yu12c05.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:233576 3' similar to contains Alu repetitive element; contains A3R repetitive element;
8429	21122	34260	0.78	2.4E-02	N69442.1	EST_HUMAN	za35g11.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:294596 3' similar to gb J02809 JATSR7K Rat (rRNA); contains A3R.b1 A3R repetitive element;
8885	21576	34718	0.57	2.4E-02	AE001125.1	NT	Borrelia burgdorferi (section 11 of 70) of the complete genome
8907	21598	34740	0.78	2.4E-02	AA625660.1	EST_HUMAN	zu91c06.s1 Soares testis NHT Homo sapiens cDNA clone IMAGE:745354 3' similar to gb:J04422 ISLET XTR repetitive element;
9591	22244	35427	0.52	2.4E-02	AF124160.1	NT	Arabidopsis thaliana mol/xylopterin synthase sulphuryase (cny5) gene, complete cds
9591	22244	35428	0.52	2.4E-02	AF124160.1	NT	Arabidopsis thaliana mol/xylopterin synthase sulphuryase (cny5) gene, complete cds
9706	22357	35553	2.38	2.4E-02	AV682954.1	EST_HUMAN	AV682954 GKG Homo sapiens cDNA clone GKGDS003 5'
9881	22531	35728	2.73	2.4E-02	AA493894.1	EST_HUMAN	nh07b12.s1 NCL_OGAP_Thy1 Homo sapiens cDNA clone IMAGE:943583 similar to contains Alu repetitive element; contains element P' TRS repetitive element;
10512	23159		0.46	2.4E-02	BE387111.1	EST_HUMAN	50127492F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3615902 5'
11565	24164	37475	1.89	2.4E-02	AF109905.1	NT	Mus musculus major histocompatibility locus class III regions Hsc70t gene, partial cds; smRNP, G7A, NG23, Muts homolog, CLCP, NG24, NG25, and NG26 genes, complete cds; and unknown genes
11565	24164	37476	1.89	2.4E-02	AF109905.1	NT	Mus musculus major histocompatibility locus class III regions Hsc70t gene, partial cds; smRNP, G7A, NG23, Muts homolog, CLCP, NG24, NG25, and NG26 genes, complete cds; and unknown genes
11938	24485		2.28	2.4E-02	9627908	NT	Bacteriophage bil67, complete genome
12081	24589	31124	1.91	2.4E-02	6753635	NT	Mus musculus Dmb homolog 1 (E. coli) (Dmb1), mRNA
12136	24625	31094	2.37	2.4E-02	BE928869.1	EST_HUMAN	MRO-F70175-310800-202-406 F70175 Homo sapiens cDNA
12186	24657	31063	1.88	2.4E-02	U78187.1	NT	Rattus norvegicus cAMP-regulated guanine nucleotide exchange factor I (cAMP-GEFI) mRNA, complete cds

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Single Exon Probes Expressed In Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12186	24657	31104	1.66	2.4E-02	U78167.1	NT	Rafus norvegicus cAMP-regulated guanine nucleotide exchange factor I (cAMP-GEFI) mRNA, complete cds
12216	24678		1.34	2.4E-02	AF163864.1	NT	Homo sapiens SNCA isoform (SNCA) gene, complete cds, alternatively spliced
12360	24764		3.88	2.4E-02	AB008569.1	NT	Caenorhabditis elegans mRNA for iron-sulfur subunit of mitochondrial succinate dehydrogenase, complete cds
1865	14603		4.28	2.3E-02	W05340.1	EST_HUMAN	zab4g08.r1 Soares_fetal_lung_NHL19W Homo sapiens cDNA clone IMAGE:289284 5'
1880	14617		10.45	2.3E-02	U94165.1	NT	4 Homo sapiens mammary tumor-associated protein INT6 (INT6) gene, exon 4
2350	15072	27809	2.08	2.3E-02	Z74283.1	NT	S.cerevisiae chromosome IV reading frame ORF YDL245c
3670	16423	29084	6.19	2.3E-02	Z20377.1	EST_HUMAN	HSAAACADH P, Human foetal Brain Whole tissue Homo sapiens cDNA
3702	16455		0.8	2.3E-02	L23429.1	NT	Carls beta-galactosides-binding lectin (LGALS3) mRNA, 3'end
4129	18871	29489	1.06	2.3E-02	L24799.1	NT	Gallus gallus connexin 45.6 (Cx45.6) gene, complete cds
4129	18871	29500	1.06	2.3E-02	L24799.1	NT	Gallus gallus connexin 45.6 (Cx45.6) gene, complete cds
4386	17123	29755	0.93	2.3E-02	AW899107.1	EST_HUMAN	CM4-NN0080-280400-160-b04 NN0080 Homo sapiens cDNA
4415	17152	29780	0.88	2.3E-02	BE935225.1	EST_HUMAN	CM3-MT0118-010900-318-g07 MT0118 Homo sapiens cDNA
4415	17152	29781	0.88	2.3E-02	BE935225.1	EST_HUMAN	CM3-MT0118-010900-318-g07 MT0118 Homo sapiens cDNA
4416	17880	29782	1.14	2.3E-02	AW593693.1	EST_HUMAN	xs25d08.x1 NCI_CGAP_U12 Homo sapiens cDNA clone IMAGE:2770671 3'
4416	17880	29783	1.14	2.3E-02	AW593693.1	EST_HUMAN	xs25d08.x1 NCI_CGAP_U12 Homo sapiens cDNA clone IMAGE:2770671 3'
4555	17280	29919	2.56	2.3E-02	BF028487.1	EST_HUMAN	601672279F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3955386 5'
4555	17290	29920	2.56	2.3E-02	BF028487.1	EST_HUMAN	601672279F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3955386 5'
5291	18096	30756	3.63	2.3E-02	U68303.1	NT	Caulobacter crescentus topoisomerase IV ParE subunit (parE) gene, complete cds, and propionyl-CoA carboxylase beta chain (pccB) homolog gene, partial cds
5522	19288	32292	4.08	2.3E-02	AL161505.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 17
6883	17659	30513	0.69	2.3E-02	BE141476.1	EST_HUMAN	MRO-HIT0080-011095-002-c09 HIT0080 Homo sapiens cDNA
7776	20472	33595	6.28	2.3E-02	U63610.1	NT	Human plectin (PLEC1) gene, exons 3-32, and complete cds
8370	21063	34204	0.94	2.3E-02	A1298105.1	NT	Homo sapiens PDX1 gene for lipoyl-containing component X, exons 1-11
8370	21063	34205	0.94	2.3E-02	A1298105.1	NT	Homo sapiens PDX1 gene for lipoyl-containing component X, exons 1-11
8597	21289	34429	0.68	2.3E-02	A1865380.1	EST_HUMAN	wa76h10.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2302147 3'
8597	21289	34430	0.68	2.3E-02	A1865380.1	EST_HUMAN	wa76h10.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2302147 3'
9036	21728	34880	0.98	2.3E-02	P41996	SWISSPROT	HYPOPHOSPHATASE 55.8 KD PROTEIN B0280.5 IN CHROMOSOME III PRECURSOR
9759	22410	35617	0.77	2.3E-02	P50332	SWISSPROT	CHROMOSOME ASSEMBLY PROTEIN XCAP-C
9928	22577	35776	1.33	2.3E-02	AE000199.1	NT	Escherichia coli K-12 MG1655 section 89 of 400 of the complete genome
9928	22577	35777	1.33	2.3E-02	AE000199.1	NT	Escherichia coli K-12 MG1655 section 89 of 400 of the complete genome
10524	23170	36397	0.46	2.3E-02	AF282894.1	NT	Bacillus licheniformis isolate N57N1 KcrA gene, partial cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10882	23373	36615	2.16	2.3E-02	P08640	SWISSPROT	GLUCOAMYLASE S1/S2 PRECURSOR (GLUCAN 1,4-ALPHA-GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN
12058	25166		5.07	2.3E-02	BE278331.1	EST_HUMAN	GLUCOHYDROLASE)
12562	24892	30697	2.19	2.3E-02	U38394.1	NT	601179958F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3546567 5'
12616	25409		2.42	2.3E-02	U11077.1	NT	Streptomyces sp. alpha-1/3/4-fucosidase precursor gene, complete cds
12807	25280		1.62	2.3E-02	11426338	NT	Dictyostellum discoideum extracellular signal-regulated protein kinase (ERK1) mRNA, complete cds
720	13494	26147	4.13	2.2E-02	AF018267.1	NT	Homo sapiens dead ringer (Drosophila)-like 1 (DRIL1), mRNA
1741	14483		1.38	2.2E-02	4557448	NT	complete cds
1755	14497	27197	1.06	2.2E-02	P07313	SWISSPROT	Homo sapiens chromodomain helicase DNA binding protein 2 (CHD2) mRNA
1755	14497	27198	1.06	2.2E-02	P07313	SWISSPROT	MYOSIN LIGHT CHAIN KINASE, SKELETAL MUSCLE (MLCK)
2008	14743	27469	2.13	2.2E-02	Z62001.1	NT	MYOSIN LIGHT CHAIN KINASE, SKELETAL MUSCLE (MLCK)
3428	16185		1.49	2.2E-02	AA577785.1	EST_HUMAN	S. pneumoniae pcpA gene and open reading frames
3637	16390		4.01	2.2E-02	AF083094.1	NT	nm24a04.s1 NCI_CGAP_Gas1 Homo sapiens cDNA clone IMAGE:1084782 3'
3834	16585	29221	1.26	2.2E-02	AW601317.1	EST_HUMAN	Infectious bursal disease virus segment B strain L4 VP1 gene, complete cds
3899	16849	29280	0.75	2.2E-02	Z74293.1	NT	PMD-BT0340-170100-004-b03 BT0340 Homo sapiens cDNA
5006	17729	30333	1.05	2.2E-02	Z73597.1	NT	S. cerevisiae chromosome IV, reading frame ORF YDL245c
7146	19833	32902	3.63	2.2E-02	AV699721.1	EST_HUMAN	S. cerevisiae chromosome XVI, reading frame ORF YPL241c
8269	20863	34104	1.62	2.2E-02	AL161515.2	NT	AV699721 GKB Homo sapiens cDNA clone GKBAND03 3'
8269	20963	34105	1.62	2.2E-02	AL161515.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 27
8709	21401	34546	0.82	2.2E-02	X79468.1	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 27
9586	22239	35422	2.22	2.2E-02	AB026898.1	NT	P. vulgaris alpha tub 2 mRNA
9586	22239	35423	2.22	2.2E-02	AB026898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
10105	22753		0.89	2.2E-02	6678140	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
11167	23634	37115	1.66	2.2E-02	BE797601.1	EST_HUMAN	Mus musculus Sjogren syndrome antigen A1 (Ssa1), mRNA
11841	24425	37766	1.54	2.2E-02	11423632	NT	601584309F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3838571 5'
12315	24737		4.07	2.2E-02	AA503553.1	EST_HUMAN	Homo sapiens transmembrane protein 1 (TMEM1), mRNA
410	13195		6.11	2.1E-02	AV761502.1	EST_HUMAN	ne47h07 st NCI_CGAP_Co3 Homo sapiens cDNA clone IMAGE:900541 3' similar to contains Alu repetitive element;
436	13222		9.88	2.1E-02	AF029726.1	NT	AV761502 MDS Homo sapiens cDNA clone MDSADG01 5'
						NT	Dictyostellum discoideum histidine kinase C (dhkC) mRNA, complete cds

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1240	13989	26656	10.32	2.1E-02	U72073.1	NT	Bacillus subtilis cotKLM cluster, CotK (cotK), CotL (cotL), and spore coat protein CotM (cotM) genes, complete cds
1366	14113	26787	1.21	2.1E-02	AF204395.1	NT	Mus musculus macrophage migration inhibitory factor (MIF) gene, 5' flanking region and partial cds
1366	14113	26788	1.21	2.1E-02	AF204395.1	NT	Mus musculus macrophage migration inhibitory factor (MIF) gene, 5' flanking region and partial cds
1775	14517	27218	1.06	2.1E-02	P02438	SWISSPROT	KERATIN, HIGH-SULFUR MATRIX PROTEIN, B2A
1775	14517	27219	1.06	2.1E-02	P02438	SWISSPROT	KERATIN, HIGH-SULFUR MATRIX PROTEIN, B2A
1775	14517	27220	1.06	2.1E-02	P02438	SWISSPROT	KERATIN, HIGH-SULFUR MATRIX PROTEIN, B2A
2028	14763	27492	1.2	2.1E-02	BE072546.1	EST_HUMAN	PM2-BT0546-120100-001-f11 BT0546 Homo sapiens cDNA
2028	14763	27493	1.2	2.1E-02	BE072546.1	EST_HUMAN	PM2-BT0546-120100-001-f11 BT0546 Homo sapiens cDNA
2591	15305	28041	1.32	2.1E-02	AA226095.1	EST_HUMAN	nc21903.r1 NCI_CGAP_P1 Homo sapiens cDNA clone IMAGE:1008820
2818	13534	26193	4.48	2.1E-02	N29266.1	EST_HUMAN	yx43h07.r1 Soares melanocyte 2NblHM Homo sapiens cDNA clone IMAGE:284541 5'
3147	14763	27492	1.07	2.1E-02	BE072546.1	EST_HUMAN	PM2-BT0546-120100-001-f11 BT0546 Homo sapiens cDNA
3147	14763	27493	1.07	2.1E-02	BE072546.1	EST_HUMAN	PM2-BT0546-120100-001-f11 BT0546 Homo sapiens cDNA
3571	18326	28973	1	2.1E-02	AA461271.1	EST_HUMAN	zx63b09.r1 Soares total fetus Nb2HF8_9w Homo sapiens cDNA clone IMAGE:796121 5'
4110	16853	29480	0.81	2.1E-02	Z74293.1	NT	S.cerevisiae chromosome IV reading frame ORF YDL245c
4275	17014	29641	0.81	2.1E-02	BF343655.1	EST_HUMAN	602015308F1 NCI_CGAP_Brn64 Homo sapiens cDNA clone IMAGE:415181 5'
4410	17147	29778	1.47	2.1E-02	U44914.1	NT	Borrelia burgdorferi plasmid pb32-2, erpC and erpD genes, complete cds; and unknown genes
4421	17157	29788	1.53	2.1E-02	A1788127.1	EST_HUMAN	wg81d11.x1 Soares NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2371509 3'
4461	17197		0.69	2.1E-02	Y19213.1	NT	Homo sapiens putative psbHBA pseudogene for hair keratin, exons 2 to 7
4682	17396	30031	4.51	2.1E-02	Y08501.1	NT	A.thaliana mitochondrial genome, part A
4762	17494	30122	1.05	2.1E-02	AL163302.2	NT	Homo sapiens chromosome 21 segment HS21C102
4769	17501	30124	0.78	2.1E-02	A1828432.1	EST_HUMAN	wh54e05.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2384528 3'
5553	18350	31259	1.13	2.1E-02	AW379529.1	EST_HUMAN	GM4-HT0244-111199-040-h05 HT0244 Homo sapiens cDNA
6966	18448	32466	0.88	2.1E-02	BF066199.1	EST_HUMAN	OV3-GN0058-120900-329-at2 GN0058 Homo sapiens cDNA
8417	21110	34249	0.6	2.1E-02		NT	Mus musculus sorting nexin 1 (Snx1), mRNA
9403	22065	35236	0.5	2.1E-02	AA084288.1	EST_HUMAN	am83e07.s1 Strategene schizo brain S11 Homo sapiens cDNA clone IMAGE:1629732 3' similar to contains
9531	22184	35368	2.61	2.1E-02	AJ243213.1	NT	Alu repetitive element/contains element MER11 repetitive element ;
9531	22184	35369	2.61	2.1E-02	AJ243213.1	NT	Homo sapiens partial 5-HT4 receptor gene, exons 2 to 5
9883	22533	35730	1.15	2.1E-02	L29324.1	NT	Homo sapiens partial 5-HT4 receptor gene, exons 2 to 5
9961	22609	35814	0.69	2.1E-02	AA984288.1	EST_HUMAN	Streptococcus pneumoniae Integrase, excisionase, repressor protein, relaxase, UmuC MucB homolog, and UmuD MucA homolog genes, complete cds; and unknown genes
10522	23188	36395	0.45	2.1E-02	AP001519.1	NT	am83e07.s1 Strategene schizo brain S11 Homo sapiens cDNA clone IMAGE:1629732 3' similar to contains
						NT	Alu repetitive element/contains element MER11 repetitive element ;
						NT	Bacillus halodurans genomic DNA, section 13/14

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Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11479	24080	37391	1.38	2.1E-02	6754255	NT	Mus musculus heat shock protein, 74 kDa, A (Hspa9a), mRNA
12296	17197		8.62	2.1E-02	Y19213.1	NT	Homo sapiens putative psbHbA pseudogene for hair keratin, exons 2 to 7
12339	25163	30801	1.89	2.1E-02	L34170.1	NT	Human germline UBE1L gene similar to the gene for ubiquitin-activating enzyme, exons 1-22
12714	24988	30869	5.71	2.1E-02	AF183913.1	NT	Azospirillum brasilense major outer membrane protein OmaA precursor (omaA) gene, complete cds
16	12844	25457	1.1	2.0E-02	BF002932.1	EST_HUMAN	7g51c08.x1 NCI_CGAP_P28 Homo sapiens cDNA clone IMAGE:3309998 3' similar to contains MER1.13
17	12845	25458	14.4	2.0E-02	AW895865.1	EST_HUMAN	MER1 repetitive element ;
252	13061	25698	3.76	2.0E-02	6753635	NT	QV4-NN0038-270400-187-h05 NN0038 Homo sapiens cDNA
288	13094	25736	2.72	2.0E-02	AA456538.1	EST_HUMAN	Mus musculus DinB homolog 1 (E. coli) (Dinb1), mRNA
781	13553	26214	2.11	2.0E-02	6753635	NT	aa15b10.r1 Soares_NihHMPu_S1 Homo sapiens cDNA clone IMAGE:813307 5'
1065	13823	26483	1.6	2.0E-02	AL096805.1	NT	Mus musculus DinB homolog 1 (E. coli) (Dinb1), mRNA
1177	13930	26595	1.17	2.0E-02	8922391	NT	Homo sapiens genomic region containing hypervariable minisatellites chromosome 1 [p36.33] of Homo sapiens
1177	13930	26596	1.17	2.0E-02	8922391	NT	Homo sapiens hypothetical protein FLJ10379 (FLJ10379), mRNA
1866	14604	27313	2.39	2.0E-02	8922453	NT	Homo sapiens hypothetical protein FLJ10379 (FLJ10379), mRNA
1866	14604	27314	2.39	2.0E-02	8922453	NT	Homo sapiens hypothetical protein FLJ10486 (FLJ10486), mRNA
2801	15606		3.24	2.0E-02	AL161532.2	NT	Homo sapiens hypothetical protein FLJ10486 (FLJ10486), mRNA
3077	12844	25457	2.11	2.0E-02	BF002932.1	EST_HUMAN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 32
3141	15905		1.4	2.0E-02	7305474	NT	7g51c08.x1 NCI_CGAP_P28 Homo sapiens cDNA clone IMAGE:3309998 3' similar to contains MER1.13
3221	15984		2.35	2.0E-02	AF085688.1	NT	Mus musculus sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6B (Sema6b), mRNA
3988	16736	28370	1.3	2.0E-02	M18095.1	NT	Arabidopsis thaliana C2H2 zinc finger protein FZF mRNA, complete cds
5548	18345	31254	0.58	2.0E-02	U34778.1	NT	P. vulgaris hydroxyproline-rich glycoprotein (HRGP) mRNA, 3' end
6807	18596	31523	0.7	2.0E-02	L35321.2	NT	Caenorhabditis elegans sma-2 mRNA, complete cds
7460	20128	33217	1.11	2.0E-02	AP000004.1	NT	Dictyostelium discoideum class VII unconventional myosin (myoI) gene, complete cds
7460	20126	33218	1.11	2.0E-02	AP000004.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 777001-994000 nt. position (4/7)
9777	22428		2.21	2.0E-02	U70408.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 777001-994000 nt. position (4/7)
10259	22907	36117	1.62	2.0E-02	A1840342.1	EST_HUMAN	Japanese encephalitis virus envelope protein mRNA, partial cds
10539	23286	36469	1.78	2.0E-02	Z73966.1	NT	wat7502.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2298315 3'
11344	24034	37337	2.17	2.0E-02	D88184.1	NT	Mycobacterium tuberculosis H37Rv complete genome; segment 83/162
11892	24277	37598	2.21	2.0E-02	10947055	NT	Equus caballus DNA for 17alpha-hydroxylase/17,20-lyase, complete cds
11892	24277	37599	2.21	2.0E-02	10947055	NT	Homo sapiens ankyrin 3, node of Ranvier (ankyrin G) (ANK3), transcript variant 1, mRNA
							Homo sapiens ankyrin 3, node of Ranvier (ankyrin G) (ANK3), transcript variant 1, mRNA

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11880	17609	30595	1.9	2.0E-02	AA158538.1	EST_HUMAN	aa15b10.r1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:813307 5'
12336	15506		1.82	2.0E-02	AL161632.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 32
12786	25038		6.4	2.0E-02	T80037.1	EST_HUMAN	y04c09.r1 Soares infant brain 1N15 Homo sapiens cDNA clone IMAGE:24676 5'
677	13452	26095	2.15	1.9E-02	AA572764.1	EST_HUMAN	nt18a07.s1 NCI_CGAP_P1 Homo sapiens cDNA clone IMAGE:914196 similar to contains L1.11 L1 repetitive element;
1811	14358	27047	1.15	1.9E-02	P18488	SWISSPROT	EMPTY SPIRACLES HOMEOTIC PROTEIN
2032	14767	27496	2.68	1.9E-02	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
2510	15227	27998	2.68	1.9E-02	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
2906	15672	28320	7.48	1.9E-02	AL161550.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 50
2952	15718	28369	1.66	1.9E-02	AA713896.1	EST_HUMAN	nw04r05.s1 NCI_CGAP_SS1 Homo sapiens cDNA clone IMAGE:1238337 3'
3558	16351		1.18	1.9E-02	AV648669.1	EST_HUMAN	AV648669 GLC Homo sapiens cDNA clone CLCBLH07 3'
3691	16444		9.58	1.9E-02	IN52250.1	EST_HUMAN	y228b02.s1 Soares_multiple_sclerosis_2NBH1MSP Homo sapiens cDNA clone IMAGE:284331 3'
3703	16456	29095	0.95	1.9E-02	BE738088.1	EST_HUMAN	601572682F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:3839584 5'
4025	16770	29402	1.49	1.9E-02	AI301183.1	EST_HUMAN	gn04c07.x1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1897260 3' similar to contains Alu repetitive element;
4170	16910	29539	1.83	1.9E-02	AF141940.1	NT	Myoplasma imitans VhaA1 precursor (VhaA1) and VhaA2 precursor (VhaA2) genes, partial cds
4170	16910	29540	1.83	1.9E-02	P09081	SWISSPROT	HOMEOTIC BICOID PROTEIN (PRD-4)
4504	17239	29872	3.21	1.9E-02	P09081	SWISSPROT	HOMEOTIC BICOID PROTEIN (PRD-4)
4951	15227	27968	4.09	1.9E-02	AI452899.1	EST_HUMAN	ij46d04.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2144551 3' similar to contains Alu repetitive element;
5233	18039	30667	0.99	1.9E-02	AL161550.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 50
5382	18182	30872	1.41	1.9E-02	AF037352.1	NT	Mus musculus T cell receptor gamma locus, TOR gamma 1 and gamma 3 gene clusters
5701	18495		0.86	1.9E-02	L47572.1	NT	Meleagris gallopavo paraoxonase-2 (PON2) mRNA, complete cds
7001	19893	32744	1.38	1.9E-02	AB019507.1	NT	Drosophila karekoi gene for glyceral-3-phosphate dehydrogenase, complete cds
7001	19893	32745	1.38	1.9E-02	U19241.1	NT	Homo sapiens interferon-gamma receptor alpha chain gene, exon 1
8469	21161	32745	1.23	1.9E-02	U19241.1	NT	Homo sapiens interferon-gamma receptor alpha chain gene, exon 1
9230	21909	35082	1.03	1.9E-02	BF318129.1	EST_HUMAN	Neisseria meningitidis serogroup A strain Z2491 complete genome, segment 3/7
9613	22266	35452	0.6	1.9E-02	L10114.1	NT	60186130F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4125462 5'
9845	22593	35786	1.05	1.9E-02	BF695832.1	NT	Nicotiana tabacum type II phytochrome (phyB) gene, complete cds
10152	22800	36017	0.54	1.9E-02	D64001.1	EST_HUMAN	601852385F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4076253 5'
10681	23372	36814	1.44	1.9E-02	AF008933.1	NT	Synechocystis sp. PCC6803 complete genome, 20/27, 2539000-2644794
12090	25171	30903	2.82	1.9E-02	AF101085.1	NT	Vibrio cholerae V86 phage putative replication protein gene, complete cds
12646	25147		1.36	1.9E-02	L11068.1	NT	Hirudo medicinalis intermediate filament gliadin mRNA, complete cds Candida albicans lambda Ca3/B fragment

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338	13137	25772	1.4	1.8E-02	AW771104.1	EST_HUMAN	hm52c06.x1 NCL_CGAP_Cot17 Homo sapiens cDNA clone IMAGE:3027274 3' similar to contains element
670	13446	28086	0.83	1.8E-02	BF308122.1	EST_HUMAN	MER29 repetitive element;
1137	13892	26553	1.32	1.8E-02	X17684.1	NT	601894328F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4139983 5'
1416	14184	28847	1.73	1.8E-02	AF243382.1	NT	H.francisci mRNA for myelin basic protein (MBP)
2685	15394	28133	1.71	1.8E-02	AE004544.1	NT	Drosophila melanogaster cytoplasmic protein encode (enc) mRNA, complete cds
3205	15988		0.94	1.8E-02	AI805828.1	EST_HUMAN	Pseudomonas aeruginosa PA01, section 105 of 529 of the complete genome
4065	16810		0.99	1.8E-02	AA861446.1	EST_HUMAN	ak24h04.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2090266 3'
4398	17133	29794	1.17	1.8E-02	AW936363.1	EST_HUMAN	QV4-DT0021-301299-071-511 DT0021 Homo sapiens cDNA
6712	18827	32871	5.02	1.8E-02	P14310	SWISSPROT	HYPOTHETICAL 7.9 KD PROTEIN IN FIXW 5'REGION
8028	20724	33857	0.69	1.8E-02	U37091.1	NT	Mus musculus carbonic anhydrase IV gene, complete cds
8367	21060	34200	0.91	1.8E-02	AW905327.1	EST_HUMAN	QV2-NN1073-220400-158-h09 NN1073 Homo sapiens cDNA
8410	21103	34242	0.8	1.8E-02	6878943	NT	Mus musculus microtubule-associated protein 2 (Map2), mRNA
9092	22054	35225	0.49	1.8E-02	BF241924.1	EST_HUMAN	601877026F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4105303 5'
9392	22054	35226	0.49	1.8E-02	BF241924.1	EST_HUMAN	601877026F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4105303 5'
9542	22195		2.41	1.8E-02	AA897643.1	EST_HUMAN	al62709.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1394921 3' similar to gb.L11672 ZINC FINGER PROTEIN 91 (HUMAN);
9983	22611	35815	1.51	1.8E-02	BE778274.1	EST_HUMAN	60146345F1 NIH_MGC_87 Homo sapiens cDNA clone IMAGE:3866963 5'
10126	22774	35987	1.37	1.8E-02	X96933.1	NT	L.stagalis mRNA for myomodulin neuropeptide precursor
11414	23181	36409	2.31	1.8E-02	AB002337.2	NT	Homo sapiens mRNA for KIAA0339 protein, partial cds
11414	23181	36410	2.31	1.8E-02	AB002337.2	NT	Homo sapiens mRNA for KIAA0339 protein, partial cds
11613	24211	37535	1.59	1.8E-02	AP000006.1	NT	Pyrococcus horikoshii O13 genomic DNA, 1166001-1485000 nt, position (617)
11626	24223	37545	3.32	1.8E-02	U62749.1	NT	Zea mays acidic ribosomal protein P2a-3 (pp2a-3) mRNA, partial cds
886	13655	26323	1.86	1.7E-02	BE394869.1	EST_HUMAN	601310626F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3632180 5'
1783	14524	27230	2.17	1.7E-02	AW573183.1	EST_HUMAN	h34a03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2933740 3' similar to contains L1.11 L1 repetitive element;
1783	14524	27231	2.17	1.7E-02	AW573183.1	EST_HUMAN	h34a03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2933740 3' similar to contains L1.11 L1 repetitive element;
1864	14602		3.41	1.7E-02	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
2108	14837		10.5	1.7E-02	AB004816.1	NT	Oryctolagus cuniculus mRNA for mitisugmin28, complete cds
2291	15016	27752	0.99	1.7E-02	S74186.1	NT	[microsatellite INRA41] [Ovis aries=sheep, Genomic, 361 nt, segment 1 of 2]
2846	15356		1.01	1.7E-02	7657495	NT	Homo sapiens putative Rab5 GDP/GTP exchange factor homologue (RABEX5), mRNA
2898	15782	28411	1.44	1.7E-02	AI147615.1	EST_HUMAN	qb22a08.x1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:1696982 3'

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3502	16258		4.67	1.7E-02	AW827368.1	EST_HUMAN	hm45a04.x1 NCL_CGAP_RDF1 Homo sapiens cDNA clone IMAGE:3015534 3' similar to contains
3614	16367		0.73	1.7E-02	P04929	SWISSPROT	MER19.b1 MER19 repetitive element ;
4148	16890		1.23	1.7E-02	AA669618.1	EST_HUMAN	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR
4178	16916		2.04	1.7E-02	R02506.1	EST_HUMAN	ac1904.s1 Stratagene ovary (#937217) Homo sapiens cDNA clone IMAGE:856927 3' similar to contains Alu repetitive element; contains element MER24 repetitive element ;
4420	17156	29787	1.49	1.7E-02	A305279.1	EST_HUMAN	ye86f08.t1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:124647 5'
4491	17227	29856	1.78	1.7E-02	AW573183.1	EST_HUMAN	qm08g07.x1 NCL_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1881276 3' similar to gb:X52359 ZINC FINGER PROTEIN 30 (HUMAN);
4666	17400	30034	1.61	1.7E-02	V00641.1	NT	h134a03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2933740 3' similar to contains L1.11 L1 repetitive element ;
4763	17495	30334	5.84	1.7E-02	A1015076.1	EST_HUMAN	Messenger RNA for anglerfish (Lophius americanus) somatostatin II
5007	17730	30334	0.69	1.7E-02	6981289	NT	ov51e02.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1640858 3'
5096	17815		0.91	1.7E-02	AJ229041.1	NT	Rattus norvegicus N-arginine dibasic convertase 1 (Nrd1), mRNA
6035	18815	31775	2.07	1.7E-02	AJ769247.1	EST_HUMAN	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3
6484	19251	32250	1.47	1.7E-02	AJ038280.1	EST_HUMAN	wg35f09.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2367113 3' similar to contains Alu repetitive element;
6950	19432	32448	1.27	1.7E-02	AF190930.1	NT	oy85h03.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1672681 3'
7103	19791	32856	2.44	1.7E-02	8400716	NT	Macaca fascicularis protein tyrosine phosphatase (PRL-1) mRNA, complete cds
7257	19941	33016	1.06	1.7E-02	L07899.1	NT	Homo sapiens nebulin (NEB), mRNA
7642	20307	33017	1.06	1.7E-02	L07899.1	NT	Human apolipoprotein (a) gene, exon 1
9336	20407	33523	0.98	1.7E-02	AJ010770.1	NT	Human apolipoprotein (a) gene, exon 1
9598	22251	35437	1.3	1.7E-02	AJ040554.1	EST_HUMAN	Homo sapiens hyperion gene, exons 1-50
11801	24391	37724	1.38	1.7E-02	5902007	NT	Caenorhabditis elegans cCAF1 protein gene, complete cds
12631	25337	30716	2.39	1.7E-02	AW903482.1	EST_HUMAN	DKFZp434i0314.t1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434i0314 5'
498	13282		3.19	1.6E-02	AL021829.1	NT	Homo sapiens serum constituent protein (MSE55), mRNA
1653	14399	27088	1.04	1.6E-02	Y18889.1	NT	GM4-NN1030-040400-130-06 NN1030 Homo sapiens cDNA
2246	14974	27711	0.9	1.6E-02	Q64176	SWISSPROT	Mycobacterium tuberculosis H37Rv complete genome; segment 13/162
2246	14974	27711	0.9	1.6E-02	Q64176	SWISSPROT	Treponema mallophilum flaB2, flaB3 and flpD genes for flagellin subunit proteins and CAP protein homologue
2570	15284	28022	1.05	1.6E-02	AJ006345.1	NT	LIVER CARBOXYLESTERASE 22 PRECURSOR (EGASYN) (ESTERASE-22)
2649	15359	28102	1.48	1.6E-02	AA484872.1	EST_HUMAN	LIVER CARBOXYLESTERASE 22 PRECURSOR (EGASYN) (ESTERASE-22)
2698	15408		0.96	1.6E-02	AB014534.1	NT	Homo sapiens KVLQ11 gene
							ne81006.s1 NCL_CGAP_Ew1 Homo sapiens cDNA clone IMAGE:910667
							Homo sapiens mRNA for KIAA0634 protein, partial cds

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3016	15782	28431	0.71	1.6E-02	AF112282.1	NT	Lassea sp. isolate lBd cytochrome oxidase III gene, partial cds; mitochondrial gene for mitochondrial product
3516	16272	28926	5.9	1.6E-02	AW850652.1	EST_HUMAN	IL3-CT0219-160200-063-C07 CT0219 Homo sapiens cDNA
3830	16581	29215	1.32	1.6E-02	AL163301.2	NT	Homo sapiens chromosome 21 segment HS21C101
4154	16896						Mus musculus major histocompatibility complex region NG27, NG28, RPS28, NADH oxidoreductase, NG29, KIFC1, Fas-binding protein, BING1, tapasin, RelGDS-like, KE2, BING4, beta 1,3-galactosyl transferase, and RPS18 genes, complete cds; Sacm21 gene, partial>
4267	17007	28640	2.49	1.6E-02	AF110520.1	NT	QV2-PT0012-140100-030-f07 PT0012 Homo sapiens cDNA
5536	18334	31241	0.97	1.6E-02	AW875407.1	EST_HUMAN	Mus musculus CD5 antigen (Cd5), mRNA
6546	19311	32316	1.25	1.6E-02	6671715	NT	Candida albicans CaGGR3 gene, complete cds
6832	19494	32517	2.05	1.6E-02	AB015281.1	NT	Saccharomyces cerevisiae CAD2 gene for cadmium resistance protein, complete cds
6832	19494	32518	1.75	1.6E-02	AB027571.1	NT	Saccharomyces cerevisiae CAD2 gene for cadmium resistance protein, complete cds
7610	20276	33384	1.75	1.6E-02	AB027571.1	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 20
8020	20715	33847	0.86	1.6E-02	AL161508.2	NT	
8078	20772		0.76	1.6E-02	AJ277662.1	NT	Homo sapiens partial TUB gene for tubby (mouse) homolog and LMO1 gene for LIM domain only 1 protein
9940	22688		1.88	1.6E-02	X05151.1	NT	Human apoC-II gene for preproapolipoprotein C-II
			2.72	1.6E-02	AF079764.1	NT	Drosophila melanogaster enhancer of polycomb (E(Pc)) mRNA, complete cds
10319	22968	36184	1.29	1.6E-02	AA572818.1	EST_HUMAN	nf19g03 st NCL CGAP_P1 Homo sapiens cDNA clone IMAGE:914260 similar to SW:TELO_RABIT
10319	22968	36185					P29294 TELOKIN. [1]:
10826	25132	36748	1.29	1.6E-02	AA572818.1	EST_HUMAN	nf19g03 st NCL CGAP_P1 Homo sapiens cDNA clone IMAGE:914260 similar to SW:TELO_RABIT
11174	23841	37124	2.38	1.6E-02	Z94828.1	NT	P29294 TELOKIN. [1]:
11174	23841	37125	2.54	1.6E-02	AL161508.2	NT	G.gallus microsatellite DNA (LE10280 (=T1611E11))
11495	24096	37407	2.54	1.6E-02	AL161508.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 20
734	13508		1.54	1.6E-02	AJ375558.1	EST_HUMAN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 20
2138	14898	27598	23.05	1.9E-02	8923734	NT	q288e10.x1 Soares_pregnant_uterus NbtPU Homo sapiens cDNA clone IMAGE:2042442 3'
2172	14901	27635	4.24	1.9E-02	N39521.1	EST_HUMAN	Homo sapiens transcription factor (HSA130894), mRNA
3057	15823	28467	1.69	1.9E-02	AL161594.2	NT	yv27b07 st Soares fetal liver spleen 1NLS Homo sapiens cDNA clone IMAGE:243925 3'
3057	15823	28468	1.6	1.9E-02	AJ006216.1	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 90
3711	16464	29103	1.6	1.9E-02	AJ006216.1	NT	Homo sapiens CACNA1F gene, exons 1 to 48
6201	18977	31955	0.98	1.9E-02	BF092942.1	EST_HUMAN	Homo sapiens CACNA1F gene, exons 1 to 48
7219	19904		1.63	1.9E-02	Q09711	SWISSPROT	MR4-TN0115-080900-201-b12 TN0115 Homo sapiens cDNA
7301	19984	33080	1.2	1.9E-02	11467282	NT	HYPOTHEICAL CALCIUM-BINDING PROTEIN C18B11.04 IN CHROMOSOME I
					11467282	NT	Oyanophora paradoxa cyanelle, complete genome
					11418713	NT	Homo sapiens KIAA1009 protein (KIAA1009), mRNA

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Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7773	20469	33592	1.63	1.5E-02	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
7781	20476	33602	3.59	1.5E-02	11417739	NT	Homo sapiens valyl-tRNA synthetase 2 (VARS2), mRNA
8729	21421	34585	0.9	1.5E-02	BF345554.1	EST_HUMAN	602019135F1 NCI_CGAP_Bn67 Homo sapiens cDNA clone IMAGE:4154504 5'
9388	21943	35251	0.51	1.5E-02	AF096774.1	NT	Homo sapiens kinase-related protein isoform 1 mRNA, complete cds
9470	22078	35251	1.47	1.5E-02	D44806.1	NT	Saccharomyces cerevisiae chromosome VI plasmid GapC
9711	22362	35559	0.98	1.5E-02	R32667.1	EST_HUMAN	yh54b10.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:133531 5'
9711	22362	35560	0.98	1.5E-02	R32667.1	EST_HUMAN	yh54b10.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:133531 5'
11121	23780	37088	3.49	1.5E-02	L40609.1	NT	Plasmodium falciparum (strain FCR3) variant-specific surface protein (var-2, var-3) genes, complete cds's
11163	23830	37109	2.14	1.5E-02	AL111238.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
11856	24440	37781	1.38	1.5E-02	AL161492.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 4
12277	25214		1.74	1.5E-02	AW750834.1	EST_HUMAN	RC4-CN0049-140100-011-c11 CN0049 Homo sapiens cDNA
12787	25039		1.45	1.5E-02	AF763127.1	EST_HUMAN	wf08h03.x1 NCI_CGAP CLL1 Homo sapiens cDNA clone IMAGE:2389493 3' similar to contains Alu repetitive element; contains element MER26 MSR1 repetitive element
408	13183		2.29	1.4E-02	AE002230.2	NT	Chlamydia pneumoniae AR39, section 58 of 94 of the complete genome
1096	13854	26513	4.42	1.4E-02	7705980	NT	Homo sapiens NESH protein (LOC51225), mRNA
1234	13983		1.24	1.4E-02	U32800.1	NT	Haemophilus influenzae Rd section 115 of 163 of the complete genome
1275	14025		3.77	1.4E-02	U67779.1	NT	Xenopus laevis neurogenin related 1b (X-NGNR-1b) mRNA, complete cds
1376	14123		1.45	1.4E-02	AF216854.1	NT	Homo sapiens headpin gene, complete cds
1507	14263		1.26	1.4E-02	AV723785.1	EST_HUMAN	AV723785 HTB Homo sapiens cDNA clone HTBAHH11 5'
3207	15870	28622					Bifidobacterium longum Na+/H+ antiporter (nhaB), cytosine deaminase, and alpha-galactosidase (aglL) genes, complete cds; and N-acetylglucosaminyltransferase repressor protein (nagC/xyfR) gene, partial cds
3393	16152	28805	2	1.4E-02	AF160869.2	NT	xb09d09.x1 NCI_CGAP_GUT Homo sapiens cDNA clone IMAGE:2575793 3'
3478	16234	28888	1.07	1.4E-02	AW074212.1	EST_HUMAN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 82
3478	16234	28889	6.33	1.4E-02	AL161586.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 82
3648	16401	29041	6.33	1.4E-02	AL161586.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 82
4455	17181	29817	8.63	1.4E-02	8996918	NT	Mus musculus histocompatibility 2, complement component factor B (H2-Bf), mRNA
4455	17191	29818	7.77	1.4E-02	AW962688.1	EST_HUMAN	EST374761 MAGG resequences, MAGG Homo sapiens cDNA
4821	17552	30174	7.77	1.4E-02	AW962688.1	EST_HUMAN	EST374761 MAGG resequences, MAGG Homo sapiens cDNA
4821	17552	30175	7.21	1.4E-02	BE733142.1	EST_HUMAN	601567403F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3842280 5'
4821	17552	30175	7.21	1.4E-02	BE733142.1	EST_HUMAN	601567403F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3842280 5'
6321	19091	32079	5.47	1.4E-02	AA559030.1	EST_HUMAN	nl11c04.s1 NCI_CGAP_B12 Homo sapiens cDNA clone IMAGE:1029880 3' similar to contains Alu repetitive element;

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLASTE Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6321	18091	32080	5.47	1.4E-02	AA59030.1	EST_HUMAN	nt11c04.s1 NCI_COAP_Br2 Homo sapiens cDNA clone IMAGE:1028890 3' similar to contains Alu repetitive element;
8038	20733		1.94	1.4E-02	AL022073.1	NT	Mycobacterium tuberculosis H37Rv complete genome; segment 88/162
8798	21488	34634	0.75	1.4E-02	M81702.1	NT	Candida bodinii methanol oxidase (AOD1) gene, complete cds
9063	21742	34900	0.84	1.4E-02	AJ272265.1	NT	Homo sapiens SPP2 gene for secreted phosphoprotein 24 precursor, exons 1-8
9300	21967	35141	2.27	1.4E-02	BE544561.1	EST_HUMAN	601078239F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3464241 5'
10455	23101		0.76	1.4E-02	AL163218.2	NT	Homo sapiens chromosome 21 segment HS21C018
11985	24526	37267	2.2	1.4E-02	X60459.1	NT	Human IFNAR gene for interferon alpha/beta receptor
12331	24747		1.37	1.4E-02	AF324985.1	NT	Arabidopsis thaliana F21J9.2 mRNA, complete cds
12601	24913		2.36	1.4E-02		NT	Homo sapiens sperm associated antigen 7 (SPAG7), mRNA
1948	14683	27395	2.21	1.3E-02	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
3208	15971	28623	2.23	1.3E-02	BF697081.1	EST_HUMAN	602129475F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4286203 5'
3208	15971	28624	2.23	1.3E-02	BF697081.1	EST_HUMAN	602129475F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4286203 5'
3951	16701		1.31	1.3E-02	AF166288.1	NT	Mus musculus beta-sarcoglycan gene, complete cds
4874	17601	30223	0.93	1.3E-02	U66061.1	NT	Human germline T-cell receptor beta chain TCRBV17S1A1T, TCRBV2S1, TCRBV10S1P, TCRBV28S1P, TCRBV16S1P, TCRBV15S1, TCRBV11S1A1T, HVB relic, TCRBV28S1P, TCRBV34S1, TCRBV14S1, TCRBV3S1, TCRBV4S1A1T, TRY4, TRY5, TRY6, TRY7, TRY8, TCRBD1, TCRBV1S1, TCRBV1S2, finger protein 92, rnmq28orf
5168	17975	30532	1.31	1.3E-02	AL049866.2	NT	Mus musculus chromosome X contigB; X-linked lymphocyte regulated 5 gene, Zinc finger protein 275, Zinc finger protein 92, rnmq28orf
5168	17975	30533	1.31	1.3E-02	AL049866.2	NT	Mus musculus chromosome X contigB; X-linked lymphocyte regulated 5 gene, Zinc finger protein 275, Zinc finger protein 92, rnmq28orf
6072	18851	31816	1.05	1.3E-02	U80017.1	NT	Homo sapiens basic transcription factor 2 p44 (btf2p44) gene, partial cds, neuronal apoptosis inhibitory protein (nail) and survival motor neuron protein (smn) genes, complete cds
6105	18883	31851	0.88	1.3E-02	M62962.1	NT	C.reinhardtii ribulose 1,5-bisphosphate carboxylase/oxygenase activase mRNA, complete cds
6665	17942	30535	1.33	1.3E-02	AL161546.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 46
6665	17942	30536	1.33	1.3E-02	AL161546.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 46
7477	20150	33244	4.9	1.3E-02	A1031593.1	EST_HUMAN	ow06g05.x1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:1646072 3' similar to contains Alu repetitive element;
8380	21073	34212	1.65	1.3E-02	AF159961.1	NT	Homo sapiens human endogenous retrovirus W gagC3.37 G gag (gag) gene, complete cds
10107	22755	35967	1.91	1.3E-02	M63707.1	NT	Mouse kidney androgen-regulated protein (KAP) gene, complete cds
10178	22826	36040	0.68	1.3E-02	AE001304.1	NT	Chlamydia trachomatis section 31 of 87 of the complete genome
10913	23593	36838	3.97	1.3E-02	AW268563.1	EST_HUMAN	xv34e03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2815036 3'
10913	23593	36839	3.87	1.3E-02	AW268563.1	EST_HUMAN	xv34e03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2815036 3'

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12337	25352		1.44	1.3E-02	Z89117.1	NT	Bacillus subtilis complete genome (section 14 of 21): from 2599481 to 2812870
12437	24807		2.41	1.3E-02	9633069	NT	Human herpesvirus 6B, complete genome
12607	25145		28.18	1.3E-02	AF192238.1	NT	Homo sapiens V1b vasopressin receptor (VPR3) gene, complete cds
345	13145	25783	3.48	1.2E-02	AA059299.1	EST_HUMAN	z665g01.1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:381840 5' similar to contains element
440	13226	25869	1.66	1.2E-02	F38898	SWISSPROT	L1 repetitive element
721	13495	26148	2.02	1.2E-02	AI183522.1	EST_HUMAN	HYPOPHYSICAL 17.1 KD PROTEIN IN PUR53 REGION
2175	14904	27637	1.81	1.2E-02	AL163213.2	NT	q68a012.x1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1734670 3' similar to contains L1.11 L1
2178	14907	27640	1.71	1.2E-02	AW172350.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C013
2444	15163	27801	1.39	1.2E-02	AW172350.1	EST_HUMAN	AV731704 HTF Homo sapiens cDNA clone HTFBHG11 5'
2642	15163	27801	1.07	1.2E-02	AW172350.1	EST_HUMAN	x37a09.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2659432 3'
3098	15863	28691	6.66	1.2E-02	AA075418.1	EST_HUMAN	x37a09.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2659432 3'
3281	16042	28691	2.1	1.2E-02	R62805.1	EST_HUMAN	zm88a03.1 Strabagene ovarian cancer (#937219) Homo sapiens cDNA clone IMAGE:545020 5'
3284	16045	28694	0.92	1.2E-02	AI668694.1	EST_HUMAN	y11b08.s1 Soares placenta N2b2HP Homo sapiens cDNA clone IMAGE:1738903 3'
4675	17409	30045	0.91	1.2E-02	AI687378.1	EST_HUMAN	z66a07.x5 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:308532 3' similar to contains element MER22 repetitive element
4859	17588	30211	2.03	1.2E-02	U91328.1	NT	wn39f04.x1 NCI CGAP_U14 Homo sapiens cDNA clone IMAGE:2438335 3'
4881	17704		1.13	1.2E-02	AB019786.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
5025	17746	30358	1.41	1.2E-02	AV731704.1	EST_HUMAN	Cynops Pyrrhogaster CpUbiqT mRNA, partial cds
5066	18461	31375	1.73	1.2E-02	D78589.1	NT	AV731704 HTF Homo sapiens cDNA clone HTFBHG11 5'
6028	18806	31767	0.72	1.2E-02	AF045555.1	NT	Rana rugosa mRNA for calreticulin, complete cds
6807	19845	32691	6.46	1.2E-02	AF175412.1	NT	Homo sapiens wbscr1 (WBSOR1) and wbscr5 (WBSOR5) genes, complete cds, alternatively spliced and replication factor C subunit 2 (RFC2) gene, complete cds
7192	19878	32952	1.36	1.2E-02	H02197.1	EST_HUMAN	Mus musculus DNA methyltransferase (Dnm1) gene, exons 2, 3, 4, and 5
7212	19897	32872	10.54	1.2E-02	AV732093.1	EST_HUMAN	y34ht12.s1 Soares placenta N2b2HP Homo sapiens cDNA clone IMAGE:150685 3'
7456	20130	33222	0.57	1.2E-02	BF216650.1	EST_HUMAN	AV732093 HTF Homo sapiens cDNA clone HTFBHG11 5'
7896	20591	33722	2.18	1.2E-02	Q11205	SWISSPROT	601882949F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4085253 5'
8092	20786	33917	1.35	1.2E-02	AF183612.1	NT	GMP-N-ACETYLNEURAMINATE-BETA-GALACTOSAMIDE-ALPHA-2,3-SIALYLTRANSFERASE (BETA-GALACTOSIDE ALPHA-2,3-SIALYLTRANSFERASE) (ALPHA 2,3-ST) (GAL-NAO6S) (GAL-BETA-1,3-GALNAc-ALPHA-2,3-SIALYLTRANSFERASE) (ST3GAL.2) (SIA T4-B)
8092	20786	33918	1.35	1.2E-02	AF183612.1	NT	Homo sapiens fringe protein mRNA, partial cds
							Homo sapiens fringe protein mRNA, partial cds

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8788	21480		1.03	1.2E-02	T76987.1	EST_HUMAN	y472c08.s1 Soares fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:113774 3'
9539	22192	35376	2.46	1.2E-02	AB031013.1	NT	Norwalk-like virus genogroup 2 gene for capsid protein, complete cds
9570	22223	35408	1.35	1.2E-02	AJ246003.1	NT	Homo sapiens Spast gene for spastin protein
12034	24559	31112	2.88	1.2E-02	O15534	SWISSPROT	PERIOD CIRCADIAN PROTEIN 1 (CIRCADIAN PACEMAKER PROTEIN RIGU1) (HPER)
12615	24922		8.02	1.2E-02	C18119.1	EST_HUMAN	C18119 Human placenta cDNA (T Fujwara) Homo sapiens cDNA clone GEN-557G06 5'
1246	13995	26662	1.49	1.1E-02	AA070384.1	EST_HUMAN	zm69e11.s1 Stratagene neuroepithelium (#937231) Homo sapiens cDNA clone IMAGE:530924 3'
1701	14444	27143	1.35	1.1E-02	X75491.1	NT	H. sapiens LIPA gene, exon 4
1701	14444	27144	1.35	1.1E-02	X75491.1	NT	H. sapiens LIPA gene, exon 4
2031	14766	27495	4.92	1.1E-02	BF345263.1	EST_HUMAN	602018037F1 NCI CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4153808 5'
2880	15647		4.05	1.1E-02	N95523.1	EST_HUMAN	zn40a05.r1 Soares fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:295040 5'
3513	16289	28924	2.98	1.1E-02	AI653508.1	EST_HUMAN	iq95b10.x1 NCI CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2216539 3' similar to SW:XP_F_HUMAN
4088	16829		0.86	1.1E-02	AW813786.1	EST_HUMAN	Q92889 DNA-REPAIR PROTEIN COMPLEMENTING XP-F CELL ;
4778	17510	30132	1.5	1.1E-02	AL048383.2	EST_HUMAN	RC3-ST0197-120200-015-g11 ST0197 Homo sapiens cDNA
							DKFZp586E0924 s1 586 (synonym: hute1) Homo sapiens cDNA clone DKFZp586E0924
6057	18837	31799	1	1.1E-02	U69480.1	NT	Bacillus subtilis SpoVK (spoVK), YnbA (ynbA), YnbB (ynbB), GlnR (glnR), glutamine synthetase (glnA), YnaA (ynaA), YnaB (ynaB), YnaC (ynaC), YnaD (ynaD), YnaE (ynaE), YnaF (ynaF), YnaG (ynaG), YnaH (ynah), YnaI (ynai), YnaJ (ynaj), YnaK (ynak), xylan beta-1,4-xylosyl>
7497	20169	33261	2.51	1.1E-02	BE149611.1	EST_HUMAN	RC1-HT0256-100300-016-h07 HT0256 Homo sapiens cDNA
8538	21230	34372	0.91	1.1E-02	AW996160.1	EST_HUMAN	QV3-BN0045-220300-128-h02 BN0045 Homo sapiens cDNA
8721	21413	34556	0.97	1.1E-02	C04803.1	EST_HUMAN	C04803 Human heart cDNA (YNakamura) Homo sapiens cDNA clone 3NHG4040
8800	21492	34639	6.45	1.1E-02	Q61982	SWISSPROT	NEUROGENIC LOCUS NOTCH 3 PROTEIN
9829	22480	35682	2.03	1.1E-02	AA082578.1	EST_HUMAN	zn24a01.r1 Stratagene neuroepithelium NT2RAM1 937234 Homo sapiens cDNA clone IMAGE:548328 5'
9994	22642	35854	3.55	1.1E-02	AA314665.1	EST_HUMAN	EST186494 Colon carcinoma (HCC) cell line II Homo sapiens cDNA 5' end
10900	23580	36830	3.23	1.1E-02	11435505	NT	Homo sapiens T-box 5 (TBX5), mRNA
11923	24484		4.16	1.1E-02	AA668239.1	EST_HUMAN	ab77f11.s1 Stratagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:853005 3' similar to contains
12878	16829		1.62	1.1E-02	AW813796.1	EST_HUMAN	Alu repetitive element
6	12833	25448	9.16	1.0E-02	AW846120.1	EST_HUMAN	RC3-ST0197-120200-015-g11 ST0197 Homo sapiens cDNA
1513	14280	26946	1.56	1.0E-02	AW368128.1	EST_HUMAN	MR3-CT0176-111099-003-e10 CT0176 Homo sapiens cDNA
2577	15291		1.57	1.0E-02	AA806389.1	EST_HUMAN	CM2-HT0177-041099-017-h12 HT0177 Homo sapiens cDNA
3087	15852	28494	2.7	1.0E-02	BE835558.1	EST_HUMAN	oc22108.s1 NCI CGAP_GC81 Homo sapiens cDNA clone IMAGE:1350495 3'
3257	16019	28669	1.49	1.0E-02	BE969999.1	EST_HUMAN	RCO-FN0025-250500-021-d02 FN0025 Homo sapiens cDNA
3861	16611	29250	0.79	1.0E-02	AI05086.1	EST_HUMAN	601649987R1 NIH_MGC_74 Homo sapiens cDNA clone IMAGE:3933689 3'
							HA0927 Human fetal liver cDNA library Homo sapiens cDNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3876	16626	29264	0.7	1.0E-02	AL163302.2	NT	Homo sapiens chromosome 21 segment HS21C102
4726	17458	30094	4.24	1.0E-02	6753521	NT	Mus musculus corticotropin releasing hormone receptor 2 (Chr2), mRNA
4793	17524	30146	5.16	1.0E-02	R96567.1	EST_HUMAN	yq54h01.r1 Soares fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:199633 5'
5331	18134	30763	0.72	1.0E-02	H62681.1	EST_HUMAN	yq36h11.r1 Soares ovary tumor N6HOT Homo sapiens cDNA clone IMAGE:235941 5'
5681	18456	31370	0.57	1.0E-02	AF309388.1	NT	Mus musculus transcription complex subunit NF-ATc4 (Nfatc4) gene, exons 1 and 2
6025	18805	31766	1.4	1.0E-02	AF257303.1	NT	Mus musculus synaptotagmin II (Sy2) gene, complete cds
6088	18868	31831	2.47	1.0E-02	AW577113.1	EST_HUMAN	MR4-BT0356-070100-201-h01 BT0356 Homo sapiens cDNA
6088	18868	31832	2.47	1.0E-02	AW577113.1	EST_HUMAN	MR4-BT0356-070100-201-h01 BT0356 Homo sapiens cDNA
6664	19581	32616	1.92	1.0E-02	Z28942.1	NT	Z.mays U3snRNA pseudogene
9293	21960	35133	4.19	1.0E-02	BF036331.1	EST_HUMAN	601459570F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3863177 5'
9293	21960	35134	4.19	1.0E-02	BF036331.1	EST_HUMAN	601459570F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3863177 5'
11229	23892		1.97	1.0E-02	AF157559.1	NT	Citridia fasciculata 27 kDa guide RNA-binding protein mRNA, complete cds; mitochondrial gene for
11283	23925						ig55h07.x1 NCI CGAP_P128 Homo sapiens cDNA clone IMAGE:2112733 3' similar to gb:X15183 cds1
11340	24030	37334	1.46	1.0E-02	A1417961.1	EST_HUMAN	HEAT SHOCK PROTEIN HSP 90-ALPHA (HUMAN); contains Alu repetitive element; contains element MER5
12003	25416		1.97	1.0E-02	AV760016.1	EST_HUMAN	repetitive element;
12059	25189	30811	1.83	1.0E-02	Q62203	SWISSPROT	AV760016 MDS Homo sapiens cDNA clone MDSBDCT0 5'
12075	25243		3.76	1.0E-02	AW935621.1	EST_HUMAN	SPLICEOSOME ASSOCIATED PROTEIN 62 (SAP 62) (SPLICING FACTOR 3A SUBUNIT 2) (SF3A68)
12592	25289		5.93	1.0E-02	S70330.1	NT	RC2-DT0007-120200-016-h02 DT0007 Homo sapiens cDNA
12803	25050	30957	3.74	1.0E-02	X62654.1	NT	Homo sapiens renal dipeptidase (RDP) gene, complete cds
			1.84	1.0E-02	AB039887.1	NT	H.sapiens gene for Me491/CD63 antigen
873	13642	26312	2.1	9.0E-03	A1796126.1	EST_HUMAN	Homo sapiens WDR4 gene for WD repeat protein, complete cds
1241	13990		2.07	9.0E-03	BE781889.1	EST_HUMAN	WH4209.x1 NCI CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2383433 3' similar to contains element
1463	14211	28899	1.1	9.0E-03	AE001270.1	NT	MER22 MER22 repetitive element;
2394	15115	27852	2.48	9.0E-03	AL181559.2	NT	601470242F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3873346 5'
2403	15124	27861	0.92	9.0E-03	AF099934.1	NT	Treponema pallidum section 86 of 87 of the complete genome
3659	16412	29050	1.21	9.0E-03	J05184.1	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 59
4927	17855	30267	1.03	9.0E-03	BE047949.1	EST_HUMAN	Mus musculus MHC class III protein RPl1 (Rpl1) mRNA, partial cds
4964	17689	30267	0.95	9.0E-03	T70044.1	EST_HUMAN	S.acidocalcarius thermophilus gene, complete cds
4964	17689	30268	0.95	9.0E-03	T70044.1	EST_HUMAN	tz44e10.y1 NCI CGAP_Bm52 Homo sapiens cDNA clone IMAGE:2261466 5'
5720	18512		1.15	9.0E-03	A1809792.1	EST_HUMAN	yc17b08.s1 Stragene lung (#937210) Homo sapiens cDNA clone IMAGE:80919 3'
6533	19269		4.88	9.0E-03	BE745988.1	EST_HUMAN	yc17b08.s1 Stragene lung (#937210) Homo sapiens cDNA clone IMAGE:80919 3'
							wf7f04.x1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2361631 3'
							601573438F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3834752 5'

Table 4

Single Exon Probes Expressed In Brain

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7382	20043	33122	0.57	9.0E-03	A1242219.1	EST_HUMAN	q87c12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1853974 3'
7374	20051	33132	0.8	9.0E-03	8922570	NT	Homo sapiens hypothetical protein FLJ10650 (FLJ10650), mRNA
7774	20470		1.05	9.0E-03	AL039991.1	EST_HUMAN	DKFZp434L0412_r1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434L0412 5'
8147	20841		0.65	9.0E-03	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
9745	22396	35601	0.47	9.0E-03	P26011	SWISSPROT	INTEGRIN BETA-7 PRECURSOR (INTEGRIN BETA-P) (M290 IEL ANTIGEN)
9762	22413	35620	1.44	9.0E-03	P20908	SWISSPROT	COLLAGEN ALPHA 1(V) CHAIN PRECURSOR
10907	23987		2.07	9.0E-03	Y18000.1	NT	Homo sapiens NF2 gene
10935	23615	36866	1.57	9.0E-03	BE395380.1	EST_HUMAN	601310881F1 NIH_MGC 44 Homo sapiens cDNA clone IMAGE:3632181 5'
11651	24248	37568	1.55	9.0E-03	L11144.1	NT	Homo sapiens preprogalanin (GAL1) gene, exons 1, 2, and 3
11651	24248	37569	1.55	9.0E-03	L11144.1	NT	Homo sapiens preprogalanin (GAL1) gene, exons 1, 2, and 3
12411	25411		2.37	9.0E-03	BE348385.1	EST_HUMAN	hw17b09.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3183161 3'
12703	24983		23.46	9.0E-03	BF351141.1	EST_HUMAN	PM1-H10452-231299-001-e09 HT0452 Homo sapiens cDNA
489	13274		4.06	8.0E-03	AA723007.1	EST_HUMAN	zh30e03.s1 Soares_pithec_gland_N3HPG Homo sapiens cDNA clone IMAGE:413596 3' similar to contains
968	13734	26399	36.32	8.0E-03	AF106656.1	NT	Alu repetitive element
2154	14884	27617	2.2	8.0E-03	AL163283.2	NT	Homo sapiens adenylosuccinate lyase gene, complete cds
2980	15726		0.93	8.0E-03	U47048.1	NT	Homo sapiens chromosome 21 segment HS21C083
3353	18113	28768	1.08	8.0E-03	AJ131016.1	NT	Escherichia coli microcin 24 region, DNA binding protein (mba), immunity protein (mif), microcin 24 (mifS), and microcin transport protein (mtbA, mtbB) genes, complete cds
3665	18418	29058	1.21	8.0E-03	P32644	SWISSPROT	Homo sapiens SCL gene locus
3665	18418	29059	1.21	8.0E-03	P32644	SWISSPROT	HYPOTHETICAL 127.0 KD PROTEIN IN RAD24-BMH1 INTERGENIC REGION
4350	17089	29721	4.88	8.0E-03	BF363327.1	EST_HUMAN	HYPOTHETICAL 127.0 KD PROTEIN IN RAD24-BMH1 INTERGENIC REGION
5083	17802	30420	1.09	8.0E-03	AU140261.1	EST_HUMAN	GM4-NN0119-300600-223-b05 NN0119 Homo sapiens cDNA
							AU140261 PLAGE2 Homo sapiens cDNA clone PLACE2000223 5'
5436	18235	30949	2.82	8.0E-03	AF110520.1	NT	Mus musculus major histocompatibility complex region NG27, NG28, RPS28, NADH oxidoreductase, NG29, KIFC1, Fas-binding protein, BING1, tapasin, RalGDS-like, KE2, BING4, beta 1,3-galactosyl transferase, and RPS18 genes, complete cds; Sacm21 gene, partial>
6106	25085	31852	1.45	8.0E-03	AP000002.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 287001-544000 nt. position (2/7)
6851	19413	32427	4.89	8.0E-03	P55577	SWISSPROT	PROBABLE PEPTIDASE Y4NA
6820	19481		0.95	8.0E-03	V01109.1	NT	Human BK virus (strain MM) genome. (Closely related to SV40.)
7107	19795	32860	1.79	8.0E-03	M17197.1	NT	A. californica (marine gastropod mollusc) neuropeptide gene (bag cell), exon 1, 5' end
7442	20119		2.03	8.0E-03	AB038267.1	NT	Tursiops truncatus mRNA for p40-phox, complete cds
8781	21473	34619	0.63	8.0E-03	P98160	SWISSPROT	BASEMENT MEMBRANE-SPECIFIC HEPARAN SULFATE PROTEOGLYCAN CORE PROTEIN PRECURSOR (HSPG) (PERLECAN) (PLC)

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8808	21500	34646	3.28	8.0E-03	AW808692.1	EST_HUMAN	MR1-ST0111-111199-011-h06 ST0111 Homo sapiens cDNA
8818	21508	34653	0.49	8.0E-03	AL139075.2	NT	Campylobacter jejuni NCTC11188 complete genome; segment 2/6
8878	21569	34713	0.58	8.0E-03	9789956	NT	Mus musculus fusion 2 (human) (Fus2), mRNA
9848	22498		4.63	8.0E-03	BE086509.1	EST_HUMAN	QV1-BT0677-040400-131-g03 BT0677 Homo sapiens cDNA
10686	23357	38597	1.36	8.0E-03	BE768441.1	EST_HUMAN	601476619F1 NIH_MGC 88 Homo sapiens cDNA clone IMAGE:3878405 5'
10906	23598		3.58	8.0E-03	Z49652.1	NT	S. cerevisiae chromosome X reading frame ORF YJR152w
11715	24309	37632	4.74	8.0E-03	AF064589.1	NT	Homo sapiens melanoma-associated antigen (MAGE-C1) gene, complete cds
11814	24402		22.71	8.0E-03	AA016180.1	EST_HUMAN	z632e11.1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:360716 5'
11853	24437	37779	1.36	8.0E-03	BF342438.1	EST_HUMAN	602013941F1 NCI_CGAP_Brm64 Homo sapiens cDNA clone IMAGE:4149418 5'
11833	24491		1.74	8.0E-03	MB9035.1	NT	Oryctolagus cuniculus eIF-2a kinase mRNA, complete cds
11980	24523		1.74	8.0E-03	AB038161.1	NT	Homo sapiens ABOG1 gene for ABC transporter (ATP-binding cassette, sub-family G (WHITE), member 1), complete cds
678	13463	26098	16.15	7.0E-03	AF097183.1	NT	Cryptosporidium parvum HC-10 gene, complete cds
678	13453	26097	16.15	7.0E-03	AF097183.1	NT	Cryptosporidium parvum HC-10 gene, complete cds
958	13721	26387	3.67	7.0E-03	AF243376.1	NT	Glycine max glutathione S-transferase GST 21 mRNA, partial cds
1094	13852	26511	3.48	7.0E-03	AV731712.1	EST_HUMAN	AV731712 HTF Homo sapiens cDNA clone HTFAZF10 5'
1343	14091		2.97	7.0E-03	Q61060	SWISSPROT	FORHEAD BOX PROTEIN D3 (HNF3/FH TRANSCRIPTION FACTOR GENESIS) (HEPATOCYTE
1374	14122	26797	5.71	7.0E-03	AA668298.1	EST_HUMAN	NUCLEAR FACTOR 3 FORKHEAD HOMOLOG 2 (HFH-2)
1491	14238	26924	3.37	7.0E-03	AW303599.1	EST_HUMAN	ab79k09.s1 Stratagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:853145 3'
1735	14477	27175	1.24	7.0E-03	AW950556.1	EST_HUMAN	xv21b02.x1 Soares_NFL_I_GBC_S1 Homo sapiens cDNA clone IMAGE:2813739 3'
1735	14477	27176	1.24	7.0E-03	AW950556.1	EST_HUMAN	EST362626 MAGE resequences, MAGA Homo sapiens cDNA
2254	15589	27722	1.86	7.0E-03	P04929	SWISSPROT	EST362626 MAGE resequences, MAGA Homo sapiens cDNA
3546	16301	28951	0.71	7.0E-03	AI150273.1	EST_HUMAN	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR
3749	16502	29137	0.8	7.0E-03	AW44463.1	EST_HUMAN	qf34h02.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1751955 3'
3792	16544	29179	1.32	7.0E-03	AF195344.1	NT	U1-H-B18-akb-c-10-0-U1.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2733691 3'
4000	16502	29137	0.83	7.0E-03	AW444463.1	EST_HUMAN	Rattus norvegicus neuronal nicotinic acetylcholine receptor subunit (Alpha10) mRNA, complete cds
4560	17295		1.24	7.0E-03	AW630888.1	EST_HUMAN	U1-H-B13-akb-c-10-0-U1.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2733691 3'
4928	17657		2.17	7.0E-03	AL163278.2	NT	hh89a05.y1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2968936 5'
5728	18521						Homo sapiens chromosome 21 segment HS21C078
6021	25083		0.75	7.0E-03	H71106.1	EST_HUMAN	y82g01.1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:211824 5' similar to
6222	18988	31972	4.9	7.0E-03	AW861059.1	EST_HUMAN	gb-X14723 CLUSTERIN PRECURSOR (HUMAN);
			1.47	7.0E-03	W68251.1	EST_HUMAN	RC1-CT0286-050400-018-c08 CT0286 Homo sapiens cDNA
							z43310.1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:342475 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6443	19211	32207	3.44	7.0E-03	AA327129.1	EST_HUMAN	EST30874 Colon I Homo sapiens cDNA 5' and
6470	19237	32237	0.75	7.0E-03	BE857385.1	EST_HUMAN	7034b10.x1 NCL CGAP Brn23 Homo sapiens cDNA clone IMAGE:3308347 3' similar to TR:Q13387
6979	19504	32529	1.67	7.0E-03	BE928133.1	EST_HUMAN	Q13387 HYPOTHETICAL PROTEIN 384D8_2, contains TAR1.2 TAR1 TAR1 repetitive element ;
7420	20097	33184	5.48	7.0E-03	Z35838.1	NT	CM2-CT0478-230800-347-511 CT0478 Homo sapiens cDNA
7420	20097	33185	5.48	7.0E-03	Z35838.1	NT	S.cerevisiae chromosome II reading frame ORF YBL077w
8010	20705	33833	2.47	7.0E-03	BE175687.1	EST_HUMAN	S.cerevisiae chromosome II reading frame ORF YBL077w
8511	21203	34348	0.51	7.0E-03	AF281074.1	NT	RC5-HT0582-160300-011-D02 HT0582 Homo sapiens cDNA
9297	21964		0.75	7.0E-03	AF111188.2	NT	Homo sapiens neurapillin 2 (NRP2) gene, complete cds
9495	22148	35330	0.72	7.0E-03	N52378.1	EST_HUMAN	Homo sapiens serine palmitoyl transferase, subunit II gene, complete cds; and unknown genes
9620	22273	35460	2.57	7.0E-03	P48982	SWISSPROT	y49c10.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:246066 3' similar to contains
9620	22273	35461	2.57	7.0E-03	P48982	SWISSPROT	Alu repetitive element;
10204	22652		1.32	7.0E-03	AV687379.1	EST_HUMAN	BETA-GALACTOSIDASE PRECURSOR (LACTASE)
10384	23030		0.77	7.0E-03	AV687379.1	EST_HUMAN	BETA-GALACTOSIDASE PRECURSOR (LACTASE)
10729	23417	36558	2.63	7.0E-03	AB008852.1	NT	AV687379 GKC Homo sapiens cDNA clone GKCAFC07 5'
10818	23501	36739	1.71	7.0E-03	AJ004862.1	NT	wc37e09.x1 NCL CGAP Pr28 Homo sapiens cDNA clone IMAGE:2320840 3'
10818	23501	36740	1.71	7.0E-03	AJ004862.1	NT	Bos taurus mRNA for NDP62, complete cds
10982	23657		1.29	7.0E-03	AJ242804.1	NT	Homo sapiens partial MUC6B gene, exon 1-29
12466	24833		1.78	7.0E-03	BE263253.1	EST_HUMAN	Homo sapiens partial MUC6B gene, exon 1-29
12593	24890		1.81	7.0E-03	Y17455.1	NT	Sporobolus stapfiarius mRNA for putative glycine and proline-rich protein
12691	25400		1.72	7.0E-03	AL163300.2	NT	601145154F2 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3160476 5'
1218	13969	26637	12.34	6.0E-03	AW511148.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C100
1218	13969	26638	12.34	6.0E-03	AW511148.1	EST_HUMAN	hd22a05.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2910224 3' similar to
2774	15479	28220	1.3	6.0E-03	AF112374.1	NT	SW:PXR_HUMAN OT5469 ORPHAN NUCLEAR RECEPTOR PXR ;
2893	15660	28305	3.36	6.0E-03	AA759135.1	EST_HUMAN	hd22a05.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2910224 3' similar to
2893	15660	28306	3.36	6.0E-03	AA759135.1	EST_HUMAN	SW:PXR_HUMAN OT5469 ORPHAN NUCLEAR RECEPTOR PXR ;
3240	16002		2.22	6.0E-03	HT5690.1	EST_HUMAN	Danio rerio odorant receptor gene cluster
3298	16060		1.31	6.0E-03	AF190338.1	NT	ah78e11.s1 Soares testis NHT Homo sapiens cDNA clone 1321772 3'
3377	16136	28793	1.18	6.0E-03	U90880.1	NT	ah78e11.s1 Soares testis NHT Homo sapiens cDNA clone 1321772 3'
							y77h04.11 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:211351 5'
							Nobolus sp. cytochrome c oxidase subunit II gene, partial cds; mitochondrial gene for mitochondrial product
							Fugu rubripes zinc finger protein, Isotocin, fatty acid binding protein, septaplerin reductase and vasobolin
							genes, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3377	16136	28794	1.18	6.0E-03	U90880.1	NT	Fugu rubripes zinc finger protein, isotocin, fatty acid binding protein, septaplerin reductase and vasotocin genes, complete cds
3534	16290		1.19	6.0E-03	W37985.1	EST_HUMAN	zct3a11.1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:322172 5'
3652	16405	28044	3.68	6.0E-03	BF510986.1	EST_HUMAN	UI-H-B14-apim-c-06-0-UI.s1 NCI_CGAP Sub8 Homo sapiens cDNA clone IMAGE:3087754 3'
3682	16435	29079	1.03	6.0E-03	BE077356.1	EST_HUMAN	RC1-BT0606-260400-014-a07 BT0606 Homo sapiens cDNA
3759	16511	29147	1.22	6.0E-03	6754028	NT	Mus musculus glucosamine-6-phosphate deaminase (Gnpl), mRNA
3902	16652	29294	0.76	6.0E-03	AW847284.1	EST_HUMAN	RC0-CT0204-240999-021-b10 CT0204 Homo sapiens cDNA
3938	16688		1.29	6.0E-03	BE250108.1	EST_HUMAN	600942904F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:2859513 5'
4331	17070		1.84	6.0E-03	AJ016833.1	EST_HUMAN	ov33c11.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1639124 3'
4647	17381	30013	5.67	6.0E-03	AA324242.1	EST_HUMAN	EST271116 Cerebellum II Homo sapiens cDNA 5' end similar to EST containing Alu repeat
5073	17792	30407	2.58	6.0E-03	Q62209	SWISSPROT	SYNAPTONEMAL COMPLEX PROTEIN 1 (SCP-1) PROTEIN
6081	25084	31802	0.67	6.0E-03	9827521	NT	Varicella virus, complete genome
6718	19633	32676	1.16	6.0E-03	O14994	SWISSPROT	SYNAPSIN III
7155	17924	30559	0.57	6.0E-03	BE253748.1	EST_HUMAN	601112353F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3353172 5'
7149	19836	32905	0.61	6.0E-03	AA299442.1	EST_HUMAN	EST11949 Uterus tumor I Homo sapiens cDNA 5' end
7149	19836	32906	0.61	6.0E-03	AA299442.1	EST_HUMAN	EST11949 Uterus tumor I Homo sapiens cDNA 5' end
7546	20216	33318	0.69	6.0E-03	AF128894.1	NT	Homo sapiens telomerase reverse transcriptase (TERT) gene, exons 7-16 and complete cds
7702	20365	33479	0.62	6.0E-03	P17964	SWISSPROT	RAS-RELATED PROTEIN RAP-2B
7757	20453	33578	6.9	6.0E-03	AJ033980.1	EST_HUMAN	ow13a04.x1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:1646670 3' similar to contains MER10.b1 MER10 repetitive element;
7874	20569	33695	2.17	6.0E-03	AW799337.1	EST_HUMAN	RC0-UJ0051-210300-032-g02 UM0051 Homo sapiens cDNA
7945	20840		1.58	6.0E-03	BF038198.1	EST_HUMAN	601454915F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3858626 5'
8454	22004	35176	7.26	6.0E-03	D10548.1	NT	Subacute sclerosing panencephalitis (SSPE) virus mRNA for fusion protein
9843	22591		2.13	6.0E-03	AJ432981.1	EST_HUMAN	l92c02.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2131202 3' similar to SW:R13A_HUMAN
10062	22710	35928	0.86	6.0E-03	AJ01849.1	NT	P40429 60S RIBOSOMAL PROTEIN L13A ; Bacillus subtilis fnd gene
10194	22842		1.14	6.0E-03	AF084555.1	NT	Homo sapiens okadaic acid-inducible and cAMP-regulated phosphoprotein 19 (ARPP-19) mRNA, complete cds
10304	22951	36166	0.59	6.0E-03	X68366.1	NT	M.thermoformicium complete plasmid pFV1 DNA
10645	23336	36575	1.75	6.0E-03	AW982164.1	EST_HUMAN	EST1374237 MAGE resequences, MAGE Homo sapiens cDNA
10713	23402		2.54	6.0E-03	11545814	NT	Homo sapiens hypothetical zinc finger protein FLJ14011 (FLJ14011), mRNA
10750	23435	36680	1.26	6.0E-03	AK20786.1	EST_HUMAN	be91c12.x1 NCI_CGAP_P28 Homo sapiens cDNA clone IMAGE:2094070 3' similar to TR:O00519 O00519 FATTY ACID AMIDE HYDROLASE. ;

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10750	23435	36681	1.26	6.0E-03	AJ420786.1	EST_HUMAN	ts91c12.x1 NCL CGAP_P28 Homo sapiens cDNA clone IMAGE:2084070 3' similar to TR:O00519 O00519
10903	23583		4.6	6.0E-03	U14556.1	NT	FATTY ACID AMIDE HYDROLASE..
10904	23594	36833	2.81	6.0E-03	BE737896.1	EST_HUMAN	Mus musculus zinc-finger protein mRNA, complete cds
12042	24563		3.25	6.0E-03	AF010496.1	NT	G01572746F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:3839747 5'
12160	25174		6.69	6.0E-03	AE000833.1	NT	Rhodobacter capsulatus strain SB1003, partial genome
12238	25235		3.17	6.0E-03	U30790.1	NT	Methanobacterium thermoautotrophicum from bases 428192 to 450298 (section 39 of 148) of the complete genome
12569	24898		1.84	6.0E-03	BE788019.1	EST_HUMAN	Pneumocystis carinii f. sp. rati guanine nucleotide binding protein alpha subunit (pog1) gene, complete cds
12568	24910		1.88	6.0E-03	AJ245480.1	NT	G01482621F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3885388 5'
654	13432	26072	2.7	5.0E-03	L25105.1	NT	Brassica napus sig gene for S-locus glycoprotein, cultivar T2
654	13432	26073	2.7	5.0E-03	L25105.1	NT	Chlamydia trachomatis partial ORFB; aminoacyl-tRNA synthase, complete cds; complete ORFA, and grpE-like protein, complete cds
655	13432	26072	3.73	5.0E-03	L25105.1	NT	Chlamydia trachomatis partial ORFB; aminoacyl-tRNA synthase, complete cds; complete ORFA, and grpE-like protein, complete cds
655	13432	26073	3.73	5.0E-03	L25105.1	NT	Chlamydia trachomatis partial ORFB; aminoacyl-tRNA synthase, complete cds; complete ORFA, and grpE-like protein, complete cds
1090	13848	26507	1.15	5.0E-03	AJ010457.1	NT	Chlamydia trachomatis partial ORFB; aminoacyl-tRNA synthase, complete cds; complete ORFA, and grpE-like protein, complete cds
2888	15397	28135	2.5	5.0E-03	AB033006.1	NT	Arabidopsis thaliana mRNA for KIAA1180 protein, partial cds
2836	15702	28351	0.88	5.0E-03	BE268057.1	EST_HUMAN	Homo sapiens mRNA for KIAA1180 protein, partial cds
3133	15898	28543	3.82	5.0E-03	T87623.1	EST_HUMAN	G01194796F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3538789 5'
3152	15915		2.83	5.0E-03	AL161491.2	NT	ye8109.s1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:22395 3'
3164	15927	28575	1.3	5.0E-03	R71794.1	EST_HUMAN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 3
3272	16033		1.12	5.0E-03	AJ297357.1	NT	y88g02.s1 Soares breast 2N1Bst Homo sapiens cDNA clone IMAGE:155866 3'
3687	16440	29082	4.03	5.0E-03	AF147449.2	NT	Homo sapiens partial LIMD1 gene for LIM domains containing protein 1 and KIAA0851 gene
3741	16494	29129	0.85	5.0E-03	U38914.1	NT	Pseudomonas aeruginosa strain PAO1 penicillin-binding protein 1B (porB) gene, complete cds
3954	16704		1.17	5.0E-03	AA298675.1	EST_HUMAN	Citrus sinensis seed storage protein citrin mRNA, complete cds
4272	16494	29129	0.82	5.0E-03	U38914.1	NT	EST121218 Ulerus Homo sapiens cDNA 5' end
4589	17304	29831	0.73	5.0E-03	AJ131016.1	NT	Citrus sinensis seed storage protein citrin mRNA, complete cds
4670	17404	30039	1.17	5.0E-03	AJ752367.1	EST_HUMAN	Homo sapiens SCL gene locus
5707	18501	31422	5.5	5.0E-03	P35500	SWISSPROT	cn15c02.x1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC_cn15c02 random
							SODIUM CHANNEL PROTEIN PARA (PARALYTIC PROTEIN)

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5953	18735	31694	2.97	5.0E-03	O00507	SWISSPROT	PROBABLE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE FAF-Y (UBIQUITIN THIOLESTERASE FAF-Y) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE FAF-Y) (DEUBIQUITINATING ENZYME FAF-Y) (FAT FACETS PROTEIN RELATED, Y-LINKED) (UBIQUITIN-SPECIFIC PROTEASE 9, Y CHROMOSOME)
5988	18769		0.91	5.0E-03	AE002234.2	NT	Chlamydomonas reinhardtii AR39, section 62 of 94 of the complete genome
6499	19264		7.58	5.0E-03	BE300091.1	EST_HUMAN	600944564T1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2960871 3'
6746	17915	30578	7.45	5.0E-03	AB026024.1	NT	Mus musculus AMD1 gene for S-adenosylmethionine decarboxylase, complete cds
6940	19422		0.84	5.0E-03	AB038287.1	NT	Tursiops truncatus mRNA for p40-phox, complete cds
7385	20065	33143	0.73	5.0E-03	T05124.1	EST_HUMAN	EST03012 Fetal brain, Stragene (cat#338206) Homo sapiens cDNA clone HFBCR93 similar to EST containing Alu repeat
7498	20170		1.21	5.0E-03	AW854327.1	EST_HUMAN	RC3-C10255-031099-011-07 CT0258 Homo sapiens cDNA
7667	20331	33442	7.5	5.0E-03	AB016816.1	NT	Homo sapiens MASL1 mRNA, complete cds
8119	20813	33948	0.48	5.0E-03	AW855907.1	EST_HUMAN	RC6-CT0281-081199-011-A05 CT0281 Homo sapiens cDNA
8119	20813	33949	0.48	5.0E-03	AW855907.1	EST_HUMAN	RC6-CT0281-081199-011-A05 CT0281 Homo sapiens cDNA
8137	20831	33965	3.29	5.0E-03	P49082	SWISSPROT	BETA-GALACTOSIDASE PRECURSOR (LACTASE)
8509	21201		5.63	5.0E-03	M61132.1	NT	Mouse complement receptor (CR2) mRNA, 3' end
8706	21398	34545	1.04	5.0E-03	D90723.1	NT	Escherichia coli genomic DNA, (19.1 - 19.4 min)
8838	21530	34676	0.71	5.0E-03	M25090.1	NT	Rabbit uteroglobin (UGL) gene, exon 1
9482	22135	35315	0.45	5.0E-03	P33750	SWISSPROT	SOF1 PROTEIN
9739	22390	35595	0.89	5.0E-03	L21710.1	NT	Plasmodium berghei 58 kDa phosphoprotein mRNA, partial cds
9871	22521	35716	0.7	5.0E-03	AW821888.1	EST_HUMAN	RC0-ST0379-210100-032-c02 ST0379 Homo sapiens cDNA
10057	22705	35923	0.45	5.0E-03	AA533143.1	EST_HUMAN	H46H10.s1 NCI_CGAP_P8 Homo sapiens cDNA clone IMAGE:995587
10231	22879	36091	0.51	5.0E-03	7682557	NT	Homo sapiens PR00471 protein (PR00471), mRNA
10377	23023		0.48	5.0E-03	AA653261.1	EST_HUMAN	ag49c10.s1 Gessler Wilms tumor Homo sapiens cDNA clone 694
10621	23314		4.99	5.0E-03	T19586.1	EST_HUMAN	694F Heart Homo sapiens cDNA clone 694
10859	23539	36785	3.42	5.0E-03	AW170334.1	EST_HUMAN	xn59g05.x1 Soares_NHCCc_cervical_tumor Homo sapiens cDNA clone IMAGE:2698040 3' similar to contains L1 L2 L1 repetitive element ;
10859	23539	36786	3.42	5.0E-03	AW170334.1	EST_HUMAN	xn59g05.x1 Soares_NHCCc_cervical_tumor Homo sapiens cDNA clone IMAGE:2698040 3' similar to contains L1 L2 L1 repetitive element ;
10971	23847	36900	1.89	5.0E-03	T49753.1	EST_HUMAN	y09e04.r1 Stragene placenta (#937225) Homo sapiens cDNA clone IMAGE:70686 5'
11021	23863	36956	1.47	5.0E-03	10946753	NT	Mus musculus hypothetical protein, MNCb-4760 (LOC98212), mRNA
11303	23962		3.54	5.0E-03	BE048055.1	EST_HUMAN	Iz46c04.y1 NCI_CGAP_Brn52 Homo sapiens cDNA clone IMAGE:2291822 5'
11774	24365	37697	1.83	5.0E-03	AJ276505.1	NT	Mus musculus genomic fragment, 279 Kb, chromosome 7
11774	24365	37698	1.53	5.0E-03	AJ276505.1	NT	Mus musculus genomic fragment, 279 Kb, chromosome 7

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12176	25367		9.28	5.0E-03	AF047874.1	NT	Gallus gallus glyceraldehyde-3-phosphate dehydrogenase mRNA, complete cds
12307	24731		4.11	5.0E-03	AF067263.1	NT	Brugia malayi Y chromosome marker
12409	24792		2.52	5.0E-03	L10347.1	NT	Human pro-alpha1 type II collagen (COL2A1) gene exons 1-54, complete cds
12441	24811		1.67	5.0E-03	AA456597.1	EST_HUMAN	zxf5a03.s1 Soares ovary tumor N6HOT Homo sapiens cDNA clone IMAGE:509548 3' similar to
12487	25183		2.78	5.0E-03	BF572332.1	EST_HUMAN	SW:DXA2 MOUSE P14685 PROBABLE DIPHENOL OXIDASE A2 COMPONENT ;
12643	24940	30980	4.2	5.0E-03	AW449109.1	EST_HUMAN	UI-H-B3-ak7-08-Q.UJ.s1 NCI CGAP_Sub5 Homo sapiens cDNA clone IMAGE:4252002 5'
12662	26253		1.76	5.0E-03	Q02389	SWISSPROT	COLLAGEN ALPHA 1(VII) CHAIN PRECURSOR (LONG-CHAIN COLLAGEN) (LC COLLAGEN)
228	13098	25675	2.98	4.0E-03	AW500198.1	EST_HUMAN	UI-HF-BN0-akc-h-04-Q-UJ.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:2734215 3'
313	13117	25755	2.29	4.0E-03	R46482.1	EST_HUMAN	Y951e04.s1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:3076831 5'
589	13369	25997	2.69	4.0E-03	AA838339.1	EST_HUMAN	on75g12.s1 Soares NFI_L_GBC S1 Homo sapiens cDNA clone IMAGE:35988 3'
857	13626	26298	2.03	4.0E-03	R46482.1	EST_HUMAN	Y951e04.s1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:35988 3'
881	13660		4.64	4.0E-03	AW749101.1	EST_HUMAN	RC3-BT0333-110100-012-01 BT0333 Homo sapiens cDNA
1128	13884	26544	29.46	4.0E-03	AA096777.1	EST_HUMAN	Z81a08.r1 Stratagene colon (#937204) Homo sapiens cDNA clone IMAGE:510998 5'
1146	13901	26563	2.4	4.0E-03	AW794740.1	EST_HUMAN	RC6-UM0014-170400-023-G01 UM0014 Homo sapiens cDNA
1280	14030	26699	1.57	4.0E-03	AA284374.1	EST_HUMAN	Z859a01.r1 NCI CGAP_GCB1 Homo sapiens cDNA clone IMAGE:701736 5'
1561	14327		1.52	4.0E-03	AV708305.1	EST_HUMAN	AV708305 ADC Homo sapiens cDNA clone ADCAKB06 5'
1737	14479	27178				NT	Rattus norvegicus type 1 astrocyte and olfactory-limbic associated protein A T1-46 mRNA, complete cds
2011	14746	27474	2.23	4.0E-03	U33472.1	NT	Z81a08.r1 Stratagene colon (#937204) Homo sapiens cDNA clone IMAGE:510998 5'
2244	14972		10.56	4.0E-03	AA099777.1	EST_HUMAN	RC6-UM0014-170400-023-G01 UM0014 Homo sapiens cDNA
2276	15002	27742	2.49	4.0E-03	BE410556.1	EST_HUMAN	RC6-UM0014-170400-023-G01 UM0014 Homo sapiens cDNA
			1.64	4.0E-03	AW794740.1	EST_HUMAN	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRTR), CDM protein (CDM), adrenoleukodystrophy protein >
2579	15293	28030	1.97	4.0E-03	U52111.2	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRTR), CDM protein (CDM), adrenoleukodystrophy protein >
2579	15293	28031	1.97	4.0E-03	U52111.2	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRTR), CDM protein (CDM), adrenoleukodystrophy protein >
2696	15405	28140	3	4.0E-03	AJ277385.1	NT	Homo sapiens polyglutamine-containing C14ORF4 gene
2696	15405	28141	3	4.0E-03	AJ277385.1	NT	Homo sapiens polyglutamine-containing C14ORF4 gene
2701	15409	28144	1.41	4.0E-03	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
3219	15982	28634	1.16	4.0E-03	BE154134.1	EST_HUMAN	PM1-HT0340-151299-003-h08 HT0340 Homo sapiens cDNA
3219	15982	28635	1.16	4.0E-03	BE154134.1	EST_HUMAN	PM1-HT0340-151299-003-h08 HT0340 Homo sapiens cDNA
3521	16277	28931	0.97	4.0E-03	AW189426.1	EST_HUMAN	X98804.x1 NCI CGAP_Cor18 Homo sapiens cDNA clone IMAGE:2665279 3'

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Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3521	16277	28932	0.97	4.0E-03	AW188426.1	EST_HUMAN	x98f04.x1 NCI_CGAP_G018 Homo sapiens cDNA clone IMAGE:2685279 3'
3612	16365	29008	0.73	4.0E-03	Q13606	SWISSPROT	OLFATORY RECEPTOR 511 (OLFATORY RECEPTOR-LIKE PROTEIN OLF1)
3909	16659	29300	0.73	4.0E-03	AF060868.1	NT	Mus musculus tumor susceptibility protein 101 (tsg101) gene, complete cds
3977	16725		1.95	4.0E-03	AJ011712.1	NT	Homo sapiens TNNT1 gene, exons 1-11 (end joined CDS)
5057	17776	30393	0.93	4.0E-03	AW103719.1	EST_HUMAN	xe83d03.x1 NCI_CGAP_Bm35 Homo sapiens cDNA clone IMAGE:2614469 3' similar to contains L1.L1 L1
5114	17832		0.97	4.0E-03	AA72898.1	EST_HUMAN	L1 repetitive element;
5194	18002	30625	1.8	4.0E-03	AF005859.1	NT	ae73a05.s1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:969776 3'
5314	18118	30774	23.91	4.0E-03	AF169825.1	NT	Drosophila melanogaster anon2D7 (anon2D7) mRNA, complete cds
5705	18499	31421	2.48	4.0E-03	P04196	SWISSPROT	Rattus norvegicus beta-catenin binding protein mRNA, complete cds
5708	18502	31423	1.74	4.0E-03	P21849	SWISSPROT	(HPRG)
5792	18563	31510	0.86	4.0E-03	AL133871.1	EST_HUMAN	MAJOR SURFACE-LABELLED TROPHOZOITE ANTIGEN PRECURSOR
5993	18774		4.11	4.0E-03	U22180.1	NT	DKFZ7611014.1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp7611014.5'
6140	18918	31888	0.95	4.0E-03	AW590572.1	EST_HUMAN	Rattus norvegicus opsin gene, complete cds
6217	18991	31967	1.6	4.0E-03	BE548453.1	EST_HUMAN	hg46c07.x1 NCI_CGAP_G03 Homo sapiens cDNA clone IMAGE:2948852 3'
6572	19338	32347	1.28	4.0E-03	AA813222.1	EST_HUMAN	601076015F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3461954 5'
6677	19594	32632	1.61	4.0E-03	U78408.1	NT	aj32f11.s1 Soares testis NHT Homo sapiens cDNA clone 192045 3'
6970	19452	32470	0.99	4.0E-03	AL163278.2	NT	Lycopodium esculentum knotted 3 protein (TKn3) mRNA, complete cds
6970	19452	32471	0.99	4.0E-03	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
7098	19787	32851	3.5	4.0E-03	Q02817	SWISSPROT	Homo sapiens chromosome 21 segment HS21C078
7331	20013	33091	1.23	4.0E-03	AI681483.1	EST_HUMAN	MUCIN 2 PRECURSOR (INTESTINAL MUCIN 2)
7333	20015	33093	0.78	4.0E-03	BE670170.1	EST_HUMAN	b37g12.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2271814 3'
7424	20101		0.74	4.0E-03	X92109.1	NT	7631b02.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3284043 3'
7843	20538	33666	0.7	4.0E-03	Q91T92	SWISSPROT	H.sapiens hcgIX gene
7947	20642	33767	5.45	4.0E-03	AF111944.1	NT	ADAM-TS 5 (A DISINTEGRIN AND METALLOPROTEINASE WITH THROMBOSPONDIN MOTIFS 5)
8103	20797	33928	2.06	4.0E-03	7662067	NT	(ADAM-TS5) (AGGRECANASE-2) (ADMP-2) (ADAM-TS 11)
8614	21306	34448	6.98	4.0E-03	AI553983.1	EST_HUMAN	Dicyostelium discoideum AX4 development protein DG1122 (DG1122) gene, partial cds
8787	21479		4.25	4.0E-03	AL163209.2	NT	Homo sapiens KIAA0345 gene product (KIAA0345), mRNA
8797	21489	34635	2.97	4.0E-03	AL163278.2	NT	te49b11.x1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2090013 3' similar to contains Alu repetitive element
9827	22478	35879	0.87	4.0E-03	H30664.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C009
10275	22923	36135	1.3	4.0E-03	AL161555.2	NT	Homo sapiens chromosome 21 segment HS21C078
10466	23112		0.45	4.0E-03	AL163281.2	NT	XP42g12.1 Soares retina N255HR Homo sapiens cDNA clone IMAGE:190150 5'
							Arabidopsis thaliana DNA chromosome 4, contig fragment No. 55
							Homo sapiens chromosome 21 segment HS21C081

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Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11074	23744	37017	4.09	4.0E-03	AL163206.2	NT	Homo sapiens chromosome 21 segment HS21C006
11777	24388	37700	1.82	4.0E-03	AE002102.1	NT	Ureaplasma urealyticum section 3 of 59 of the complete genome
12147	25385		1.78	4.0E-03	BE815173.1	EST_HUMAN	PM4-BN0138-180600-002-508 BN0138 Homo sapiens cDNA
12167	24649		2.38	4.0E-03	BE298290.1	EST_HUMAN	601118164F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3028095 5'
12246	24694		2.27	4.0E-03	AW504273.1	EST_HUMAN	U1-HF-BN0-4p-g-04-UJ.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3080622 5'
12480	24841		3.41	4.0E-03	BF224125.1	EST_HUMAN	7q74c09.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3080622 5' element; contains element MER31 repetitive element;
12521	25293		2.08	4.0E-03	AW614596.1	EST_HUMAN	h102c07.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2953932 3' similar to contains element LTR5 repetitive element;
12801	25048	30956	2.17	4.0E-03	11436955	NT	Homo sapiens Grib2-associated binder 2 (KIAA0571), mRNA
362	13160	25803	2.38	3.0E-03	AF011920.1	NT	Homo sapiens protein kinase CK2 catalytic subunit alpha gene, exon 1
859	13628	26299	5.37	3.0E-03	AF011920.1	NT	Homo sapiens protein kinase CK2 catalytic subunit alpha gene, exon 1
1657	14403	27091	3.35	3.0E-03	AA488110.1	EST_HUMAN	nc73cd5.s1 NCI_CGAP_Pr2 Homo sapiens cDNA clone IMAGE:782984 similar to contains Alu repetitive element;
2255	14982		1.38	3.0E-03	AF056066.1	NT	Homo sapiens MHC class 1 region
2292	15017	27753	6.44	3.0E-03	Z32521.1	NT	S.cereale (cv. Halo) mRNA for triosephosphate isomerase
2293	15018	27754	1.09	3.0E-03	U46858.1	NT	Mus musculus intestinal trefoil factor gene, partial cds
3081	15946	28488	1.09	3.0E-03	U46858.1	NT	Mus musculus intestinal trefoil factor gene, partial cds
3149	15912	28557	3.31	3.0E-03	BE379286.1	EST_HUMAN	601237982F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3609933 5'
3412	16170	28819	2.52	3.0E-03	AW802687.1	EST_HUMAN	IL2-UM0076-240300-056-D03 UM0076 Homo sapiens cDNA
3420	16177		1.72	3.0E-03	U34606.1	NT	Mus musculus alpha-1(XVII) collagen (COL18A1) gene, exon 1 and 2
3959	16708	29348	5.97	3.0E-03	Y12500.1	NT	C.elegans sermo gene
3959	16708	29349	6.97	3.0E-03	AV762392.1	EST_HUMAN	AV762392 MDS Homo sapiens cDNA clone MDSBSG01 5'
4016	16762	29390	6.97	3.0E-03	AV762392.1	EST_HUMAN	AV762392 MDS Homo sapiens cDNA clone MDSBSG01 5'
4130	16872		1.35	3.0E-03	AI792278.1	EST_HUMAN	af04409.y5 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:1156889 5'
4384	17102	29737	1	3.0E-03	Z32521.1	NT	S.cereale (cv. Halo) mRNA for triosephosphate isomerase
4428	17164		5.63	3.0E-03	AJ011432.1	NT	Rattus norvegicus gdnf gene
4482	17217	29844	0.73	3.0E-03	BE348739.1	EST_HUMAN	h168p08.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3151934 3'
4782	17514	30136	4.97	3.0E-03	AJ536141.1	EST_HUMAN	xu8.P10.H3 conorm Homo sapiens cDNA 3'
4802	17533	30165	2.38	3.0E-03	AI732754.1	EST_HUMAN	ab18a08.x6 Stralagene lung (4937210) Homo sapiens cDNA clone IMAGE:841142 3' similar to contains Alu repetitive element;
5184	17992	30508	7.94	3.0E-03	BE787945.1	EST_HUMAN	601482715F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3885483 5'
5488	18287	31159	3.66	3.0E-03	8922499	NT	Homo sapiens hypothetical protein FLJ10539 (FLJ10539), mRNA
			1.98	3.0E-03	AJ249981.1	NT	Mus musculus mRNA for hypothetical protein (ORF2 ortholog)

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Single Exon Probes Expressed in Brain

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5539	18337	31244	0.99	3.0E-03	U35323.1	NT	Mus musculus H2-M alpha chain (H2-Ma) gene, H2-M beta 2 chain (H2-Mb2) gene, H2-M beta 1 chain (H2-Mb1) gene, low molecular weight protein 2 Lmp2 (Lmp2) gene, complete cds
6458	19225	32225	11.75	3.0E-03	AA458701.1	EST_HUMAN	aa13f10.r1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:813163 5'
7104	19792	32857	1.38	3.0E-03	AJ011419.1	NT	Kluyveromyces marxianus pcp13 gene for purine-cytosine permease
7422	20099	33187	3.64	3.0E-03	AB021736.1	NT	Oryza sativa gene for bZIP protein, complete cds
7839	20534	33662	0.82	3.0E-03	BF333058.1	EST_HUMAN	RCO-BT0812-250900-032-e07 BT0812 Homo sapiens cDNA
7839	20534	33662	0.82	3.0E-03	BF333058.1	EST_HUMAN	RCO-BT0812-250900-032-e07 BT0812 Homo sapiens cDNA
8056	20750	33981	1.54	3.0E-03	N92580.1	EST_HUMAN	zb27b04.s1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:304783 3'
8214	20908		0.51	3.0E-03	M63498.1	NT	S.cerevisiae UGA35 gene, complete cds
8360	21053	34194	1.32	3.0E-03	P51989	SWISSPROT	HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A2 HOMOLOG 1 (HNRNP A2(A))
8381	21074	34213	1.47	3.0E-03	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C068
8485	21177		1.29	3.0E-03	Q9QM81	SWISSPROT	NONSTRUCTURAL PROTEIN V
8890	21581		11.08	3.0E-03	AW613774.1	EST_HUMAN	hh80f10.x1 NCI CGAP_GU1 Homo sapiens cDNA clone IMAGE:2969131 3' similar to contains L1.t1 L1 repetitive element;
8943	21634	34778	4.01	3.0E-03	AL161589.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 85
8967	21657	34808	6.44	3.0E-03	AJ016731.1	EST_HUMAN	ov03d12.x1 NCI CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1636247 3' similar to gbX57138_ma1 HISTONE H2B.2 (HUMAN);
8977	21687	34817	0.73	3.0E-03	BF338078.1	EST_HUMAN	602035880F1 NCI CGAP_Brr64 Homo sapiens cDNA clone IMAGE:4183638 5'
9309	21976		0.83	3.0E-03	D80601.1	NT	Synechocystis sp. PCC6803 complete genome, 3/27, 271600-402289
9347	20418	33538	0.83	3.0E-03	BE154870.1	EST_HUMAN	PM3-HT0344-071299-003-d07 HT0344 Homo sapiens cDNA
9536	22189		0.54	3.0E-03	P03355	SWISSPROT	POLYPROTEIN [CONTAINS: PROTEASE; REVERSE TRANSCRIPTASE; RIBONUCLEASE H]
9606	22259		3.88	3.0E-03	P08672	SWISSPROT	CIRCUMSPOROZITE PROTEIN PRECURSOR (CS)
9795	22446	35551	1.3	3.0E-03	P11369	SWISSPROT	RETROVIRUS-RELATED POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE; ENDONUCLEASE]
9898	22546	35740	1.29	3.0E-03	P51989	SWISSPROT	HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A2 HOMOLOG 1 (HNRNP A2(A))
10040	22698	35906	3.97	3.0E-03	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
10752	23437		1.9	3.0E-03	5803028	NT	Homo sapiens A TP/GTP-binding protein (HEAB), mRNA
11137	20099	33187	2.65	3.0E-03	AB021736.1	NT	Oryza sativa gene for bZIP protein, complete cds
11353	24043	37346	1.69	3.0E-03	AF009222.1	NT	Pneumocystis carinii kexin-like serine endoprotease mRNA, partial cds
11424	23191	36422	2.52	3.0E-03	AF265285.1	NT	Homo sapiens golgin-like protein (GLP) gene, complete cds
11462	24065	37372	2.72	3.0E-03	AF094481.1	NT	Homo sapiens trinucleotide repeat DNA binding protein p20-CGGBP (CGGBP) gene, complete cds
11482	24085	37373	2.72	3.0E-03	AF094481.1	NT	Homo sapiens trinucleotide repeat DNA binding protein p20-CGGBP (CGGBP) gene, complete cds
11543	24143	37452	1.58	3.0E-03	P11369	SWISSPROT	RETROVIRUS-RELATED POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE; ENDONUCLEASE]

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11784	24374		1.48	3.0E-03	AW294812.1	EST_HUMAN	UI-H-B12-ah1-d-06-0-UJ.s1 NCI_CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2726842 3'
11927	25186		2.86	3.0E-03	AI525096.1	EST_HUMAN	prom1a-5.E07.r bvtumor Homo sapiens cDNA 5'
11962	24510	37256	1.88	3.0E-03	AA993154.1	EST_HUMAN	ot7b10.s1 Soares total_fetus Nb2HF8_9w Homo sapiens cDNA clone IMAGE:1622779 3' similar to contains L1.13 MER26 repetitive element;
12016	25321		2.26	3.0E-03	AB009688.1	NT	Homo sapiens gene for CMP-N-acetylneuraminic acid hydroxylase, partial cds
12190	24661	31066	2.71	3.0E-03	AJ296282.1	NT	Rattus norvegicus mRNA for connexin36 (cx36 gene)
502	13286	25919	1.83	2.0E-03	Q04652	SWISSPROT	RING CANAL PROTEIN (KELCH PROTEIN)
502	13286	25920	1.83	2.0E-03	Q04652	SWISSPROT	RING CANAL PROTEIN (KELCH PROTEIN)
768	15552		12.31	2.0E-03	T70874.1	EST_HUMAN	y415h03.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:108341 5'
1342	14090	26766	2.07	2.0E-03	M20783.1	NT	Human alpha-2-plasmin inhibitor gene, exons 6 and 7
1345	14093	26768	1.4	2.0E-03	AA661605.1	EST_HUMAN	hu8801.s1 NCI_CGAP_A1V1 Homo sapiens cDNA clone IMAGE:1217593
1354	14102	26777	16.16	2.0E-03	AF284446.1	NT	Homo sapiens tumor-related protein DRC2 (DRC2) gene, complete cds
1473	14220	26906	1.73	2.0E-03	P48509	SWISSPROT	PLATELET-ENDOTHELIAL TETRASPAN ANTIGEN 3 (PETA-3) (GP27) (MEMBRANE GLYCOPROTEIN SFA-1) (CD151 ANTIGEN)
1506	14252	26938	1.84	2.0E-03	4557836	NT	Homo sapiens procollagen-lysine, 2-oxoglutarate 5-dioxygenase (lysine hydroxylase, Ehlers-Danlos syndrome type VI) (PLOD) mRNA
1506	14252	26939	1.84	2.0E-03	4557836	NT	Homo sapiens procollagen-lysine, 2-oxoglutarate 5-dioxygenase (lysine hydroxylase, Ehlers-Danlos syndrome type VI) (PLOD) mRNA
1586	14332		6.31	2.0E-03	P29400	SWISSPROT	COLLAGEN ALPHA 5(V) CHAIN PRECURSOR
1764	14506	27207	1.13	2.0E-03	AA460138.1	EST_HUMAN	z42a10.r1 Soares total_fetus Nb2HF8_9w Homo sapiens cDNA clone IMAGE:789114 5'
1872	14610		1.01	2.0E-03	BE144908.1	EST_HUMAN	GM2-HT0183-061099-018-403 HT0183 Homo sapiens cDNA
1888	14724	27445	1.57	2.0E-03	AF302691.1	NT	Mus musculus myelin expression factor-3-like protein gene, partial cds
2247	14975	27713	1.16	2.0E-03	AL163302.2	NT	Homo sapiens chromosome 21 segment HS21C102
2558	15272	28007	4.01	2.0E-03	AF187974.1	NT	8 Homo sapiens concentrative nucleoside transporter (CNT1) gene, exon 12
2558	15272	28008	4.01	2.0E-03	AF187974.1	NT	8 Homo sapiens concentrative nucleoside transporter (CNT1) gene, exon 12
2584	15298		4.57	2.0E-03	AW137782.1	EST_HUMAN	UI-H-B11-adi-g-10-0-UJ.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2717010 3'
3411	16169	28818	4.3	2.0E-03	AA450139.1	EST_HUMAN	z42a10.r1 Soares total_fetus Nb2HF8_9w Homo sapiens cDNA clone IMAGE:789114 5'
3417	16174	28823	1.13	2.0E-03	BF568955.1	EST_HUMAN	602183960T1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:4300070 3'
3657	16410	29048	6.62	2.0E-03	X87344.1	NT	H. sapiens DNA, DMB, HLA-Z1, IPP2, LMP2, TAP1, LMP7, TAP2, DOB, DOB2 and RING8, 9, 13 and 14 genes
4093	16835	29461	1.96	2.0E-03	P03374	SWISSPROT	ENV POLYPROTEIN [CONTAINS: COAT PROTEIN GP82; COAT PROTEIN GP36]
4195	16936		11.03	2.0E-03	U68491.1	NT	Rattus norvegicus 5-hydroxytryptamine7 receptor gene, partial cds
4393	17130		1.12	2.0E-03	AW297380.1	EST_HUMAN	UI-H-BW0-air-g-03-0-UJ.s1 NCI_CGAP_Sub6 Homo sapiens cDNA clone IMAGE:2730413 3'
4397	17134	29785	0.97	2.0E-03	A1064746.1	EST_HUMAN	HA0507 Human fetal liver cDNA library Homo sapiens cDNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4508	17244	29877	2.2	2.0E-03	L42512.1	NT	Drosophila melanogaster shortighted class 2 (shs) mRNA, complete cds
4509	17244	29878	2.2	2.0E-03	L42512.1	NT	Drosophila melanogaster shortighted class 2 (shs) mRNA, complete cds
4663	17397		1.84	2.0E-03	R87773.1	EST_HUMAN	yc45a02.s1 Soares adult brain N2b4HB55Y Homo sapiens cDNA clone IMAGE:180890 3'
4858	17882	30280	2.57	2.0E-03	AF003528.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
5092	17811	30427	1	2.0E-03	BE798380.1	EST_HUMAN	801833004F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3937560 5'
5398	18189	30893	1.38	2.0E-03	BF241410.1	EST_HUMAN	801876385F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4104892 5'
5540	25070	31245	2.06	2.0E-03	AB014593.1	NT	Homo sapiens mRNA for KIAA0893 protein, partial cds
5623	18420	31333	1.86	2.0E-03	U63711.1	NT	Xenopus laevis xefillin mRNA, complete cds
6019	18800	31760	3.58	2.0E-03	P23477	SWISSPROT	ATP-DEPENDENT NUCLEASE SUBUNIT B
6019	18800	31761	3.58	2.0E-03	P23477	SWISSPROT	ATP-DEPENDENT NUCLEASE SUBUNIT B
8253	19027	32001	2.17	2.0E-03	Q95203	SWISSPROT	CARBONIC ANHYDRASE-RELATED PROTEIN 2 PRECURSOR (CARP 2) (CA-RP II) (CA-XI)
8253	19027	32002	2.17	2.0E-03	Q95203	SWISSPROT	CARBONIC ANHYDRASE-RELATED PROTEIN 2 PRECURSOR (CARP 2) (CA-RP II) (CA-XI)
8255	19029	32004	7.5	2.0E-03	BF308187.1	EST_HUMAN	801887434F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4121408 5'
8291	19064	32046	2.44	2.0E-03	Q9UKP4	SWISSPROT	ADAM-TS 7 PRECURSOR (A DISINTEGRIN AND METALLOPROTEINASE WITH THROMBOSPONDIN MOTIFS 7) (ADAMTS-7) (ADAM-TS7)
8292	19065	32047	0.98	2.0E-03	AV709075.1	EST_HUMAN	AV709075 ADC Homo sapiens cDNA clone ADCAEF09 5'
8320	19090	32078	1.62	2.0E-03	X94451.1	NT	L. esculentum mRNA for lysyl-tRNA synthetase (LysRS)
8508	19271		1.16	2.0E-03	A1991089.1	EST_HUMAN	wu35h09.x1 Soares Dieckgraebe_colon_NHCD Homo sapiens cDNA clone IMAGE:2522177 3' similar to SW:RL29 HUMAN P47914 60S RIBOSOMAL PROTEIN L29 ; contains element MSR1 repetitive element ;
8541	19305	32311	0.61	2.0E-03	AA877831.1	EST_HUMAN	z13a11.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:430852 3'
8862	17939	30575	1.52	2.0E-03	AB036502.1	NT	Caenorhabditis elegans mRNA for galectin LEC-11, complete cds
8939	19674	32720	0.8	2.0E-03	5031864	NT	Homo sapiens lipoma HMGIC fusion partner (LHFP) mRNA
8939	19674	32721	0.8	2.0E-03	5031864	NT	Homo sapiens lipoma HMGIC fusion partner (LHFP) mRNA
8981	19508	32531	3.55	2.0E-03	BE067986.1	EST_HUMAN	GM4-BT0366-061299-054-d01 BT0366 Homo sapiens cDNA
7044	19735	32705	0.58	2.0E-03	A1298883.1	EST_HUMAN	qm99d1.1.x1 NCI CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1896885 3'
7193	19879	32853	0.8	2.0E-03	T86589.1	EST_HUMAN	yt77g10.11 Soares fetal liver spleen_1NFLS Homo sapiens cDNA clone IMAGE:114306 5'
7517	20188	33281	1.18	2.0E-03	P07384	SWISSPROT	PROTEOGLYCAN LINK PROTEIN PRECURSOR (CARTILAGE LINK PROTEIN) (LP)
7850	20645	33788	1.96	2.0E-03	AW592004.1	EST_HUMAN	ht37b06.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2934035 3' similar to TR:Q60976 Q60976 JERKY ;
8116	20810	33944	6.07	2.0E-03	N20287.1	EST_HUMAN	yx42g06.s1 Soares melanocyte 2Nb1M Homo sapiens cDNA clone IMAGE:264442 3' similar to contains L1.b2.L1 repetitive element ;

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8116	20810	33945	6.07	2.0E-03	N20287.1	EST_HUMAN	YX4206.s1 Soares melanocyte 2Nb-IM Homo sapiens cDNA clone IMAGE:264442 3' similar to contains L1.b2 L1 repetitive element
8162	20856	33987	0.54	2.0E-03	Q92350	SWISSPROT	HYPOTHETICAL 32.8 KD PROTEIN C639.05 IN CHROMOSOME 1
8184	20878	34015	1.19	2.0E-03	P19137	SWISSPROT	LAMININ ALPHA-1 CHAIN PRECURSOR (LAMININ A CHAIN)
8239	20933	34089	0.81	2.0E-03	6005855	NT	Homo sapiens Retina-derived POU-domain factor-1 (RPF-1), mRNA
8239	20933	34070	0.81	2.0E-03	6005855	NT	Homo sapiens Retina-derived POU-domain factor-1 (RPF-1), mRNA
8264	20958	34097	0.86	2.0E-03	AU136679.1	EST_HUMAN	AU136679 PLACE1 Homo sapiens cDNA clone PLACE1004839 5'
8318	21011		0.91	2.0E-03	AJ400877.1	NT	Homo sapiens ASL3 gene, CEGP1 gene, C11orf14 gene, C11orf15 gene, C11orf16 gene and C11orf17 gene
8570	21262	34400	0.54	2.0E-03	AB035256.1	NT	Oryctolagus cuniculus mRNA for eukaryotic polypeptide chain release factor 3, partial cds
9094	18419	31331	0.74	2.0E-03	AW786111.1	EST_HUMAN	MR2-UM0025-300300-102-f02 UM0025 Homo sapiens cDNA
9094	18419	31332	0.74	2.0E-03	AW786111.1	EST_HUMAN	MR2-UM0025-300300-102-f02 UM0025 Homo sapiens cDNA
9139	21827	34992	0.64	2.0E-03	AF224669.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
9426	22104	35276	0.89	2.0E-03	H50832.1	EST_HUMAN	yp86a09.s1 Soares fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:194296 3'
9426	22104	35277	0.89	2.0E-03	H50832.1	EST_HUMAN	yp86a09.s1 Soares fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:194296 3'
9458	22008	35178	3.46	2.0E-03	P24821	SWISSPROT	TENASCIN PRECURSOR (TN) (HEXABRACHION) (CYTOTACTIN) (NEURONECTIN) (GMEM) (JI)
9566	22219	35404	1.38	2.0E-03	P48982	SWISSPROT	(MOTENDINOUS ANTIGEN) (GLIOMA-ASSOCIATED-EXTRA CELLULAR MATRIX ANTIGEN) (GP 150-
9566	22219	35405	1.38	2.0E-03	P48982	SWISSPROT	BETA-GALACTOSIDASE PRECURSOR (LACTASE)
9623	22276	35464	0.53	2.0E-03	AF097732.1	NT	BETA-GALACTOSIDASE PRECURSOR (LACTASE)
9623	22276	35465	0.53	2.0E-03	AF097732.1	NT	Homo sapiens caspase recruitment domain-containing protein (BCL10) gene, complete cds
9815	22486	35668	0.81	2.0E-03	AF097732.1	NT	QV3-CT0064-060400-144-e01 OT0064 Homo sapiens cDNA
9942	22590		5.75	2.0E-03	AA251376.1	EST_HUMAN	zs10a06.s1 NCI_CGAP_GCB1 Homo sapiens cDNA
10508	23152	36377	0.45	2.0E-03	AW361176.1	EST_HUMAN	RC1-CT0251-141099-072-d01 CT0251 Homo sapiens cDNA
10508	23152	36378	0.45	2.0E-03	AW361176.1	EST_HUMAN	RC1-CT0251-141099-072-d01 CT0251 Homo sapiens cDNA
10938	23618		2.97	2.0E-03	M86524.1	NT	Human dystrophin gene
11470	20188	33281	2.56	2.0E-03	P07354	SWISSPROT	PROTEOLYCAN LINK PROTEIN PRECURSOR (CARTILAGE LINK PROTEIN) (LP)
11531	24131		2.14	2.0E-03	BF330909.1	EST_HUMAN	RC3-BT0333-310800-115-g04 BT0333 Homo sapiens cDNA
11538	24138	37448	9.1	2.0E-03	Z11740.1	NT	H. sapiens variable number tandem repeat (VNTR) locus DNA
11909	24473		3.23	2.0E-03	AJ625745.1	EST_HUMAN	y65103.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2283989 3' similar to SW:VATG_MANSE
11926	24487	37807	2.41	2.0E-03	AF157516.2	NT	Q25632 VACUOLAR ATP SYNTHASE SUBUNIT G ; Homo sapiens SEL1L (SEL1L) gene, partial cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11949	24502	37810	2.41	2.0E-03	A1084325.1	EST_HUMAN	oy43g06.s1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:1668634 3' similar to
11972	17907		9.37	2.0E-03	AJ245167.1	NT	TR:P97535 P97535 PS-PLA1 PRECURSOR. ;
12172	25361		2.98	2.0E-03	AV697966.1	EST_HUMAN	Camelus dromedarius cvhp19 gene for immunoglobulin heavy chain variable region
12262	24707	31050	1.76	2.0E-03	Y00508.1	NT	AV697966 GKC Homo sapiens cDNA clone GKCGXD05 5'
12433	25224		1.48	2.0E-03	A1376037.1	EST_HUMAN	H. sapiens M1 gene for muscarinic acetylcholine receptor
							ta66f02.x1 Soares_total_fetus_Nb2HF8_gw Homo sapiens cDNA clone IMAGE:2048051 3' similar to
							contains Alu repetitive element;
12542	24882		1.64	2.0E-03	AF129756.1	NT	Homo sapiens MSH55 gene, partial cds; and CLIC1, DDAH, G6b, G6c, G6d, G6e, G6f, BAT5, G5b,
12713	25175		2.65	2.0E-03	AV697966.1	EST_HUMAN	CSK2B, BAT4, G4, Apo M, BAT3, BAT2, AIF-1, 1C7, LST-1, LTB, TNF, and LTA genes, complete cds
429	13215	25860	1.28	1.0E-03	H96471.1	EST_HUMAN	AV697966 GKC Homo sapiens cDNA clone GKCGXD05 5'
810	13681	26248	2.31	1.0E-03	A1720263.1	EST_HUMAN	y68c08.r1 Soares_pineal_gland_N3-HPG Homo sapiens cDNA clone IMAGE:232334 5'
810	13581	26249	2.31	1.0E-03	A1720263.1	EST_HUMAN	as70b08.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2334039 3' similar to TR:Q13825
1073	13831	26489	3.76	1.0E-03	A1865788.1	EST_HUMAN	Q13825 AU-BINDING PROTEINENOYL-COA HYDRATASE. ;
1083	13851	26510	1.78	1.0E-03	A1854572.1	EST_HUMAN	as70b08.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2334039 3' similar to TR:Q13825
2021	14756	27486	3.38	1.0E-03	P47608	SWISSPROT	wk86a08.x1 NCI CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2422268 3'
2150	14880	27614	12.13	1.0E-03	AJ131016.1	NT	wk83e10.x1 NCI CGAP_Mel15 Homo sapiens cDNA clone IMAGE:2551242 3'
2979	15745	28393	1.37	1.0E-03	AB033117.1	NT	HIGH MOLECULAR WEIGHT FORM OF MYOSIN I (HMMWI)
							Homo sapiens SCL gene locus
3186	15949	28599	2.21	1.0E-03	P18915	SWISSPROT	Homo sapiens mRNA for KIAA1281 protein, partial cds
3186	15949	28600	2.21	1.0E-03	P18915	SWISSPROT	CARBONIC ANHYDRASE VI PRECURSOR (CARBONATE DEHYDRATASE VI) (CA-VI) (SECRETED)
3656	16409		1.65	1.0E-03	AB044400.1	NT	CARBONIC ANHYDRASE VI PRECURSOR (SALIVARY CARBONIC ANHYDRASE)
4402	17139	29767	1.28	1.0E-03	BE939162.1	EST_HUMAN	CARBONIC ANHYDRASE VI PRECURSOR (CARBONATE DEHYDRATASE VI) (CA-VI) (SECRETED)
4441	17177	29803	4.05	1.0E-03	BE246536.1	EST_HUMAN	Homo sapiens SVMT gene for synaptic vesicle monoamine transporter, exons 14, 15
4615	17350	29885	0.84	1.0E-03	U26449.1	NT	RC1-TN0128-160800-021-g01 TN0128 Homo sapiens cDNA
4773	17505	30127	1.68	1.0E-03	A1073485.1	EST_HUMAN	TCBAP1D4909 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBAP Homo
4773	17505	30128	1.68	1.0E-03	A1073485.1	EST_HUMAN	sapiens cDNA clone TCBAP4909
4774	17506		4.29	1.0E-03	BE154087.1	EST_HUMAN	Caenorhabditis elegans spliced leader RNA (SL3 alpha), (SL4), and (SL5) genes
5018	17739	30348	7.24	1.0E-03	O46409	SWISSPROT	ov45c04.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1640282 3'
							ov45c04.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1640282 3'
							PM0-HT0339-200400-010-D02 HT0339 Homo sapiens cDNA
							APOLIPOPROTEIN A-IV PRECURSOR (APO-AIV)

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5225	18032	30658	1.87	1.0E-03	AA290951.1	EST_HUMAN	zs44701.1 NCI_QGAP_GCB1 Homo sapiens cDNA clone IMAGE:700345 5'
5317	18121	30778	3.12	1.0E-03	AJ006345.1	NT	Homo sapiens KVLQT1 gene
5369	18170	30858	1.85	1.0E-03	K03332.1	NT	Epstein-Barr virus (AG876 isolate) U2-IR2 domain encoding nuclear protein EBNA2, complete cds
5369	18170	30857	1.85	1.0E-03	K03332.1	NT	Epstein-Barr virus (AG876 isolate) U2-IR2 domain encoding nuclear protein EBNA2, complete cds
5485	18284	31182	0.83	1.0E-03	BE796491.1	EST_HUMAN	601589841F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3943954 5'
5491	18280	31187	2.07	1.0E-03	Q02388	SWISSPROT	COLLAGEN ALPHA 1(VI) CHAIN PRECURSOR (LONG-CHAIN COLLAGEN) (LC COLLAGEN)
5546	18343	31251	0.67	1.0E-03	N41974.1	EST_HUMAN	yy07h06.r1 Soares melanocyte 2NbhM Homo sapiens cDNA clone IMAGE:270587 5' similar to contains element MER6 repetitive element;
5546	18343	31252	0.67	1.0E-03	N41974.1	EST_HUMAN	yy07h06.r1 Soares melanocyte 2NbhM Homo sapiens cDNA clone IMAGE:270587 5' similar to contains element MER6 repetitive element;
5930	18714		2.75	1.0E-03	X07699.1	NT	Mouse nucleolin gene
5968	18750	31711	1.07	1.0E-03	BE863939.2	EST_HUMAN	601657516R1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3875683 3'
6099	18877		8.76	1.0E-03	11526176	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1), mRNA
6242	19016	31990	1.14	1.0E-03	T87761.1	EST_HUMAN	yd83a11.r1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:115772 5'
6315	19086		1.7	1.0E-03	AW902585.1	EST_HUMAN	QV3-NN1024-260400-171-g05 NN1024 Homo sapiens cDNA
6657	19418	32432	1.37	1.0E-03	L77570.1	NT	Homo sapiens DiGeorge syndrome critical region, centromeric end
7052	19743	32905	2.54	1.0E-03	D16826.1	NT	Human gene for fourth somatostatin receptor subtype
7539	20209	33308	1.8	1.0E-03	U52111.2	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMK1), creatine transporter (CRT), CDM protein (CDM), adrenoleukodystrophy protein >
7608	20274	33382	3.37	1.0E-03	M63376.1	NT	Human TRPM-2 protein gene, exons 1,2 and 3
7656	20320	33429	0.98	1.0E-03	BE880044.1	EST_HUMAN	601491081F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3893276 5'
7789	20484	33608	0.83	1.0E-03	AF274581.1	NT	Homo sapiens prolactin-releasing peptide receptor gene, 5' flanking region
7850	20545	33673	5.18	1.0E-03	AJ251973.1	NT	Homo sapiens partial steerin-1 gene
8043	20737	33870	1	1.0E-03	AA122270.1	EST_HUMAN	zh97c09.s1 Soares_pregnant_uterus_NbhPU Homo sapiens cDNA clone IMAGE:490768 3' similar to contains L1 L1 L1 repetitive element;
8142	20836	33968	1.94	1.0E-03	AF153980.1	NT	Homo sapiens exostosin-like protein 1 (EXTL1) gene, exons 2 through 11, and complete cds
8329	21022	34158	0.68	1.0E-03	U28397.1	NT	Rattus norvegicus plasma membrane Ca2+ ATPase isoform 3 (PMCA3) gene, 5' flanking region
8492	21184	34326	0.61	1.0E-03	AA001613.1	EST_HUMAN	zh82606.s1 Soares_fetal_liver_spleen_INFLS_s1 Homo sapiens cDNA clone IMAGE:427810 3'
8492	21184	34327	0.61	1.0E-03	AA001613.1	EST_HUMAN	zh82606.s1 Soares_fetal_liver_spleen_INFLS_s1 Homo sapiens cDNA clone IMAGE:427810 3'
8842	21534		1.36	1.0E-03	Y11204.1	NT	V carter gene encoding volvoxpsin
8859	21560	34705	0.62	1.0E-03	AW840353.1	EST_HUMAN	CM3-LT0078-170200-092-e07 LT0078 Homo sapiens cDNA

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Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8978	21668		0.58	1.0E-03	U52111.2		Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRT), CDM protein (CDM), adrenoleukodystrophy protein >
9017	21707	34858	3.68	1.0E-03	M30471.1	NT	Human class III alcohol dehydrogenase (ADH5) cDNA subunit mRNA, complete cds
9017	21707	34859	3.68	1.0E-03	M30471.1	NT	Human class III alcohol dehydrogenase (ADH5) cDNA subunit mRNA, complete cds
9507	22160	35340	1.66	1.0E-03	AF011400.1	NT	Thermotoga neopolitana alpha-1,6-galactosidase (aglA) gene, complete cds
9507	22160	35341	1.66	1.0E-03	AF011400.1	NT	Thermotoga neopolitana alpha-1,6-galactosidase (aglA) gene, complete cds
9720	22371	35570	0.81	1.0E-03	Q01129	SWISSPROT	BONE PROTEOGLYCAN II PRECURSOR (PG-S2) (DECORIN) (PG40) (DERMATAN SULFATE
10063	22711	35829	0.85	1.0E-03	AF003528.1	NT	PROTEOGLYCAN-II (DSPG)
10088	22716		0.75	1.0E-03	AF097485.1	NT	Homo sapiens glypican 3 (GPC3) gene, partial cds and flanking repeat regions
10214	22862	36075	1.72	1.0E-03	AJ024350.1	EST_HUMAN	Homo sapiens transducin beta-like 2 (TBL2) gene, complete cds
10503	23149						ov7508.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1843175 3' similar to contains MER39.b1
10563	23259	36495	0.46	1.0E-03	AA708202.1	EST_HUMAN	ag93f12.s1 Stratagene hNT neuron (#937233) Homo sapiens cDNA clone IMAGE:1142063 3' similar to contains Alu repetitive element
10563	23259	36496	1.79	1.0E-03	AW362393.1	EST_HUMAN	RC1-CT0279-181099-011-a09 CT0279 Homo sapiens cDNA
10563	23259	36498	1.79	1.0E-03	AW362393.1	EST_HUMAN	RC1-CT0279-181099-011-a09 CT0279 Homo sapiens cDNA
10651	23342	36580	2.78	1.0E-03	BE170859.1	EST_HUMAN	QV3-HT0543-220300-130-a03 HT0543 Homo sapiens cDNA
10725	23413						tf73e12.x1 NCL CGAP_HSC3 Homo sapiens cDNA clone IMAGE:2246446 3' similar to TR:Q26195 Q26195
10808	23491	36727	3.29	1.0E-03	AJ583847.1	EST_HUMAN	PVA1 GENE ;
11106	23776		1.38	1.0E-03	AW237482.1	EST_HUMAN	xm72d12.x1 NCL CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2889751 3'
11905	24470	37805	3.05	1.0E-03	AV759949.1	EST_HUMAN	AV759949 MDS Homo sapiens cDNA clone MDSDDF11 5'
12124	24616		4.48	1.0E-03	BE894488.1	EST_HUMAN	601433087Ft NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3918524 5'
12371	25342		1.38	1.0E-03	AV731520.1	EST_HUMAN	AV731520 HTF Homo sapiens cDNA clone HTFAJG05 5'
12478	25365	30612	1.98	1.0E-03	AJ347355.1	EST_HUMAN	tc05h11.x1 NCL CGAP_Cot16 Homo sapiens cDNA clone IMAGE:2063013 3' similar to contains Alu repetitive element
12821	25187	30809	7.05	1.0E-03	BE780572.1	EST_HUMAN	601498878Ft NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3872035 5'
5130	17848	30465	1.37	1.0E-03	AW847341.1	EST_HUMAN	RC0-CT0205-240989-021-d02 CT0205 Homo sapiens cDNA
5596	18391		0.7	9.0E-04	P08548	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
6165	18942		1.28	9.0E-04	P06727	SWISSPROT	APOLIPOPROTEIN A-IV PRECURSOR (APO-AIV)
6395	19164	32165	0.6	9.0E-04	AJ006345.1	NT	Homo sapiens KVLQT1 gene
9543	22196		0.96	9.0E-04	P02381	SWISSPROT	MITOCHONDRIAL RIBOSOMAL PROTEIN VAR1
1471	14218		1.42	9.0E-04	AB037203.1	NT	Glycerhiza glabra GgPAS1 mRNA for beta-amylin synthase, complete cds
			1.02	8.0E-04	X96469.1	NT	X.laavis mRNA for C4SR protein

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Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4159	16899		4.37	8.0E-04	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
4713	17445	30078	2.39	8.0E-04	U29185.1	NT	Homo sapiens prion protein (PrP) gene, complete cds
11092	23762		2.93	8.0E-04	AA777084.1	EST_HUMAN	z24c10.s1 Soares fetal heart_NbHH19W Homo sapiens cDNA clone IMAGE:377874 3'
11266	23928		1.96	8.0E-04	AI571089.1	EST_HUMAN	fn85a08.x1 NCI CGAP_U12 Homo sapiens cDNA clone IMAGE:2176310 3'
2398	15119	27858	0.97	7.0E-04	U29185.1	NT	Homo sapiens prion protein (PrP) gene, complete cds
2719	15428	28164	1.19	7.0E-04	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
3274	16035	28685	1	7.0E-04	4885170	NT	Homo sapiens chromosome X open reading frame 6 (CXORF6) mRNA
6005	18786	31748	0.84	7.0E-04	AA516212.1	EST_HUMAN	wg36f09.x1 Soares NSF_F8 gW_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:939718 similar to contains L1.b3 L1 L1
6420	19186		2.47	7.0E-04	AI769331.1	EST_HUMAN	repetitive element;
7126	19816		0.78	7.0E-04	AK024445.1	NT	Homo sapiens mRNA for FLJ00035 protein, partial cds
9703	22354	35549	0.53	7.0E-04	P13497	SWISSPROT	BONE MORPHOGENETIC PROTEIN 1 PRECURSOR (BMP-1)
9703	22354	35550	0.53	7.0E-04	P13497	SWISSPROT	BONE MORPHOGENETIC PROTEIN 1 PRECURSOR (BMP-1)
11557	24156		2.28	7.0E-04	U78027.1	NT	Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein
11588	24185	37500	4.04	7.0E-04	Z40581.1	EST_HUMAN	(L44L) and FTP3 (FTP3) genes, complete cds
12642	24939		2.31	7.0E-04	R17336.1	EST_HUMAN	HSC28A072 normalized infant brain cDNA Homo sapiens cDNA clone c-28a07 3'
12869	24964		5.98	7.0E-04	6005855	NT	Homo sapiens infant brain 1N1B Homo sapiens cDNA clone IMAGE:32298 5'
3941	16691	26329	1.83	8.0E-04	AI862525.1	EST_HUMAN	Homo sapiens Retina-derived POU-domain factor-1 (RPF-1), mRNA
4068	18812	29440	0.78	8.0E-04	K01315.1	NT	Homo sapiens epsilon-1 pseudogene (IGHF1) gene, 5' flanking region
4068	18812	29441	0.78	8.0E-04	K01315.1	NT	Homo sapiens epsilon-1 pseudogene (IGHF1) gene, 5' flanking region
4162	18902	29531	3.79	8.0E-04	U45983.1	NT	Homo sapiens CCR8 chemokine receptor (CMKBR8) gene, complete cds
7478	20151	33245	0.81	8.0E-04	Q15034	SWISSPROT	GLUCOSE TRANSPORTER TYPE 5, SMALL INTESTINE (FRUCTOSE TRANSPORTER)
7765	20461		3.33	8.0E-04	P48408	SWISSPROT	LOR1 repetitive element;
7914	20809		0.82	8.0E-04	H92947.1	EST_HUMAN	RC2-BN0120-250400-012-h11 BN0120 Homo sapiens cDNA
9880	22530		3.5	8.0E-04	AL048507.2	EST_HUMAN	Lytechinus variegatus embryonic blastocoelar extracellular matrix protein precursor (ECM3) mRNA, complete
9980	22628	35837	2.26	8.0E-04	BE005650.1	EST_HUMAN	cds
10238	22886		0.71	8.0E-04	AF287478.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22, segment 2/3
11467	24070	37378	2.53	8.0E-04	AJ229042.1	NT	UIH-B10-aab-e-09-0-UI.s1 NCI CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2708825 3'
11558	24157	37467	3.46	8.0E-04	AW013847.1	EST_HUMAN	NUCLEOSIDE DIPHOSPHATE KINASE B (NDK B) (NDP KINASE B) (NM23-M2) (P18)
11636	24233		2.17	8.0E-04	Q01768	SWISSPROT	RC1-HT0269-261199-012-408 HT0269 Homo sapiens cDNA
12082	25249		2.81	8.0E-04	AW380519.1	EST_HUMAN	

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Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12816	25058						wf76g11.x1 NCI_CGAP_Lu10 Homo sapiens cDNA clone IMAGE:2408804 3' similar to contains element L1
638	13415	26051	1.34	6.0E-04	AI817088.1	EST_HUMAN	repetitive element ;
1490	14237		6.81	5.0E-04	O10341	SWISSPROT	HYPOTHETICAL 29.3 KD PROTEIN (ORF92)
			1.4	5.0E-04	AW851844.1	EST_HUMAN	QV0-C10225-021089-030-a07 CT0225 Homo sapiens cDNA
3408	16166	28815				EST_HUMAN	nk27e11.s1 NCI_CGAP_Col1 Homo sapiens cDNA clone IMAGE:1014764 3' similar to contains Alu
			1.35	5.0E-04	AA548831.1	EST_HUMAN	repetitive element ;
3704	18457	28096	2.32	5.0E-04	Q9UKP4	SWISSPROT	ADAM-TS 7 PRECURSOR (A DISINTEGRIN AND METALLOPROTEINASE WITH THROMBOSPONDIN
5386	18186	30877					MOTIFS 7) (ADAMTS-7) (ADAM-TS7)
6532	19298	32303	2.89	5.0E-04	AF248054.1	NT	Bos taurus micromolar calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds
7276	19960	33037	7.89	5.0E-04	AA156080.1	EST_HUMAN	zo33b08.r1 Striatagene cdon (#337204) Homo sapiens cDNA clone IMAGE:588663 5'
			3.75	5.0E-04	M23604.1	NT	Gorilla gorilla involucrin gene medium allele, complete cds
7856	20551	33677					qd13f06.x1 Soares_placenta_8to8weeks_2NbrHP809W Homo sapiens cDNA clone IMAGE:1723619 3'
			5.2	5.0E-04	AI188982.1	EST_HUMAN	similar to gb:X51602_cds1 VASCULAR ENDOTHELIAL GROWTH FACTOR RECEPTOR 1
8202	20896	34033					(HUMAN) contains Alu repetitive element ;
9177	21847	35013	0.96	5.0E-04	AA814519.1	EST_HUMAN	ob96e02.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:13392226 3' similar to contains element
			1.39	5.0E-04	AA846545.1	EST_HUMAN	MER22 repetitive element ;
9271	22025	35195					q156h03.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1394357 3'
9418	22098	35268	0.88	5.0E-04	N83765.1	EST_HUMAN	KK2745F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone KK2745 5' similar to
9509	22162	35344	1.44	5.0E-04	P29128	SWISSPROT	REPTITIVE ELEMENT
10177	22825		4.1	5.0E-04	AW270938.1	EST_HUMAN	BIFUNCTIONAL ENDO-1,4-BETA-XYLANASE XYLA PRECURSOR
10897	23577		0.48	5.0E-04	U50871.1	NT	xs06e02.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2768858 3'
			2.38	5.0E-04	AL048507.2	EST_HUMAN	Human familial Alzheimer's disease (STM2) gene, complete cds
11713	18186	30877					DKFZp566M2024_r1 586 (synonym: huter1) Homo sapiens cDNA clone DKFZp566M2024
12020	25184		14.08	5.0E-04	AF248054.1	NT	Bos taurus micromolar calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cdc
658	13435	26076	5.04	5.0E-04	AA568513.1	EST_HUMAN	nf15h02.s1 NCI_CGAP_P11 Homo sapiens cDNA clone IMAGE:913875
			1.46	4.0E-04	U32748.1	NT	Haemophilus influenzae Rd section 63 of 163 of the complete genome
827	13597	26267					as70b08.x1 Barslead colon HPLR87 Homo sapiens cDNA clone IMAGE:2334039 3' similar to TR:Q13825
			1.79	4.0E-04	AI720263.1	EST_HUMAN	Q13825 AU-BINDING PROTEIN/ENOYL-COA HYDRATASE ;
827	13597	26268					as70b08.x1 Barslead colon HPLR87 Homo sapiens cDNA clone IMAGE:2334039 3' similar to TR:Q13825
1449	14198	26880	1.79	4.0E-04	AI720263.1	EST_HUMAN	Q13825 AU-BINDING PROTEIN/ENOYL-COA HYDRATASE ;
2076	14907	27538	3.18	4.0E-04	AW753356.1	EST_HUMAN	RC3-CT0254-130100-023-f01 CT0254 Homo sapiens cDNA
			1.81	4.0E-04	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2129	14860		1	4.0E-04	AL046704.1	EST_HUMAN	DKFZp434D059.1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434D059.5
2633	15345	28088	2.21	4.0E-04	O96615	SWISSPROT	SERPIN-2 (SILK GUM PROTEIN 2)
3162	15925	28572	0.95	4.0E-04	AF281074.1	NT	Homo sapiens neuropilin 2 (NRP2) gene, complete cds, alternatively spliced
4289	17028	29653	3.18	4.0E-04	AA576331.1	EST_HUMAN	h10a10.s1 NCI_CGAP_Co1 Homo sapiens cDNA clone IMAGE:951930.3 similar to gb:M21121 T-CELL SPECIFIC RANTES PROTEIN PRECURSOR (HUMAN);
4289	17028	29654	3.18	4.0E-04	AA576331.1	EST_HUMAN	h10a10.s1 NCI_CGAP_Co1 Homo sapiens cDNA clone IMAGE:951930.3 similar to gb:M21121 T-CELL SPECIFIC RANTES PROTEIN PRECURSOR (HUMAN);
4500	17236	29868	1.76	4.0E-04	AA086324.1	EST_HUMAN	zn61c08.s1 Stragene muscle 937209 Homo sapiens cDNA clone IMAGE:562670.3
5028	17748	30360	3.1	4.0E-04	BE560660.1	EST_HUMAN	601345895F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3678910.5
7168	19855	32925	1.3	4.0E-04	P48442	SWISSPROT	EXTRACELLULAR CALCIUM-SENSING RECEPTOR PRECURSOR (CASR) (PARATHYROID CELL CALCIUM-SENSING RECEPTOR)
7434	20111		0.76	4.0E-04	AL161596.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 66
7618	20284	33394	0.56	4.0E-04	AL122079.1	EST_HUMAN	AU122079 MAMMA1 Homo sapiens cDNA clone MAMMA1001620.5
8434	21127	34284	1.07	4.0E-04	BF240712.1	EST_HUMAN	601875985F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4099700.5
8442	21134	34270	1.5	4.0E-04	N25507.1	EST_HUMAN	yx39e12.r1 Soares melanocyte 2N8HM Homo sapiens cDNA clone IMAGE:264142.5
9590	22243	35428	3.24	4.0E-04	AI025699.1	EST_HUMAN	ov87h03.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1644341.3
9740	22391		1.22	4.0E-04	AF022855.1	NT	Mus musculus neuropilin-2 (e17) mRNA, alternatively spliced, complete cds
12380	25157		2.05	4.0E-04	AF254822.1	NT	Homo sapiens SMARCA4 isoform (SMARCA4) gene, complete cds, alternatively spliced
152	12967	25608	3.46	3.0E-04	AL119428.1	EST_HUMAN	DKFZp761J221.1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761J221.5
190	13003	25844	2.24	3.0E-04	P49259	SWISSPROT	180 KD SECRETORY PHOSPHOLIPASE A2 RECEPTOR PRECURSOR (PLA2-R)
860	13629	26300	1.32	3.0E-04	U83991.1	NT	Human short chain acyl CoA dehydrogenase gene, exons 1 and 2
1831	14570	27282	1.08	3.0E-04	AI262100.1	EST_HUMAN	qz28d03.y1 NCI_CGAP_K1d11 Homo sapiens cDNA clone IMAGE:2028197.5
1846	14584		1.21	3.0E-04	AI399674.1	EST_HUMAN	tn23a02.x1 NCI_CGAP_P128 Homo sapiens cDNA clone IMAGE:2119082.3
3303	16084	28712	3.43	3.0E-04	P25147	SWISSPROT	INTERNALIN B PRECURSOR
3308	16068	28717	0.7	3.0E-04	AA203342.1	EST_HUMAN	z56a04.r1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:446478.5
3946	16696	28335	4.07	3.0E-04	P49448	SWISSPROT	GLUTAMATE DEHYDROGENASE 2 PRECURSOR (GDH)
4034	16779		1.33	3.0E-04	AJ271735.1	NT	Homo sapiens Xa pseudautosomal region, segment 1/2
4072	16816		1.12	3.0E-04	BE140609.1	EST_HUMAN	RCO-HT0014-310598-028 HT0014 Homo sapiens cDNA
4766	17498		4.72	3.0E-04	BE153778.1	EST_HUMAN	PMO-HT00399-190200-007-g12 HT0339 Homo sapiens cDNA
4827	17558	30180	0.95	3.0E-04	AW937723.1	EST_HUMAN	QV3-DT0045-221299-046-009 DT0045 Homo sapiens cDNA
5083	17782	30399	0.96	3.0E-04	AA613145.1	EST_HUMAN	nq08g09.s1 NCI_CGAP_Lu1 Homo sapiens cDNA clone IMAGE:1143328.3
6052	18832		7.86	3.0E-04	AL163281.2	NT	Homo sapiens chromosome 21 segment HS21C081
6722	19596	32586	2.82	3.0E-04	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
7491	20183	33256	0.84	3.0E-04	P23468	SWISSPROT	PROTEIN-TYROSINE PHOSPHATASE DELTA PRECURSOR (R-PTP-DELTA)

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Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8157	20851	33983	3.23	3.0E-04	P22607	SWISSPROT	FIBROBLAST GROWTH FACTOR RECEPTOR 3 PRECURSOR (FGFR-3)
9820	22471	35673	1.34	3.0E-04	AA454055.1	EST_HUMAN	zx48d08.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:795471 5' similar to gb:M62762
10078	22726	35943	0.65	3.0E-04	A1992139.1	EST_HUMAN	VACUOLAR ATP SYNTHASE 16 KD PROTEOLIPID SUBUNIT (HUMAN);
10356	23003	36220	3.73	3.0E-04	AA781201.1	EST_HUMAN	w75at11.x1 Soares_thymus_NHT Homo sapiens cDNA clone IMAGE:2513276 3'
10495	23141	36367	0.54	3.0E-04	P13816	EST_HUMAN	a124g05.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:2513276 3'
11555	24154	37466	1.38	3.0E-04	4501960	SWISSPROT	RIBOSOMAL PROTEIN L7A (HUMAN);
11976	25386	30617	4.81	3.0E-04	AA228301.1	EST_HUMAN	GLUTAMIC ACID-RICH PROTEIN PRECURSOR
12338	25230	30818	3.08	3.0E-04	AB018292.1	NT	Homo sapiens adrenole, alpha-1A-, receptor (ADRA1A), mRNA
12730	25000		2.75	3.0E-04	AL134483.1	EST_HUMAN	nc39e04.r1 NC1_CGAP_P12 Homo sapiens cDNA clone IMAGE:1010430 similar to contains L1 L2 L1 repetitive element:
171	12984	25624	2.65	2.0E-04	AF217796.1	NT	Homo sapiens mRNA for KIAA0749 protein, partial cds
466	13251	25892	1.8	2.0E-04	AU146707.1	EST_HUMAN	DKFZp547L185_r1 547 (synonym: hrbf1) Homo sapiens cDNA clone DKFZp547L185 6'
887	13656	26324	10.71	2.0E-04	M86524.1	NT	Homo sapiens SCG10 like-protein, helicase-like protein NHL, M68, and ADP-ribosylation factor related protein 1 (ARFRP1) genes, complete cds
887	13656	26325	10.71	2.0E-04	M86524.1	NT	AU146707 HEMBB1 Homo sapiens cDNA clone HEMBB1001253 3'
1156	13911		3.93	2.0E-04	A1286021.1	EST_HUMAN	Human dystrophin gene
1163	13917		2.18	2.0E-04	AL163203.2	NT	qh98e11.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1855052 3' similar to contains MER3.b2 MER3 repetitive element;
1824	14563		1.12	2.0E-04	AF224268.1	NT	Homo sapiens chromosome 21 segment HS21C003 Mus musculus 5' flanking region of Pitd3 gene
2581	15295	28033	4.47	2.0E-04	U66081.1	NT	Human germline T-cell receptor beta chain TORBV17S1A1T, TORBV2S1, TORBV10S1P, TORBV29S1P, TORBV19S1P, TORBV15S1, TORBV11S1A1T, HVB relic, TORBV28S1P, TORBV34S1, TORBV14S1, TORBV3S1, TORBV4S1A1T, TRY4, TRY6, TRY6, TRY7, TRY8, TCRBD1, TCRBJ1S1, TCRBJ1S2,>
2986	15752	28398	1.11	2.0E-04	A1124629.1	EST_HUMAN	am58c08.x1 Johnston frontal cortex Homo sapiens cDNA clone IMAGE:1539780 3'
3328	16088	28740	1.1	2.0E-04	5174736	NT	Homo sapiens tubulin, beta, 4 (TUBB4) mRNA
3429	16186	28834	1.89	2.0E-04	BE082317.1	EST_HUMAN	QV2-BT0636-070500-194-b07 BT0636 Homo sapiens cDNA
3892	16842	29282	0.79	2.0E-04	AW978441.1	EST_HUMAN	EST1390550 MAGE resequences, MAGP Homo sapiens cDNA
4122	16864		4.93	2.0E-04	U01029.1	NT	Phasolus vulgaris nitrate reductase (PVNR2) gene, complete cds
4620	17355	29690	1.74	2.0E-04	H96265.1	EST_HUMAN	y01e11.r1 Soares_pituitary_gland_N3HPG Homo sapiens cDNA clone IMAGE:232556 5'
4620	17355	29691	1.74	2.0E-04	H96265.1	EST_HUMAN	y01e11.r1 Soares_pituitary_gland_N3HPG Homo sapiens cDNA clone IMAGE:232556 5'
4742	17474		1.63	2.0E-04	U09226.1	NT	Gallus gallus proteasome 28 kDa subunit homolog mRNA, complete cds
4998	17721	30324	1.1	2.0E-04	AB037597.1	NT	Danio rerio hagoromo gene, exons 1 to 6, partial cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6089	17808	30424	1.04	2.0E-04	P35748	SWISSPROT	MYOSIN HEAVY CHAIN, SMOOTH MUSCLE ISOFORM (SMMHC)
6457	18256	31148	0.73	2.0E-04	AV654352.1	EST_HUMAN	AV654352 GLC Homo sapiens cDNA clone GLCJUH10 3'
5469	18268	31160	1.75	2.0E-04	AI690862.1	EST_HUMAN	ICQ3b11.x1 NCI CGAP_U13 Homo sapiens cDNA clone IMAGE:2207709 3'
5684	18459	31373	0.96	2.0E-04	AA266652.1	EST_HUMAN	EST11191 Uterus Homo sapiens cDNA 5' end similar to EST containing O family repeat
5857	18644	31584	0.81	2.0E-04	4758179	NT	Homo sapiens cell cycle progression 3 protein (DNJ3) mRNA
6144	18822	31892	0.59	2.0E-04	AF140708.1	NT	Mus musculus G protein coupled receptor gene, complete cds; and unknown gene
7130	18818		2.6	2.0E-04	AU121712.1	EST_HUMAN	AU121712 MAMMA1 Homo sapiens cDNA clone MAMMA1000788 5'
7225	18910		0.55	2.0E-04	AW860963.1	EST_HUMAN	QV0-CT0387-180300-167-e10 CT0387 Homo sapiens cDNA
7520	20191		14.88	2.0E-04	P08548	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
7530	20200	33285	1.42	2.0E-04	P54296	SWISSPROT	MYOMESIN 2 (M-PROTEIN) (165 KD TITIN-ASSOCIATED PROTEIN) (165 KD CONNECTIN-ASSOCIATED PROTEIN)
7855	20550	33675	1.06	2.0E-04	U32444.2	NT	Solanum lycopersicum phytochrome F (PHYF) gene, partial cds
7855	20550	33676	1.06	2.0E-04	U32444.2	NT	Solanum lycopersicum phytochrome F (PHYF) gene, partial cds
8182	20876	34012	1.23	2.0E-04	AB026898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
8182	20876	34013	1.23	2.0E-04	AB026898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
8463	21155	34298	1.96	2.0E-04	AF020503.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHIT) gene, exon 5
8842	21334	34478	0.49	2.0E-04	X57331.1	NT	Human immunoglobulin C(mu) and C(delta) heavy chain genes (constant regions)
9233	21912	35086	0.49	2.0E-04	AA725700.1	EST_HUMAN	ai22a12.s1 Soares testis_NHT Homo sapiens cDNA clone 1343518 3'
9319	21986	35158	0.6	2.0E-04	P18715	SWISSPROT	GASTRULA ZINC FINGER PROTEIN XLOGF26.1
9875	22525	35719	1.19	2.0E-04	BE149303.1	EST_HUMAN	RC3-HT0264-151099-011-b05 HT0264 Homo sapiens cDNA
9916	22565	35761	1.77	2.0E-04	AA405777.1	EST_HUMAN	zu66c11.1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:742964 5'
10755	23440	36684	5.23	2.0E-04	AV730373.1	EST_HUMAN	AV730373 HTF Homo sapiens cDNA clone HTFAAA01 5'
11128	23796		1.61	2.0E-04	AJ243213.1	NT	Homo sapiens partial 5-HT4 receptor gene, exons 2 to 5
11276	23937	37226					ij01f11.x1 NCI CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2140269 3' similar to contains Alu repetitive element;
11403	24052	37356	3.06	2.0E-04	AI440282.1	EST_HUMAN	UI-H-B1-adm-c-04-0-UI.s1 NCI CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2717190 3'
11857	24441	37782	2.86	2.0E-04	AW136740.1	EST_HUMAN	y679b10.x5 Stragene ovary (#937217) Homo sapiens cDNA clone IMAGE:77371 3'
			2.77	2.0E-04	AI821304.1	EST_HUMAN	RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ; ENDONUCLEASE]
1053	13812	26472	3.3	1.0E-04	P11369	SWISSPROT	
1082	13850	26508	4.74	1.0E-04	AW013847.1	EST_HUMAN	UI-H-B10-aab-e-09-0-UI.s1 NCI CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2708825 3'
1092	13850	26509	4.74	1.0E-04	AW013847.1	EST_HUMAN	UI-H-B10-aab-e-09-0-UI.s1 NCI CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2708825 3'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1309	14057		3.12	1.0E-04	U62918.1	NT	Anguilla anguilla dopamine D1A1 receptor (d1A1) gene, complete cds
1623	14370	27058	3.25	1.0E-04	AF148805.1	NT	Kaposi's sarcoma-associated herpesvirus ORF 68 gene, partial cds; and ORF 69, kaposin, v-FLIP, v-cyclin, latent nuclear antigen, ORF K14, v-GPCR, putative phosphoribosylformylglycinamide synthase, and LAMP (LAMP) genes, complete cds
1623	14370	27058	3.25	1.0E-04	AF148805.1	NT	Kaposi's sarcoma-associated herpesvirus ORF 68 gene, partial cds; and ORF 69, kaposin, v-FLIP, v-cyclin, latent nuclear antigen, ORF K14, v-GPCR, putative phosphoribosylformylglycinamide synthase, and LAMP (LAMP) genes, complete cds
1854	14592	27308	2.09	1.0E-04	AB048342.1	NT	Kaposi's sarcoma-associated herpesvirus ORF 68 gene, partial cds; and ORF 69, kaposin, v-FLIP, v-cyclin, latent nuclear antigen, ORF K14, v-GPCR, putative phosphoribosylformylglycinamide synthase, and LAMP (LAMP) genes, complete cds
3278	16039	28689	1.06	1.0E-04	Q62203	SWISSPROT	Equus caballus DNA, chromosome 24q14, microsatellite TKY38
3719	16472	29110	0.91	1.0E-04	AI440282.1	EST_HUMAN	SPLICEOSOME ASSOCIATED PROTEIN 62 (SAP 62) (SPLICING FACTOR 3A SUBUNIT 2) (SF3A66)
4037	16782	29412	2.11	1.0E-04	M14042.1	NT	[J01111.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2140289 3' similar to contains Alu repetitive element;
4062	16807	29437	1.15	1.0E-04	AV647727.1	EST_HUMAN	Mouse alpha 1 type-IV collagen mRNA
5036	17755	30368	1.28	1.0E-04	7662015	NT	AV647727 GLC Homo sapiens cDNA clone G1CB8D04 3'
5036	17755	30369	1.28	1.0E-04	7662015	NT	Homo sapiens KIAA0237 gene product (KIAA0237), mRNA
5769	18560	31487	1.49	1.0E-04	P08547	SWISSPROT	Homo sapiens KIAA0237 gene product (KIAA0237), mRNA
5834	18623	31556	0.57	1.0E-04	T19615.1	EST_HUMAN	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
5834	18623	31557	0.57	1.0E-04	T19615.1	EST_HUMAN	753F Heart Homo sapiens cDNA clone 753
6346	19116	32105	0.95	1.0E-04	AA177111.1	EST_HUMAN	753F Heart Homo sapiens cDNA clone 753
6738	19572	32605	0.92	1.0E-04	AA564561.1	EST_HUMAN	inc02a12.s1 NCI_CGAP_P3 Homo sapiens cDNA clone IMAGE:252
7086	19776	32841	15.6	1.0E-04	AI251980.1	EST_HUMAN	n25a04.s1 NCI_CGAP_AA1 Homo sapiens cDNA clone IMAGE:993486 3' similar to gb:M97252
7470	19776	32841	17.82	1.0E-04	AI251980.1	EST_HUMAN	KALLMANN SYNDROME PROTEIN PRECURSOR (HUMAN); contains Alu repetitive element;
7894	20589	33719	0.95	1.0E-04	AA630463.1	EST_HUMAN	qv57d10.x1 NCI_CGAP_Ov32 Homo sapiens cDNA clone IMAGE:1885683 3'
9236	21915	35088	2.27	1.0E-04	AI806220.1	EST_HUMAN	qv57d10.x1 NCI_CGAP_Ov32 Homo sapiens cDNA clone IMAGE:1885683 3'
9247	21926	35097	1.46	1.0E-04	O88989	SWISSPROT	ab94g08.s1 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:854664 3'
9325	21992		0.49	1.0E-04	T77153.1	EST_HUMAN	w26a08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2356742 3'
9546	22199	35381	1.86	1.0E-04	10863876	NT	CYSTATIN-RELATED EPIDIDYMAL SPERMATOGENIC PROTEIN PRECURSOR (CYSTATIN 8)
10079	22727		2.74	1.0E-04	P08547	SWISSPROT	y472c08.1 Soares fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:113774 5'
10115	22763	35975	1	1.0E-04	P08548	SWISSPROT	Homo sapiens phospholipid scramblase 1 (PLSCR1), mRNA
11312	23971		2.13	1.0E-04	M25587.1	NT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
11567	24166	37479	2.05	1.0E-04	AW205336.1	EST_HUMAN	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
11567	24166	37480	2.05	1.0E-04	AW205336.1	EST_HUMAN	Mouse alpha leukocyte interferon gene, complete cds
11649	24246	37566	1.76	1.0E-04	AB032898.1	NT	UI-H-B11-aeaw-a-02-Q-UI.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2720546 3'
							UI-H-B11-aeaw-a-02-Q-UI.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2720546 3'
							Homo sapiens mRNA for KIAA1142 protein, partial cds

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11692	24287	37609	2.01	1.0E-04	AW269061.1	EST_HUMAN	xv49g12.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2816518 3'
11725	24319	37643	2	1.0E-04	Q03696	SWISSPROT	NEURONAL-GLIAL CELL ADHESION MOLECULE PRECURSOR (NG-CAM)
11725	24319	37644	2	1.0E-04	Q03696	SWISSPROT	NEURONAL-GLIAL CELL ADHESION MOLECULE PRECURSOR (NG-CAM)
12131	25203		2.51	1.0E-04	BE876399.1	EST_HUMAN	7729a10.x1 NCL_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:3286058 3' similar to contains L1.13 L1
982	13457	26102	2.76	9.0E-05	AA718933.1	EST_HUMAN	repetitive element ;
1897	14733	27455	1.14	9.0E-05	AW868218.1	EST_HUMAN	af45c11.s1 Scores_testis_NHT Homo sapiens cDNA clone 1292468 3'
5873	18660	31601	1.81	9.0E-05	Q60716	SWISSPROT	QV4-SN0023-070400-166-b04 SN0023 Homo sapiens cDNA
7476	20149	33242	0.6	9.0E-05	AW204958.1	EST_HUMAN	PROLYL 4-HYDROXYLASE ALPHA-2 SUBUNIT PRECURSOR
7476	20149	33243	0.6	9.0E-05	AW204958.1	EST_HUMAN	UI-H-B11-aer-d-05-0-UI.s1 NCL_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2720289 3'
8378	21951		3.02	9.0E-05	D85606.1	NT	UI-H-B11-aer-d-05-0-UI.s1 NCL_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2720289 3'
9378	21953	35125	2.78	9.0E-05	AF120982.1	NT	Homo sapiens gene for cholecystokinin type-A receptor, complete cds
11082	23752	37027	2.68	9.0E-05	AW073078.1	EST_HUMAN	Homo sapiens methyl-CpG binding protein 1 (MBD1) gene, exon 15b
11207	23870	37158	1.75	9.0E-05	AI287878.1	EST_HUMAN	xa34g05.x1 NCL_CGAP_Br18 Homo sapiens cDNA clone IMAGE:2568728 3' similar to contains L1.12 L1
11617	18660	31601	3.5	9.0E-05	Q60716	SWISSPROT	repetitive element ;
							q123f06.x1 NCL_CGAP_Lym6 Homo sapiens cDNA clone IMAGE:1982436 3' similar to contains element
							MIR repetitive element ;
							PROLYL 4-HYDROXYLASE ALPHA-2 SUBUNIT PRECURSOR
12176	26259		6.63	9.0E-05	AF129758.1	NT	Homo sapiens MSH55 gene, partial cds; and CLIC1, DDAH, G6b, G6c, G5b, G6d, G6e, G6f, BAT5, G5b,
802	13574	26237	1.97	8.0E-05	AJ251646.1	NT	CSK2B, BAT4, G4, Apo M, BAT3, BAT2, AIF-1, 1C7, LST-1, LTB, TNF, and LTA genes, complete cds
844	13614		2.75	8.0E-05	AJ251646.1	NT	Pisum sativum mRNA for beta-1,3 glucanase (gns2 gene)
2950	15716		0.73	8.0E-05	MB83576.1	NT	Pisum sativum mRNA for beta-1,3 glucanase (gns2 gene)
4448	17184	29808	0.87	8.0E-05	AW044605.1	EST_HUMAN	Human platelet-derived growth factor A chain (PDGFA) gene, exons only
11099	23769	37045	1.84	8.0E-05	MB9197.1	NT	wy78a04.x1 Scores_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2554638 3'
							Human heptoglobin and heptoglobin-related protein (HP and HPR) genes, complete cds
12765	25242		4.85	8.0E-05	AA279333.1	EST_HUMAN	zs88h01.s1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:704593 3' similar to contains Alu
337	13138	25773	1.14	7.0E-05	AW847445.1	EST_HUMAN	repetitive element; contains element MSR1 repetitive element ;
337	13138	25774	1.14	7.0E-05	AW847445.1	EST_HUMAN	RC3-C10208-220999-011-E04 C10208 Homo sapiens cDNA
554	13337	25965	1.1	7.0E-05	L49075.1	EST_HUMAN	RC3-C10208-220999-011-E04 C10208 Homo sapiens cDNA
554	13337	25966	1.1	7.0E-05	L49075.1	EST_HUMAN	HUM072014F Human fovea cDNA Homo sapiens cDNA clone EST HFD072014
							HUM072014F Human fovea cDNA Homo sapiens cDNA clone EST HFD072014
1033	13793	26453	1.4	7.0E-05	Q22949	SWISSPROT	PROBABLE GLYCEROL-3-PHOSPHATE ACYLTRANSFERASE, MITOCHONDRIAL PRECURSOR
2724	15431	28168	2.99	7.0E-05	AL163278.2	NT	(GPAT)
							Homo sapiens chromosome 21 segment HS21C078

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3156	15919	28555	5.72	7.0E-05	AB009080.1	NT	Dicotyledonum discoidium gene for TRFA, complete cds
4339	17078	29707	1.71	7.0E-05	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
4412	17149	29776	0.95	7.0E-05	U60980.1	NT	Caenorhabditis elegans Skp1p homolog mRNA, complete cds
4871	17598	30221	0.71	7.0E-05	9845300	NT	Rat cytomegalovirus Maastricht, complete genome
8124	20818	33934	1.09	7.0E-05	AA505582.1	EST_HUMAN	h93901.s1 NCI_CGAP_Br2 Homo sapiens cDNA clone IMAGE:968096 3'
9453	22003	35175	2.97	7.0E-05	T07095.1	EST_HUMAN	EST04984 Fetal brain, Stragene (cat#936206) Homo sapiens cDNA clone HFBED60
11112	23782		3.09	7.0E-05	10835046	NT	Homo sapiens sarcoglycan, epsilon (SGCE), mRNA
2020	14793	27484	1.69	6.0E-05	4885170	NT	Homo sapiens chromosome X open reading frame 6 (CXORF6) mRNA
2020	14755	27485	1.69	6.0E-05	4885170	NT	Homo sapiens chromosome X open reading frame 6 (CXORF6) mRNA
2595	15309	28046	1.19	6.0E-05	AI655241.1	EST_HUMAN	W54H06.x1 NCI_CGAP_G08 Homo sapiens cDNA clone IMAGE:2309531 3' similar to gb:J03260 DNA
2690	15399	28137	1.1	6.0E-05	Z84506.1	NT	TOPOISOMERASE I (HUMAN);
2690	15399	28138	1.1	6.0E-05	Z84506.1	NT	H. sapiens flow-sorted chromosome 6 HindIII fragment, SC6pA28B10
2817	13440	26080	3.07	6.0E-05	AF050630.1	NT	H. sapiens flow-sorted chromosome 6 HindIII fragment, SC6pA28B10
5822	18611	31541	3.61	6.0E-05	Q12860	SWISSPROT	Homo sapiens monocyte/neutrophil elastase inhibitor gene, complete cds
5822	18611	31542	3.61	6.0E-05	Q12860	SWISSPROT	CONTACTIN PRECURSOR (GLYCOPROTEIN GP135)
6309	19081	32068	1.4	6.0E-05	N72829.1	EST_HUMAN	CONTACTIN PRECURSOR (GLYCOPROTEIN GP135)
6834	19496	32520	0.95	6.0E-05	AA897680.1	EST_HUMAN	y60g11.r1 Scores fetal liver spleen TNFSL Homo sapiens cDNA clone IMAGE:246212 5'
7983	20578	33803	0.76	6.0E-05	BE084410.1	EST_HUMAN	q80a03.s1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1504588 3'
7983	20578	33804	0.76	6.0E-05	BE084410.1	EST_HUMAN	RC4-BT0311-141199-011-h06 BT0311 Homo sapiens cDNA
8342	21035	34172	0.62	6.0E-05	AA150482.1	EST_HUMAN	RC4-BT0311-141199-011-h06 BT0311 Homo sapiens cDNA
8347	21040	34171	2.22	6.0E-05	AW896629.1	EST_HUMAN	z108c08.s1 Scores_pregnant_uterus_NbhPU Homo sapiens cDNA clone IMAGE:491726 3' similar to contains element MER28 repetitive element ;
8479	21171	34316	0.63	6.0E-05	O60401	SWISSPROT	PM4-NN0050-310300-001-410 NN0050 Homo sapiens cDNA
9151	21882	35050	1.21	6.0E-05	P08607	SWISSPROT	COMPLEMENT DECAY-ACCELERATING FACTOR PRECURSOR
9151	21882	35051	1.21	6.0E-05	P08607	SWISSPROT	C4B-BINDING PROTEIN PRECURSOR (C4BP)
9421	22099	35271	0.85	6.0E-05	T94149.1	EST_HUMAN	C4B-BINDING PROTEIN PRECURSOR (C4BP)
9621	22274	35462	0.59	6.0E-05	AW627985.1	EST_HUMAN	ye28c12.r1 Stragene lung (#937210) Homo sapiens cDNA clone IMAGE:119082 5'
10649	23340	36579	3.06	6.0E-05	R75639.1	EST_HUMAN	h37a03.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2974444 3'
11502	24103	37415	3.36	6.0E-05	AA044015.1	EST_HUMAN	y59c08.s1 Scores placenta Nb2HP Homo sapiens cDNA clone IMAGE:143535 3' similar to contains Alu repetitive element; contains LTR7 repetitive element ;
12387	25238	30822	14.34	6.0E-05	AW890110.1	EST_HUMAN	zk58f02.r1 Scores_pregnant_uterus_NbhPU Homo sapiens cDNA clone IMAGE:487035 5'
12810	25053		1.4	6.0E-05	BE559403.1	EST_HUMAN	MRO-NT0038-250400-001-409 NT0038 Homo sapiens cDNA
1382	14128	26802	10.48	5.0E-05	AW392086.1	EST_HUMAN	7g28a08.x1 NCI_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:3307766 3'

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1855	14593		1.2	5.0E-05	8923891	NT	Homo sapiens 22kDa peroxisomal membrane protein-like (LOC555895), mRNA
2551	15266	28001	1.1	5.0E-05	P23249	SWISSPROT	PROTEIN MOV-10
3961	16710	26350	2.41	5.0E-05	AJ251884.1	NT	Homo sapiens partial SLC22A3 gene for extraneuronal monoamine transporter (EMT), exon 1
5074	17793	30408	0.72	5.0E-05	Q28422	SWISSPROT	LIMULUS CLOTTING FACTOR C PRECURSOR (FC)
5074	17793	30409	0.72	5.0E-05	Q28422	SWISSPROT	LIMULUS CLOTTING FACTOR C PRECURSOR (FC)
5438	18237	30951	13.38	5.0E-05	X38885.1	NT	Human MLC1 gene for embryonic myosin alkaline light chain, 3'UTR
5903	18888	31636	3.75	5.0E-05	AV553544.1	EST_HUMAN	AV553544 GLC Homo sapiens cDNA clone GLCMA06 3'
6076	18855	31822	0.99	5.0E-05	AF260225.1	NT	Homo sapiens TESTIN 2 and TESTIN 3 genes, complete cds, alternatively spliced
7231	19918		0.87	5.0E-05	AF260225.1	NT	Mus musculus gene for calretinin, exon 1
12175	24810		3.64	5.0E-05	P49193	SWISSPROT	RETINAL-BINDING PROTEIN (RALBP)
12440	24810		4.72	5.0E-05	P49193	SWISSPROT	RETINAL-BINDING PROTEIN (RALBP)
2810	13032		3.84	4.0E-05	U12821.1	NT	Human retin (REN) gene, 5' flanking region
4449	17185	29809	0.73	4.0E-05	P49193	SWISSPROT	RETINAL-BINDING PROTEIN (RALBP)
4449	17185	29810	0.73	4.0E-05	P49193	SWISSPROT	RETINAL-BINDING PROTEIN (RALBP)
4820	17551		1.16	4.0E-05	AF164488.1	NT	Cryptosporidium parvum isolate Zaire 15 kDa glycoprotein gp15 gene, partial cds
4955	17681	30289	0.75	4.0E-05	AF212313.1	NT	Drosophila melanogaster senseless protein (sens) gene, complete cds
6941	19503	32528	0.74	4.0E-05	U01947.1	NT	Macaca mulatta haptoglobin (HP) gene, 5' region
8423	22101		7.57	4.0E-05	AF202635.1	NT	Homo sapiens PP1200 mRNA, complete cds
9901	22550	35745	0.47	4.0E-05	P11369	SWISSPROT	RETROVIRUS-RELATED POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE; ENDONUCLEASE]
10306	22953	36168	0.59	4.0E-05	P23780	SWISSPROT	BETA-GALACTOSIDASE PRECURSOR (LACTASE) (ACID BETA-GALACTOSIDASE)
10668	23359	36599	4.18	4.0E-05	AW627946.1	EST_HUMAN	h136c07.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2974380 3' similar to contains element MIR repetitive element
12140	24629		1.48	4.0E-05	AW117580.1	EST_HUMAN	xd53909.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2605192 3'
12789	25041		1.71	4.0E-05	AA417756.1	EST_HUMAN	z01e11.st NCJ CGAP_GCB1 Homo sapiens cDNA clone IMAGE:746252 3'
665	13441	26082	1.6	3.0E-05	A1248061.1	EST_HUMAN	q164c10.x1 Soares_fetal_liver_spleen_NFL.S.S1 Homo sapiens cDNA clone IMAGE:1849458 3' similar to contains Alu repetitive element/contains element KER repetitive element
1037	13797	26457	0.86	3.0E-05	AW273851.1	EST_HUMAN	x24g03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2814100 3'
1109	13866	26523	1.01	3.0E-05	BF037898.1	EST_HUMAN	601461463F1 NIH_MGC 66 Homo sapiens cDNA clone IMAGE:3865142 5'
1109	13866	26524	1.01	3.0E-05	BF037898.1	EST_HUMAN	601461463F1 NIH_MGC 66 Homo sapiens cDNA clone IMAGE:3865142 5'
3287	16048		0.73	3.0E-05	A1288919.1	EST_HUMAN	q191g11.x1 Soares_NHMPu.S1 Homo sapiens cDNA clone IMAGE:1879748 3' similar to TR:O08632
4349	17088	29719	7.96	3.0E-05	BE169211.1	EST_HUMAN	PM1-HT0521-120200-001-e10 HT0521 Homo sapiens cDNA
4349	17088	29720	7.96	3.0E-05	BE169211.1	EST_HUMAN	PM1-HT0521-120200-001-e10 HT0521 Homo sapiens cDNA

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Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4434	17170	28798	0.94	3.0E-05	AA368879.1	EST_HUMAN	EST179996 Placenta Homo sapiens cDNA similar to similar to p53-associated protein
4434	17170	28799	0.94	3.0E-05	AA368879.1	EST_HUMAN	EST179996 Placenta Homo sapiens cDNA similar to similar to p53-associated protein
4550	17285		0.99	3.0E-05	AL169302.2	NT	Homo sapiens chromosome 21 segment HS21C102
4686	17420	30056	1	3.0E-05	P97468	SWISSPROT	CHEMOKINE RECEPTOR-LIKE 1 (G-PROTEIN COUPLED RECEPTOR DEZ)
4785	13441	26092	0.82	3.0E-05	A1248061.1	EST_HUMAN	qh64c10.x1 Soares_fetal_liver_spleen_1NLS_S1 Homo sapiens cDNA clone IMAGE:1849458 3' similar to contains Alu repetitive element; contains element KER repetitive element;
4791	17622	30144	0.97	3.0E-05	AU126721.1	EST_HUMAN	AU125721 N27RM4 Homo sapiens cDNA clone NT2RM4002075 5'
5470	18269	31181	1.66	3.0E-06	11072102	NT	Mus musculus myosin light chain 2, precursor lymphocyte-specific (Myc2pl), mRNA
6659	19419	32433	1.17	3.0E-05	AJ226782.1	NT	Homo sapiens SYBL1 gene, exons 6-8
6659	19419	32434	1.17	3.0E-05	AJ226782.1	NT	Homo sapiens SYBL1 gene, exons 6-8
7799	20494	33616	2.33	3.0E-05	BE733167.1	EST_HUMAN	601567451F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3842282 5'
8250	20944	34082	1.47	3.0E-05	AA284049.1	EST_HUMAN	zs60b05.s1 Striatagene schizo brain S11 Homo sapiens cDNA clone IMAGE:701841 3'
8791	21483	34630	1.58	3.0E-05	AW770982.1	EST_HUMAN	h194e08.x1 NCJ_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3009638 3'
8795	21487	34633	1.23	3.0E-05	6912431	NT	Homo sapiens interleukin-1 receptor antagonist homolog 1 (IL1HY1), mRNA
8799	21491	34638	0.51	3.0E-05	P43361	SWISSPROT	MELANOVA-ASSOCIATED ANTIGEN 8 (IMAGE 8 ANTIGEN)
9028	21719		0.56	3.0E-05	X03273.1	NT	Human Alu-family cluster 5' of alpha(1)-acid glycoprotein gene
9220	21899	35068	1.22	3.0E-05	AA372562.1	EST_HUMAN	EST84475 Colon adenocarcinoma IV Homo sapiens cDNA 5' end
9563	22216		2.92	3.0E-05	A1769331.1	EST_HUMAN	wg3809.x1 Soares_NSF_FB_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2367209 3'
10433	23079	36303	0.98	3.0E-05	Q62918	SWISSPROT	PROTEIN KINASE C-BINDING PROTEIN NELL2 PRECURSOR (NELL-LIKE PROTEIN 2)
10433	23079	36304	0.98	3.0E-05	Q62918	SWISSPROT	PROTEIN KINASE C-BINDING PROTEIN NELL2 PRECURSOR (NELL-LIKE PROTEIN 2)
12072	24585		1.77	3.0E-05	L77570.1	NT	Homo sapiens DiGeorge syndrome critical region, centromeric end
2323	15048	27784					qh98e11.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1855052 3' similar to contains
2587	15301	28037	1.09	2.0E-05	A1286021.1	EST_HUMAN	MER3.b2 MER3 repetitive element;
			2.43	2.0E-05	M13792.1	NT	Human adenosine deaminase (ADA) gene, complete cds
2718	15425		7.45	2.0E-05	AA180562.1	EST_HUMAN	zq48a12.r1 Striatagene hNT neuron (#937233) Homo sapiens cDNA clone IMAGE:632734 5' similar to contains Alu repetitive element; contains element L1 repetitive element;
3134	15899	28544	1.23	2.0E-05	BE068036.1	EST_HUMAN	RC3-BT0319-120200-014-P08 BT0319 Homo sapiens cDNA
3343	16102	28754	0.93	2.0E-05	AF184614.1	NT	Homo sapiens p47-phox (NCF1) gene, complete cds
3362	16121	28779	1.22	2.0E-05	X89211.1	NT	H. sapiens DNA for endogenous retroviral like element
3485	16242		0.71	2.0E-05	X95465.1	NT	S. cerevisiae 12.8 Kbp fragment of the left arm of chromosome XV
3787	18639		0.78	2.0E-05	AL039107.1	EST_HUMAN	DKFZp6661064_r1 566 (synonym: hfkcd2) Homo sapiens cDNA clone DKFZp6661064 5'
4643	17377		1.09	2.0E-05	BE378471.1	EST_HUMAN	601236455F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3608653 5'
5672	18467	31382	1.92	2.0E-05	AJ011712.1	NT	Homo sapiens TNNT1 gene, exons 1-11 (and joined CDS)

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Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5827	18616		0.69	2.0E-05	AF029308.1	NT	Homo sapiens chromosome 9 duplication of the T cell receptor beta locus and trypsinogen gene families
5860	18666	31608	0.76	2.0E-05	Q13183	SWISSPROT	RENAL SODIUM/DICARBOXYLATE COTRANSPORTER (NA(+)/DICARBOXYLATE COTRANSPORTER)
5880	18668	31607	0.76	2.0E-05	Q13183	SWISSPROT	RENAL SODIUM/DICARBOXYLATE COTRANSPORTER (NA(+)/DICARBOXYLATE COTRANSPORTER)
6065	18944	31808	0.61	2.0E-05	A1149272.1	EST_HUMAN	qc72a02.x1 Soares_placenta_8tc6weeks_2NbhP8tc6w Homo sapiens cDNA clone IMAGE:1715114 3'
6527	19283	32297	2.28	2.0E-05	AA714330.1	EST_HUMAN	similar to contains L1 t3 L1 repetitive element ;
6801	19462	32483	3.27	2.0E-05	Y08926.1	NT	inv06d12.s1 NCI_CGAP_SS1 Homo sapiens cDNA clone IMAGE:1238519 3'
6814	19475	32497	1.12	2.0E-05	A1492960.1	EST_HUMAN	P.falciptarum mRNA for AARP1 protein, partial
6824	19485		9.37	2.0E-05	A1991025.1	EST_HUMAN	qz47b06.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2030003 3' similar to TR.O02711
7053	19744	32806	1.93	2.0E-05	AF224262.1	NT	wu35b07.x1 Soares_Dieckgraebe_colon_NHCD Homo sapiens cDNA clone IMAGE:2522077 3'
7053	19744	32807	1.93	2.0E-05	AF224262.1	NT	Heterodontus francisci HoxA10 (HoxA10), HoxA9 (HoxA9), HoxA7 (HoxA7), HoxA6 (HoxA6), HoxA5 (HoxA5), HoxA4 (HoxA4), HoxA3 (HoxA3), HoxA2 (HoxA2), and HoxA1 (HoxA1) genes, complete cds
7267	19951		0.83	2.0E-05	AF128847.1	NT	Heterodontus francisci HoxA10 (HoxA10), HoxA9 (HoxA9), HoxA7 (HoxA7), HoxA6 (HoxA6), HoxA5 (HoxA5), HoxA4 (HoxA4), HoxA3 (HoxA3), HoxA2 (HoxA2), and HoxA1 (HoxA1) genes, complete cds
7785	20480	33605	1.71	2.0E-05	A1381040.1	EST_HUMAN	Homo sapiens indolethylamine N-methyltransferase (INMT) mRNA, INMT-2 allele, complete cds
9020	21710	34862	0.53	2.0E-05	BE244840.1	EST_HUMAN	ig20h05.x1 NCI_CGAP_QLL1 Homo sapiens cDNA clone IMAGE:2109369 3'
9020	21710	34863	0.53	2.0E-05	BE244840.1	EST_HUMAN	TCBAP2E1590 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP1590
9167	21837	35002	0.58	2.0E-05	P49457	SWISSPROT	TCBAP2E1590 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP1590
9167	21837	35003	0.58	2.0E-05	P49457	SWISSPROT	COMPLEMENT DECAY-ACCELERATING FACTOR (CD55)
9823	22474	35677	0.49	2.0E-05	AL163207.2	NT	COMPLEMENT DECAY-ACCELERATING FACTOR (CD55)
10035	22683	35900	0.87	2.0E-05	BF055939.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C007
10457	23103	36333	0.54	2.0E-05	AJ131024.1	NT	7175g09.y1 NCI_CGAP_Bm20 Homo sapiens cDNA clone IMAGE:3340576 5'
10457	23103	36334	0.54	2.0E-05	AJ131024.1	NT	Homo sapiens olase gene, exon 1-alpha
10489	23135	36362	1.98	2.0E-05	N41751.1	EST_HUMAN	Homo sapiens olase gene, exon 1-alpha
							yw91a06.r1 Soares_placenta_8tc6weeks_2NbhP8tc6w Homo sapiens cDNA clone IMAGE:259570 5'

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Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10489	23135	36363	1.98	2.0E-05	N41751.1	EST_HUMAN	yw91a06.t1 Soares_placenta_8to9weeks_2Nbl-P8b9W Homo sapiens cDNA clone IMAGE:259570 5'
10541	19485		2.42	2.0E-05	A1891026.1	EST_HUMAN	wu35h07.x1 Soares_Dieckgraefe_colon_NHCD Homo sapiens cDNA clone IMAGE:2522077 3'
11287	23948	37243	1.33	2.0E-05	A1493285.1	EST_HUMAN	h30h09.x1 NCL_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2132033 3' similar to TR:Q13538 Q13538 ORF2: FUNCTION UNKNOWN.
11287	23948	37244	1.33	2.0E-05	A1493285.1	EST_HUMAN	h30h09.x1 NCL_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2132033 3' similar to TR:Q13538 Q13538 ORF2: FUNCTION UNKNOWN.
11430	23197	36428	2.27	2.0E-05	BE175801.1	EST_HUMAN	h30h09.x1 NCL_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2132033 3' similar to TR:Q13538 Q13538 ORF2: FUNCTION UNKNOWN.
12186	25168		4.86	2.0E-05	BE348229.1	EST_HUMAN	h30h09.x1 NCL_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2132033 3' similar to TR:Q13538 Q13538 ORF2: FUNCTION UNKNOWN.
12342	25165		2.27	2.0E-05	AF275948.1	NT	h30h09.x1 NCL_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2132033 3' similar to TR:Q13538 Q13538 ORF2: FUNCTION UNKNOWN.
12874	25247		1.44	2.0E-05	D16883.1	NT	h30h09.x1 NCL_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2132033 3' similar to TR:Q13538 Q13538 ORF2: FUNCTION UNKNOWN.
2265	14991	27731	3.22	1.0E-05	P27448	SWISSPROT	h30h09.x1 NCL_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2132033 3' similar to TR:Q13538 Q13538 ORF2: FUNCTION UNKNOWN.
2700	15603	28143	1.6	1.0E-05	AL163282.2	NT	h30h09.x1 NCL_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2132033 3' similar to TR:Q13538 Q13538 ORF2: FUNCTION UNKNOWN.
3641	16394	29034	1.91	1.0E-05	AF088273.1	NT	h30h09.x1 NCL_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2132033 3' similar to TR:Q13538 Q13538 ORF2: FUNCTION UNKNOWN.
3793	16545		1.02	1.0E-05	AF223391.1	NT	h30h09.x1 NCL_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2132033 3' similar to TR:Q13538 Q13538 ORF2: FUNCTION UNKNOWN.
3949	16699	29337	9.2	1.0E-05	P81274	SWISSPROT	h30h09.x1 NCL_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2132033 3' similar to TR:Q13538 Q13538 ORF2: FUNCTION UNKNOWN.
4152	18894	29523	1.2	1.0E-05	AL163203.2	NT	h30h09.x1 NCL_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2132033 3' similar to TR:Q13538 Q13538 ORF2: FUNCTION UNKNOWN.
4244	16985	29608	2.52	1.0E-05	AA431119.1	EST_HUMAN	h30h09.x1 NCL_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2132033 3' similar to TR:Q13538 Q13538 ORF2: FUNCTION UNKNOWN.
4799	17530	30152	1.81	1.0E-05	AW419134.1	EST_HUMAN	h30h09.x1 NCL_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2132033 3' similar to TR:Q13538 Q13538 ORF2: FUNCTION UNKNOWN.
6853	19415	32428	1.22	1.0E-05	AJ246003.1	NT	h30h09.x1 NCL_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2132033 3' similar to TR:Q13538 Q13538 ORF2: FUNCTION UNKNOWN.
6980	19505	32530	2.58	1.0E-05	AA641846.1	EST_HUMAN	h30h09.x1 NCL_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2132033 3' similar to TR:Q13538 Q13538 ORF2: FUNCTION UNKNOWN.
6982	19675	32722	3.28	1.0E-05	4505844	NT	h30h09.x1 NCL_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2132033 3' similar to TR:Q13538 Q13538 ORF2: FUNCTION UNKNOWN.
7677	20341		1.16	1.0E-05	P19474	SWISSPROT	h30h09.x1 NCL_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2132033 3' similar to TR:Q13538 Q13538 ORF2: FUNCTION UNKNOWN.
8813	21505		2.24	1.0E-05	AL163227.2	NT	h30h09.x1 NCL_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2132033 3' similar to TR:Q13538 Q13538 ORF2: FUNCTION UNKNOWN.
8958	21649	34799	3.02	1.0E-05	AA452578.1	EST_HUMAN	h30h09.x1 NCL_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2132033 3' similar to TR:Q13538 Q13538 ORF2: FUNCTION UNKNOWN.
9187	21857	35022	12.45	1.0E-05	AA236110.1	EST_HUMAN	h30h09.x1 NCL_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2132033 3' similar to TR:Q13538 Q13538 ORF2: FUNCTION UNKNOWN.
9268	22020	35189	0.62	1.0E-05	AV732190.1	EST_HUMAN	h30h09.x1 NCL_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2132033 3' similar to TR:Q13538 Q13538 ORF2: FUNCTION UNKNOWN.
9738	22389	35593	0.74	1.0E-05	AW150902.1	EST_HUMAN	h30h09.x1 NCL_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2132033 3' similar to TR:Q13538 Q13538 ORF2: FUNCTION UNKNOWN.

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Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9738	22389	35594	0.74	1.0E-05	AW510902.1	EST_HUMAN	hd41b02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2912043 3' similar to contains
8818	22467	35689	1.16	1.0E-05	AW291521.1	EST_HUMAN	OFRT1 OFR repetitive element
9818	22467	35670	1.10	1.0E-05	AW291521.1	EST_HUMAN	UI-H-B12-agk-a-08-0-JL.s1 NCI_CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2724398 3'
10084	22732		1.87	1.0E-05	AW466995.1	EST_HUMAN	UI-H-B12-agk-a-08-0-JL.s1 NCI_CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2724398 3'
							ha07c10.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2873010 3' similar to contains L1.12 L1 repetitive element
10836	23518	36780	1.97	1.0E-05	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
10836	23518	36761	1.97	1.0E-05	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
11654	24438	37780	1.38	1.0E-05	AF111167.2	NT	Homo sapiens jun dimerization protein gene, partial cds, cfos gene, complete cds, and unknown gene
2678	15387	28128	4.8	9.0E-06	AF583811.1	EST_HUMAN	h73a06.x1 NCI_CGAP_HSC3 Homo sapiens cDNA clone IMAGE:2245386 3'
3082	15857	28498	3.53	9.0E-06	AF218983.1	EST_HUMAN	qg11b08.x1 Soares_placenta_8tp5weeks_2Nblp8b9W Homo sapiens cDNA clone IMAGE:1759191 3'
3597	16350		2.82	9.0E-06	M61755.1	NT	Human alanine glyoxylate aminotransferase (AGXT) gene, exons 1 and 2
5815	18604	31532	2.61	9.0E-06	L23416.1	NT	Homo sapiens differentiation antigen CD20 gene, exons 5, 6
6765	19509	32534	0.8	9.0E-06	BE065042.1	EST_HUMAN	RC1-B10313-110500-017-a07 BT0313 Homo sapiens cDNA
7340	20021	33099	0.95	9.0E-06	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
7873	20337	33450	13.94	9.0E-06	A034370.1	EST_HUMAN	ox20g01.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1656912 3' similar to contains Alu repetitive element
8363	21056	34197	1.1	9.0E-06	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
8881	21572	34715	2.69	9.0E-06	Q63769	SWISSPROT	SUSHI REPEAT-CONTAINING PROTEIN SRPX PRECURSOR (DRS PROTEIN) (DOWN-REGULATED BY V-SRC)
8881	21572	34716	2.69	9.0E-06	Q63769	SWISSPROT	SUSHI REPEAT-CONTAINING PROTEIN SRPX PRECURSOR (DRS PROTEIN) (DOWN-REGULATED BY V-SRC)
9122	21810	34976	4.3	9.0E-06	U35114.1	NT	Human apolipoprotein E (APOE) gene, hepatic control region HCR-2
10858	23538	36784	3.46	9.0E-06	Q10364	SWISSPROT	PUTATIVE SERINE/THREONINE-PROTEIN KINASE C22E12.14C
2532	15597	27986	1.27	8.0E-06	AW362539.1	EST_HUMAN	RC3-CT0283-201159-011-h11 CT0283 Homo sapiens cDNA
10430	23076	36298	0.75	8.0E-06	P34083	SWISSPROT	FASCLIN II, PHOSPHATIDYLINOSITOL-LINKED ISOFORM PRECURSOR (FAS II)
10430	23076	36299	0.75	8.0E-06	P34083	SWISSPROT	FASCLIN II, PHOSPHATIDYLINOSITOL-LINKED ISOFORM PRECURSOR (FAS II)

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
958	13723		2.89	7.0E-06	AA669729.1	EST_HUMAN	ab30f10.s1 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:854251 3' similar to contains
1419	14167	26851	3.42	7.0E-06	7882177	NT	MER20.t1 MER20 repetitive element;
2876	15643		5.93	7.0E-06	AI368252.1	EST_HUMAN	Homo sapiens KIAA0555 gene product (KIAA0555), mRNA
3551	16308		0.92	7.0E-06	AA385542.1	EST_HUMAN	qw16g09.x1 NCI_CGAP_U13 Homo sapiens cDNA clone IMAGE:1991296 3' similar to contains Alu repetitive
5609	18405		5.68	7.0E-06	AW883141.1	EST_HUMAN	element;
5715	18508	31429	1.01	7.0E-06	N98845.1	EST_HUMAN	EST199205 Thyroid Homo sapiens cDNA 5' end similar to EST containing L1 repeat
8688	21380	34524	0.7	7.0E-06		NT	QV2-OT0062-250400-173-h01 OT0062 Homo sapiens cDNA
9800	22451		0.45	7.0E-06	Q61147	SWISSPROT	yy65c07.r1 Scores_multiple_sclerosis_2NBHMSF Homo sapiens cDNA clone IMAGE:278412 5'
11930	25336	30608	2.32	7.0E-06	BF215972.1	EST_HUMAN	Homo sapiens DNA segment, numerous copies, expressed probes (GS1 gene) (DXF68S1E), mRNA
2918	15684	28329	1.28	6.0E-06	BE069189.1	EST_HUMAN	CERULOPLASMIN PRECURSOR (FERROXIDASE)
3680	16433	29076	1.08	6.0E-06	BE069189.1	EST_HUMAN	601881622F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4093972 5'
4705	15708	28359	1.91	6.0E-06	Q01456	SWISSPROT	QV3-BT0379-010300-105-d11 BT0379 Homo sapiens cDNA
4710	17442	30074	2.21	6.0E-06	AI040099.1	EST_HUMAN	QV3-BT0379-010300-105-d11 BT0379 Homo sapiens cDNA
5265	18071	30700	1.32	6.0E-06	AF167441.1	NT	OVARIAN ABUNDANT MESSAGE PROTEIN (OAM PROTEIN)
5324	18127	30787	1.06	6.0E-06	Q02040	SWISSPROT	ox08602.x1 Scores_feat_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1665738 3' similar to
9756	22407		1.48	6.0E-06	AW801912.1	EST_HUMAN	contains MER8.12 MER8 repetitive element;
12755	25018	30979	2.27	6.0E-06	11418157	NT	Mus musculus E-cadherin binding protein E7 mRNA, complete cds
5970	18752	31713	3.27	5.0E-06	AL163246.2	NT	PROTEIN XE7
6245	19019	31993	2.31	5.0E-06	U07561.1	NT	IL5-UM0070-110400-063-g02 UM0070 Homo sapiens cDNA
7134	19821	32887	1.1	5.0E-06	AB007546.1	NT	Homo sapiens calcium channel, voltage-dependent, alpha 11 subunit (CACNA11), mRNA
8359	21052	34192	0.53	5.0E-06	AW856972.1	EST_HUMAN	Homo sapiens ABL gene, exon 1b and Intron 1b, and putative M8604 Met protein (M8604 Met) gene, complete cds
8359	21052	34193	0.53	5.0E-06	AW856972.1	EST_HUMAN	Homo sapiens gene for LECT2, complete cds
10002	22650	35862	6.16	5.0E-06	AA313620.1	EST_HUMAN	RC1-CT0302-120200-013-h02 CT0302 Homo sapiens cDNA
10410	23056	36273	0.45	5.0E-06	P06681	SWISSPROT	RC1-CT0302-120200-013-h02 CT0302 Homo sapiens cDNA
12849	24953	30987	2.83	5.0E-06	AI055045.1	EST_HUMAN	EST185498 Colon carcinoma (HCC) cell line Homo sapiens cDNA 5' end
632	13411	28046	6.1	4.0E-06	R16287.1	EST_HUMAN	COMPLEMENT C2 PRECURSOR (C3/C5 CONVERTASE)
826	13596	26296	7.07	4.0E-06	AW103354.1	EST_HUMAN	HA0877 Human fetal liver cDNA library Homo sapiens cDNA
							ya48c03.r1 Scores_infant brain_1NIB Homo sapiens cDNA clone IMAGE:53254 5' similar to contains Alu
							repetitive element; contains L1 repetitive element;
							xc69g12.x1 NCI_CGAP_Eso2 Homo sapiens cDNA clone IMAGE:2589574 3' similar to contains Alu
							repetitive element; contains element MER21 repetitive element;

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1311	14059	26733	4.84	4.0E-06	A1334928.1	EST_HUMAN	tb33e09.x1 NCI_CGAP_HSC2 Homo sapiens cDNA clone IMAGE:2056168 3'
1311	14059	26734	4.84	4.0E-06	A1334928.1	EST_HUMAN	tb33e09.x1 NCI_CGAP_HSC2 Homo sapiens cDNA clone IMAGE:2056168 3'
1457	14204	26889	1.8	4.0E-06	BF365612.1	EST_HUMAN	QV2-NT0046-200600-250-H07 NT0046 Homo sapiens cDNA
2261	14988	27728	2.17	4.0E-06	AW015401.1	EST_HUMAN	UI-H-B10-aat-f-05-U1.s1 NCI_CGAP_Sub1 Homo sapiens cDNA
3060	15828	28471	0.9	4.0E-06	AF198349.1	NT	Gallus gallus Dach2 protein (Dach2) mRNA, complete cds
3874	16624	29262	1.05	4.0E-06	AW848295.1	EST_HUMAN	IL3-CT0214-150200-074-B03 CT0214 Homo sapiens cDNA
4756	17488	30115	1.89	4.0E-06	A1895939.1	EST_HUMAN	w194c10.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2432562 3' similar to contains element
8397	21090	34225	0.56	4.0E-06	O15393	SWISSPROT	MER22 repetitive element;
8699	21391	34536	3.56	4.0E-06	AF009660.1	NT	TRANSMEMBRANE PROTEASE, SERINE 2
9607	22280	35446	1.24	4.0E-06	AJ272285.1	NT	Homo sapiens T cell receptor beta locus, TCRBV7S3A2 to TCRBV12S2 region
11427	23194	36425	4.21	4.0E-06	AB007956.1	NT	Homo sapiens SPP2 gene for secreted phosphoprotein 24 precursor, exons 1-8
2160	14890	27624	1.75	3.0E-06	AA700562.1	EST_HUMAN	Homo sapiens mRNA, chromosome 1 specific transcript KIAA0496
2160	14890	27625	1.76	3.0E-06	AA700562.1	EST_HUMAN	z134b08.s1 Scores_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:432663 3' similar to contains L1.1 L1 repetitive element;
2263	14989		1.44	3.0E-06	AF202835.1	NT	z134b08.s1 Scores_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:432663 3' similar to contains L1.1 L1 repetitive element;
2922	15688	28332	1.05	3.0E-06	AA868218.1	EST_HUMAN	Homo sapiens PP1200 mRNA, complete cds
3259	16021		2.05	3.0E-06	A1857779.1	EST_HUMAN	ek48g11.s1 Scores_testis_NHT Homo sapiens cDNA clone IMAGE:1409252 3' similar to contains LTR1.13
3763	16515	29152	1.13	3.0E-06	BE047094.1	EST_HUMAN	LINE-1 LIKE PROTEIN; contains L1.12 L1 repetitive element;
3763	16515	29153	1.13	3.0E-06	BE047094.1	EST_HUMAN	hg64d12.x1 NCI_CGAP_HN13 Homo sapiens cDNA clone IMAGE:3124151 3'
4524	17259	29893	3.74	3.0E-06	X54816.1	NT	hg64d12.x1 NCI_CGAP_HN13 Homo sapiens cDNA clone IMAGE:3124151 3'
6088	18847	31811	0.93	3.0E-06	AU159412.1	EST_HUMAN	Homo sapiens gene for alpha-1-microglobulin-bikunin, exons 1-5 (encoding alpha-1-microglobulin, N-terminus.)
7129	19817		2.43	3.0E-06	P08548	SWISSPROT	AU159412 THYRO1 Homo sapiens cDNA clone THYRO1001602 3'
7981	20676	33801	0.83	3.0E-06	BE562964.1	EST_HUMAN	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
8584	21276	34413	0.66	3.0E-06	P07743	SWISSPROT	601336213F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3690314 5'
12349	24755		3.84	3.0E-06	AW385262.1	EST_HUMAN	PAROTID SECRETORY PROTEIN PRECURSOR (PSP)
197	13010		2.81	2.0E-06	P54366	SWISSPROT	RCQ-LT0001-261199-011-A03 LT0001 Homo sapiens cDNA
1681	14308		4.45	2.0E-06	P21414	SWISSPROT	HOMEOBOX PROTEIN GOOSECOID
2376	15098	27838	4.8	2.0E-06	A1672138.1	EST_HUMAN	POL POLYPROTEIN [CONTAINS: PROTEASE: REVERSE TRANSCRIPTASE; ENDONUCLEASE]
							w194d03.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2297068 3' similar to contains MER30.b1
							MER30 repetitive element;

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Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2469	15187	27826	2.37	2.0E-06	P04928	SWISSPROT	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR
2571	15285	28023	1.68	2.0E-06	P06719	SWISSPROT	KNOB-ASSOCIATED HISTIDINE-RICH PROTEIN PRECURSOR (KAHRP)
3509	16285	28919	1.12	2.0E-06	AV657555.1	EST_HUMAN	AV657555 GLC Homo sapiens cDNA clone GLCFDB05 3'
3744	16487	29132	1.59	2.0E-06	AA173518.1	EST_HUMAN	z002e05.r1 Stratagene ovarian cancer (#937219) Homo sapiens cDNA clone IMAGE:595232 5'
3753	16505	29141	0.82	2.0E-06	AW450215.1	EST_HUMAN	U1H-B13-aky-g-05-Q-UI.s1 NCI CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2736176 3'
3758	16510	29146	1.82	2.0E-06	AB030896.1	NT	Mus musculus gene for odorant receptor A16, complete cds
5988	18778		0.63	2.0E-06	AA974932.1	EST_HUMAN	on34h01.s1 NCI CGAP_Lu6 Homo sapiens cDNA clone IMAGE:1568609 3' similar to contains Alu repetitive element;
6028	18808	31768	0.83	2.0E-06	AI539448.1	EST_HUMAN	te51105.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2090241 3' similar to TR:Q13537
6348	19118	32108	5.47	2.0E-06	AI819424.1	EST_HUMAN	Q13537 MER37 TRANSPOSABLE ELEMENT, COMPLETE CONSENSUS SEQUENCE ;
7818	20513		1.63	2.0E-06	AW869223.1	EST_HUMAN	w90504.x1 NCI CGAP_Lym12 Homo sapiens cDNA clone IMAGE:2410063 3'
7888	20683	33809	0.57	2.0E-06	T12338.1	EST_HUMAN	MR3-SN0067-120400-002-402 SN0067 Homo sapiens cDNA
8735	21427		0.6	2.0E-06	AA772497.1	EST_HUMAN	A447R Heart Homo sapiens cDNA clone A447
8747	21439	34586	1.8	2.0E-06	H62051.1	EST_HUMAN	z127c11.s1 Soares_pinea_gland_N3-HPG Homo sapiens cDNA clone IMAGE:413300 3' similar to TR:P70467 P70467 REVERSE TRANSCRIPTASE ;
9116	21804	34969	0.82	2.0E-06	AF003529.1	EST_HUMAN	y037c04.r1 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:235974 5' similar to gb:X74929
9116	21804	34970	0.82	2.0E-06	AF003529.1	NT	KERATIN, TYPE II CYTOSKELETAL 8 (HUMAN);
9135	21823		0.46	2.0E-06	AI473450.1	EST_HUMAN	Homo sapiens glypican 3 (GPC3) gene, partial cds and flanking repeat regions
9600	22253	35438	1	2.0E-06	N30576.1	EST_HUMAN	Homo sapiens glypican 3 (GPC3) gene, partial cds and flanking repeat regions
9819	22470		0.63	2.0E-06	AV748969.1	EST_HUMAN	g16g10.x1 NCI CGAP_Gas4 Homo sapiens cDNA clone IMAGE:214730 3'
12251	25357	30609	2.1	2.0E-06	P23249	SWISSPROT	yw68e03.s1 Soares_placenta_8b9weeks_2NbhP8to9w Homo sapiens cDNA clone IMAGE:257212 3'
32	12860	25477	2.39	1.0E-06	O76082	SWISSPROT	AV748969 NPC Homo sapiens cDNA clone NP:CAXD05 5'
642	13421	26050	2.62	1.0E-06	AF084364.1	NT	PROTEIN MOV-10
1434	14181	26886	1.61	1.0E-06	P09125	SWISSPROT	ORGANIC CATION/CARNITINE TRANSPORTER 2 (SOLUTE CARRIER FAMILY 22, MEMBER 5) (HIGH-AFFINITY SODIUM-DEPENDENT CARNITINE COTRANSPORTER)
1514	14261	26947	1.67	1.0E-06	AL163278.2	NT	Mus musculus D8Mm5E protein (D8Mm5e) mRNA, complete cds
1564	14311	26987	1.27	1.0E-06	AA034141.1	EST_HUMAN	MEROZOITE SURFACE PROTEIN CMZ-8
1564	14311	26998	1.27	1.0E-06	AA034141.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C078
1578	14325		1.34	1.0E-06	P27625	SWISSPROT	z106a12.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:429982 3' similar to contains Alu repetitive element;
							z106a12.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:429982 3' similar to contains Alu repetitive element;
							DNA-DIRECTED RNA POLYMERASE III LARGEST SUBUNIT

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1987	14723	27443	5.09	1.0E-06	AF184614.1	NT	Homo sapiens p47-phox (NCF1) gene, complete cds
1987	14723	27444	5.09	1.0E-06	AF184614.1	NT	Homo sapiens p47-phox (NCF1) gene, complete cds
4336	17075	29703	12.81	1.0E-06	U07961.1	NT	Human ABL gene, exon 1b and intron 1b, and putative M8604 Met protein (M8604 Met) gene, complete cds
5208	18016	30638	5.07	1.0E-06	BF333015.1	EST_HUMAN	MR1-BT0800-030700-002-c06 BT0800 Homo sapiens cDNA
5232	18038	30665	0.83	1.0E-06	BE834518.1	EST_HUMAN	MR3-FN0004-090600-001-e04 FN0004 Homo sapiens cDNA
5232	18038	30666	0.93	1.0E-06	BE834518.1	EST_HUMAN	MR3-FN0004-090600-001-e04 FN0004 Homo sapiens cDNA
5389	18189	30881	1.22	1.0E-06	BE063518.1	EST_HUMAN	15 KDA SELENOPROTEIN PRECURSOR
5706	18500		0.78	1.0E-06	BE063518.1	SWISSPROT	GM0-BT0281-031198-087-H04 BT0281 Homo sapiens cDNA
6773	19517	32545	6.91	1.0E-06	P02671	EST_HUMAN	FIBRINOGEN ALPHA1(A) CHAIN PRECURSOR
7644	25427		0.63	1.0E-06	BE186330.1	EST_HUMAN	IL5-HT0730-020500-074-g01 HT0730 Homo sapiens cDNA
7900	20595		0.77	1.0E-06	AA912623.1	EST_HUMAN	cl26c08.s1 Scores_NFL_I_GBC_S1 Homo sapiens cDNA
8171	20865	33897	1.2	1.0E-06	AB347010.1	EST_HUMAN	ap54e02.x1 NCL_CGAP_C08 Homo sapiens cDNA
8387	21080	34215	1.31	1.0E-06	AI287878.1	EST_HUMAN	q123106.x1 NCL_CGAP_C08 Homo sapiens cDNA
9204	22083	35255	0.84	1.0E-06	N74835.1	EST_HUMAN	MIR repetitive element
9278	22033	35205	0.55	1.0E-06	Q39575	EST_HUMAN	za56e01.s1 Scores_NFL_I_GBC_S1 Homo sapiens cDNA
9581	22234	35417	4.28	1.0E-06	U82668.1	SWISSPROT	q123106.x1 NCL_CGAP_C08 Homo sapiens cDNA
9581	22234	35418	4.28	1.0E-06	U82668.1	SWISSPROT	q123106.x1 NCL_CGAP_C08 Homo sapiens cDNA
9827	22280	35470	4.78	1.0E-06	AA132611.1	EST_HUMAN	DIENEIN GAMMA CHAIN, FLAGELLAR OUTER ARM
9888	22340		3.37	1.0E-06	AA449257.1	EST_HUMAN	Homo sapiens shox gene, alternatively spliced products, complete cds
10385	23031		1.68	1.0E-06	AL163203.2	EST_HUMAN	Homo sapiens shox gene, alternatively spliced products, complete cds
11646	24245		3.85	1.0E-06	AW890941.1	EST_HUMAN	z017e08.r1 Stratagene colon (#837204) Homo sapiens cDNA
11724	24318	37641	1.38	1.0E-06	AA164914.1	EST_HUMAN	z04d411.s1 Scores_Total_Tetus_Nb2HF8_9w Homo sapiens cDNA
11724	24318	37642	1.38	1.0E-06	AA164914.1	EST_HUMAN	gb:ID26129 RIBONUCLEASE PANCREATIC PRECURSOR (HUMAN);
12390	14723	27443	1.79	1.0E-06	AF184614.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C003
12390	14723	27444	1.79	1.0E-06	AF184614.1	EST_HUMAN	RC4-NT0054-120500-012-b03 NT0054 Homo sapiens cDNA
351	13150	25790	2.24	9.0E-07	AF003529.1	NT	zq42c02.s1 Stratagene hNT neuron (#837233) Homo sapiens cDNA
351	13150	25791	2.24	9.0E-07	AF003529.1	NT	SW_POL_SMSAV P03359 POL POLYPROTEIN;
8308	21000		0.53	9.0E-07	AL163280.2	NT	SW_POL_SMSAV P03359 POL POLYPROTEIN;
11212	23875	37161	2.87	9.0E-07	AL163281.2	NT	Homo sapiens p47-phox (NCF1) gene, complete cds
							Homo sapiens glypican 3 (GPC3) gene, partial cds and flanking repeat regions
							Homo sapiens glypican 3 (GPC3) gene, partial cds and flanking repeat regions
							Homo sapiens chromosome 21 segment HS21C080
							Homo sapiens chromosome 21 segment HS21C081

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Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11733	24328	37950	1.3	9.0E-07	AF087913.1	NT	Human endogenous retrovirus HERV-P-T47D
4719	17451	30084	3.26	8.0E-07	A1288596.1	EST_HUMAN	ql82g07.x1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:1878876 3'
4719	17451	30085	3.26	8.0E-07	A1288596.1	EST_HUMAN	ql82g07.x1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:1878876 3'
5798	18587		9.43	8.0E-07	P21414	SWISSPROT	POL POLYPROTEIN [CONTAINS: PROTEASE; REVERSE TRANSCRIPTASE; ENDONUCLEASE]
7901	20598		9.73	8.0E-07	AF135418.1	NT	Homo sapiens UDP-glucuronosyltransferase gene, complete cds
11622	24219		6.59	8.0E-07	T07770.1	EST_HUMAN	EST05680 Fetal brain, Strategene (cat#936206) Homo sapiens cDNA clone HFBEN89
11912	24476		8.22	8.0E-07	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
1858	14596	27312	0.91	7.0E-07	AF167341.1	NT	Homo sapiens membrane interleukin 1 receptor accessory protein (IL1RAP) gene, exons 10 and 11
5432	18231	30844	0.72	7.0E-07	6005700	NT	Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 8 (ABCA8), mRNA
5432	18231	30945	0.72	7.0E-07	6005700	NT	Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 8 (ABCA8), mRNA
1905	14642	27352	2.98	6.0E-07	AW855558.1	EST_HUMAN	CM3-CT0277-221089-024-e11 CT0277 Homo sapiens cDNA
2496	15213	27956	4.52	6.0E-07	AF019413.1	NT	Homo sapiens HLA class III region containing tenascin X (tenascin-X) gene, partial cds; cytochrome P450 21-hydroxylase (CYP21B), complement component C4 (C4B) G11, helicase (SKI2W), RD, complement factor B (BF), and complement component C2 (C2) genes, >
3955	16705		1.83	6.0E-07	P41479	SWISSPROT	HYPOTHEICAL 24.1 KD PROTEIN IN LEF4-P33 INTERGENIC REGION
9040	21730	34885	1.52	8.0E-07	BF001897.1	EST_HUMAN	7694907.x1 NCI_CGAP_Corf6 Homo sapiens cDNA clone IMAGE:3314149 3' similar to TR:O75920 O75920 4FEL
11835	24420	37761	1.3	6.0E-07	BE083509.1	EST_HUMAN	CM0-BT0281-031189-087-e03 BT0281 Homo sapiens cDNA
12156	25307		2.26	6.0E-07	AW503222.1	EST_HUMAN	CM4-NN1029-260300-121-h12 NN1029 Homo sapiens cDNA
318	13121		1.94	5.0E-07	A1831893.1	EST_HUMAN	wh84f10.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2385547 3'
1035	13795		4.25	5.0E-07	AA380630.1	EST_HUMAN	EST93615 Supt cells Homo sapiens cDNA 5' end
3028	15784		0.88	5.0E-07	A1831893.1	EST_HUMAN	wh84f10.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2385547 3'
6029	18809	31769	0.9	5.0E-07	U65067.1	NT	Mus musculus OG-2 homeodomain protein (OG-2) gene, partial cds
6864	19448	32463	1.69	5.0E-07	A1393981.1	EST_HUMAN	tg06b05.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2107953 3' similar to contains Alu repetitive element; contains element A3R repetitive element
6864	19448	32464	1.69	5.0E-07	A1393981.1	EST_HUMAN	tg06b05.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2107953 3' similar to contains Alu repetitive element; contains element A3R repetitive element
7248	19933	33008	17	5.0E-07	AW070885.1	EST_HUMAN	xa31a02.x1 NCI_CGAP_Br18 Homo sapiens cDNA clone IMAGE:2568362 3' similar to gb:U15341 CYTOCHROME C OXIDASE POLYPEPTIDE VIA-LIVER (HUMAN);
8173	20867	33999	0.74	5.0E-07	Q9WUQ1	SWISSPROT	ADAM-TS 1 PRECURSOR (A DISINTEGRIN AND METALLOPROTEINASE WITH THROMBOSPONDIN MOTIFS 1) (ADAMTS-1) (ADAM-TS1)
8388	21081		0.82	5.0E-07	P09593	SWISSPROT	S-ANTIGEN PROTEIN PRECURSOR
10265	22913	36123	4.94	5.0E-07	A1908587.1	EST_HUMAN	CM-BT178-220499-014 BT178 Homo sapiens cDNA

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10560	23256	36493	1.28	5.0E-07	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
11500	24101	37413	4.04	5.0E-07	P11087	SWISSPROT	COLLAGEN ALPHA 1(I) CHAIN PRECURSOR
11574	24173		2.52	5.0E-07	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
12561	25211		3.48	5.0E-07	AW882537.1	EST_HUMAN	QV0-CT0383-210400-204-b12 CT0383 Homo sapiens cDNA
3981	16729	29364	2.02	4.0E-07	AW009602.1	EST_HUMAN	ws84h05.x1 NCL_CGAP_C03 Homo sapiens cDNA clone IMAGE:2504697 3'
7078	19769		0.83	4.0E-07	AJ272265.1	NT	Homo sapiens SPP2 gene for secreted phosphoprotein 24 precursor, exons 1-8
7187	19854	32923	1.74	4.0E-07	Q922V6	SWISSPROT	HISTONE DEACETYLASE 5 (HD5) (HISTONE DEACETYLASE MHD41)
7187	19854	32924	1.74	4.0E-07	Q922V6	SWISSPROT	HISTONE DEACETYLASE 5 (HD5) (HISTONE DEACETYLASE MHD41)
7823	20518	33644	0.8	4.0E-07	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C007
8949	21640	34787	5.41	4.0E-07	AW419134.1	EST_HUMAN	xy49g11.x1 NCL_CGAP_Lu34.1 Homo sapiens cDNA clone IMAGE:2856548 3'
10027	22675	35890	0.47	4.0E-07	BE901975.1	EST_HUMAN	601676748F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3959651 5'
10027	22675	35891	0.47	4.0E-07	BE901975.1	EST_HUMAN	601676748F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3959651 5'
10223	22871	36084	0.49	4.0E-07	AL163218.2	NT	Homo sapiens chromosome 21 segment HS21C018
10856	23536	36781	3.14	4.0E-07	A1765528.1	EST_HUMAN	w181b08.x1 NCL_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2399703 3'
10856	23536	36782	3.14	4.0E-07	A1765528.1	EST_HUMAN	w181b08.x1 NCL_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2399703 3'
11184	23849		1.66	4.0E-07	BE001828.1	EST_HUMAN	PM1-BN0083-030300-003-e12 BN0083 Homo sapiens cDNA
431	13217	25862					Human microtubule-associated glycoprotein (MFAP2) gene, putative promoter region and alternatively spliced untranslated exons
569	13350	25978	9.64	3.0E-07	U19719.1	NT	
1353	14101	26776	2.12	3.0E-07	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
1822	14369		2.87	3.0E-07	M99149.1	NT	Human polymorphic microsatellite DNA
			2.03	3.0E-07	M64857.1	NT	Human Igk subgroup I germline gene, exons 1 and 2, V-region 018 allele
2039	14773		1.42	3.0E-07	AA526763.1	EST_HUMAN	n156b09.s1 NCL_CGAP_Ov2 Homo sapiens cDNA clone IMAGE:980825 similar to contains Alu repetitive element; contains L1 L3 L1 repetitive element ;
2286	15011	27749	1.83	3.0E-07	M99149.1	NT	Human polymorphic microsatellite DNA
2472	15180	27930	7.61	3.0E-07	BE005077.1	EST_HUMAN	MFO-BN0115-020300-001-f11 BN0115 Homo sapiens cDNA
2472	15180	27931	7.61	3.0E-07	BE005077.1	EST_HUMAN	MFO-BN0115-020300-001-f11 BN0115 Homo sapiens cDNA
3031	15797	28443	1.16	3.0E-07	T84704.1	EST_HUMAN	y450f12.r1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:11695 5'
3157	15920	28566	1.45	3.0E-07	P38739	SWISSPROT	HYPOTHETICAL 63.8 KD PROTEIN IN GUT1-RIM1 INTERGENIC REGION PRECURSOR
4678	17412	30047	7.42	3.0E-07	AV650201.1	EST_HUMAN	AV650201 GLC Homo sapiens cDNA clone GLCCCD01 3'
4711	17443	30075	0.86	3.0E-07	A1797236.1	EST_HUMAN	we88b012.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2347987 3'
5004	17727	30330	1.3	3.0E-07	T57850.1	EST_HUMAN	yc14h09.s1 Stratiagene lung (#837210) Homo sapiens cDNA clone IMAGE:80705 3' similar to similar to gb:M62982 ARACHIDONATE 12-LIPOXYGENASE (HUMAN)
5004	17727	30331	1.3	3.0E-07	T57850.1	EST_HUMAN	yc14h09.s1 Stratiagene lung (#837210) Homo sapiens cDNA clone IMAGE:80705 3' similar to similar to gb:M62982 ARACHIDONATE 12-LIPOXYGENASE (HUMAN)

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Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5580	18377	31290	12.43	3.0E-07	O88807	SWISSPROT	PROTEIN-ARGININE DEIMINASE TYPE IV (PEPTIDYLARGININE DEIMINASE IV) (PAD-R4)
5883	18669	31610	0.83	3.0E-07	O42280	SWISSPROT	WNT-14 PROTEIN PRECURSOR
6603	18368		5.57	3.0E-07	AA815175.1	EST_HUMAN	LOC40410.s1 NCI CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1339890 3'
7409	20086	33170	3.48	3.0E-07	AW797168.1	EST_HUMAN	QV1-UM0036-2003000-115-g02 UM0036 Homo sapiens cDNA
7561	20231		0.79	3.0E-07	A1591065.1	EST_HUMAN	tw28f11.x1 NCI CGAP_Ov65 Homo sapiens cDNA clone IMAGE:2261037 3' similar to contains Alu repetitive element; contains element MSR1 MSR1 repetitive element;
8028	21718	34872	0.85	3.0E-07	P33240	SWISSPROT	CLEAVAGE STIMULATION FACTOR, 64 KD SUBUNIT (CSTF 64 KD SUBUNIT) (CF-1 64 KD SUBUNIT)
8028	21718	34873	0.85	3.0E-07	P33240	SWISSPROT	CLEAVAGE STIMULATION FACTOR, 64 KD SUBUNIT (CSTF 64 KD SUBUNIT) (CF-1 64 KD SUBUNIT)
11484	24085		1.45	3.0E-07	BE439408.1	EST_HUMAN	HTM1-Q25F1 HTM1 Homo sapiens cDNA
11656	24253		1.75	3.0E-07	AF028308.1	NT	Homo sapiens chromosome 9 duplication of the T cell receptor beta locus and tyrosinogen gene families
12791	25043		5.1	3.0E-07	AJ132352.1	NT	Rattus norvegicus mRNA for 45 kDa secretory protein, partial
27	12855	25471	4.15	2.0E-07	AF282988.1	NT	Homo sapiens TRF2-interacting telomeric RAP1 protein (RAP1) mRNA, complete cds
150	12965	25606	9	2.0E-07	L77569.1	NT	Homo sapiens DiGeorge syndrome critical region, telomeric end
150	12965	25607	9	2.0E-07	L77569.1	NT	Homo sapiens DiGeorge syndrome critical region, telomeric end
177	12989	25629	44.15	2.0E-07	U38849.1	NT	Fugu rubripes beta-cytoplasmic(vascular) actin gene, complete cds
731	13505	26160	2.45	2.0E-07	AF003530.1	NT	Homo sapiens homeobox protein CDX4 (CDX4) gene, complete cds and flanking repeat regions
731	13505	26161	2.45	2.0E-07	AF003530.1	NT	Homo sapiens homeobox protein CDX4 (CDX4) gene, complete cds and flanking repeat regions
744	13517		0.82	2.0E-07	P11369	SWISSPROT	RETROVIRUS-RELATED POLYPROTEIN (CONTAINS: REVERSE TRANSCRIPTASE);
922	13689	26353	3.73	2.0E-07	AA223260.1	EST_HUMAN	z08b07.s1 Stragene NT2 neuronal precursor 937230 Homo sapiens cDNA clone IMAGE:650869 3' similar to gb:U131860 GLYCOPHORIN A PRECURSOR (HUMAN); contains Alu repetitive element;
923	13690	26354	2.15	2.0E-07	T63042.1	EST_HUMAN	ye15g04.s1 Stragene lung (#937210) Homo sapiens cDNA clone IMAGE:80790 3' similar to contains L1 repetitive element;
1140	13805	26556	1.37	2.0E-07	Q26798	SWISSPROT	I/6 AUTOANTIGEN
1596	14342	27032	2.86	2.0E-07	Q09701	SWISSPROT	HYPOPHYSICAL 72.5 KD PROTEIN C2F7.10 IN CHROMOSOME 1
3676	16429	28070	15.83	2.0E-07	AF125348.1	NT	Homo sapiens caveolin 1 (CAV1) gene, exon 3 and partial cds
5059	17778	30395	0.84	2.0E-07	AW070965.1	EST_HUMAN	xa05h07.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2567485 3' similar to WP:038H2.1 CE00923 PROBABLE RABGAP DOMAINS;

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5059	17778	30396				EST_HUMAN	xe05h07.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2567485 3' similar to WP:C38H2.1
5260	18068	30894	0.84	2.0E-07	AW070995.1	EST_HUMAN	CE00923 PROBABLE RABGAP DOMAINS
6456	25090	32223	1.21	2.0E-07	AW898066.1	EST_HUMAN	RC3-NN0068-260400-021-g11 NN0068 Homo sapiens cDNA
6565	19330	32337	0.81	2.0E-07	AW448988.1	EST_HUMAN	UIH-BI3-ake-b-01-0-UI.s1 NCI_CGAP_Sub6 Homo sapiens cDNA
7568	20238	33342	1.79	2.0E-07	A1208715.1	EST_HUMAN	q956405.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:2734008 3'
8369	21062		0.67	2.0E-07	X95159.1	NT	H.sapiens brca2 gene exon 9
8595	21287	34426	4.08	2.0E-07	AV729390.1	EST_HUMAN	AV729390 HTC Homo sapiens cDNA clone HTCAEG02 5'
9861	22313		0.97	2.0E-07	AA035198.1	EST_HUMAN	zk27g09.s1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:471808 3'
10167	22815	36033	2.8	2.0E-07	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
10386	23032	36245	5.41	2.0E-07	AW892507.1	EST_HUMAN	GM4-NN0003-280300-124-e08 NN0003 Homo sapiens cDNA
10386	23032	36246	0.9	2.0E-07	P00751	SWISSPROT	COMPLEMENT FACTOR B PRECURSOR (C3/C5 CONVERTASE) (PROPERDIN FACTOR B)
10386	23032	36246	0.9	2.0E-07	P00751	SWISSPROT	COMPLEMENT FACTOR B PRECURSOR (C3/C5 CONVERTASE) (GBG) (PBF2)
11871	24945		2.44	2.0E-07	BE153717.1	EST_HUMAN	GLYCINE-RICH BETA GLYCOPROTEIN (GBG) (PBF2)
11953	25212		2.39	2.0E-07	AI732462.1	EST_HUMAN	PM0-HT0339-260100-006-H07 HT0339 Homo sapiens cDNA
1080	13838		1.97	1.0E-07	AL163282.2	NT	zn85h11.x5 Stralagene lung carcinoma 937218 Homo sapiens cDNA clone IMAGE:565029 3' similar to contains THR.b2 THR repetitive element
2381	15103	27842	1.11	1.0E-07	P10263	SWISSPROT	Homo sapiens chromosome 21 segment HS21C082
2830	14259	28945	2.51	1.0E-07	P08256	SWISSPROT	RETROVIRUS-RELATED GAG POLYPROTEIN (VERSION 1)
3727	13838		1.29	1.0E-07	AL163282.2	NT	GLYCOPROTEIN GPV
4260	17001	29631	2.76	1.0E-07	AV718662.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C082
4260	17001	29632	2.76	1.0E-07	AV718662.1	EST_HUMAN	AV718662 GLC Homo sapiens cDNA clone GLCFNF04 5'
4690	17424		0.93	1.0E-07	O75820	SWISSPROT	AV718662 GLC Homo sapiens cDNA clone GLCFNF04 5'
5072	17781	30408	0.93	1.0E-07	AA019181.1	EST_HUMAN	ZINC FINGER PROTEIN 189
6410	19178	32177				NT	ze56g02.r1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:363026 5'
6768	19512	32537	0.87	1.0E-07	UB2671.2	NT	Homo sapiens chromosome Xq28 melanoma antigen family A2a (MAGEA2A), melanoma antigen family A12 (MAGEA12), melanoma antigen family A2b (MAGEA2B), melanoma antigen family A3 (MAGEA3), caltracin (CALT), NAD(P)H dehydrogenase-like protein (NSDHL), and LI>
6768	19512	32538	5.24	1.0E-07	BE047871.1	EST_HUMAN	tz43d06.y1 NCI_CGAP_Bm52 Homo sapiens cDNA clone IMAGE:2291339 5'
7392	20071	33150	5.24	1.0E-07	BE047871.1	EST_HUMAN	tz43d06.y1 NCI_CGAP_Bm52 Homo sapiens cDNA clone IMAGE:2291339 5'
7548	20218	33320	9.08	1.0E-07	N55081.1	EST_HUMAN	yz43c07.s1 Soares_fetal_liver_spleen_TN0024 Homo sapiens cDNA clone IMAGE:245484 3'
7548	20218	33321	0.67	1.0E-07	BF375909.1	EST_HUMAN	PM4-TN0024-030800-002-b05 TN0024 Homo sapiens cDNA
7577	20246	33351	0.67	1.0E-07	BF375909.1	EST_HUMAN	PM4-TN0024-030800-002-b05 TN0024 Homo sapiens cDNA
7577	20246	33351	1.31	1.0E-07	AL163281.2	NT	Homo sapiens chromosome 21 segment HS21C081

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7721	20385	33499	0.64	1.0E-07	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
8114	20808	33941	2.73	1.0E-07	P97435	SWISSPROT	ENTEROPEPTIDASE (ENTEROKINASE)
8114	20808	33942	2.73	1.0E-07	P97435	SWISSPROT	ENTEROPEPTIDASE (ENTEROKINASE)
8853	21544	34691	2.78	1.0E-07	AA693576.1	EST_HUMAN	z51e10 s1 Scores_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:434346 3'
9170	21840	35005	0.97	1.0E-07	P57110	SWISSPROT	MOTIFS 8 (ADAMTS-8) (ADAM-TS8) (METH-2)
9517	22170	35353	0.45	1.0E-07	BE327843.1	EST_HUMAN	h28h06.x1 NCL_CGAP_Mel15 Homo sapiens cDNA clone IMAGE:3171419 3' similar to contains MER18.13
9836	22487	35889	2.77	1.0E-07	BF674524.1	EST_HUMAN	h28h06.x1 NCL_CGAP_Mel15 Homo sapiens cDNA clone IMAGE:3171419 3' similar to contains MER18.13
9844	22495	35896	1.21	1.0E-07	AA386311.1	EST_HUMAN	EST165054 Brain IV NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4274426 5'
10362	23009		1.28	1.0E-07	AL163282.2	NT	Homo sapiens chromosome 21 segment HS21C082
12212	25188	30810	3.83	1.0E-07	BE048770.1	EST_HUMAN	h53c11.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3132212 3' similar to TR:O95722 O95722
12514	24864		1.87	1.0E-07	X51755.1	NT	Human lambda-immunoglobulin constant region complex (germline)
7181	19867	32940	0.84	9.0E-08	AI539362.1	EST_HUMAN	h53c11.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3132212 3' similar to TR:O95722 O95722
9767	22438	35645	1.89	9.0E-08	AV734819.1	EST_HUMAN	h53c11.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3132212 3' similar to TR:O95722 O95722
11136	23804	37082	1.71	8.0E-08	AI891052.1	EST_HUMAN	h53c11.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3132212 3' similar to TR:O95722 O95722
11668	24263	37987	2.8	9.0E-08	AL163301.2	EST_HUMAN	h53c11.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3132212 3' similar to TR:O95722 O95722
12166	24648		4.44	9.0E-08	AJ251873.1	NT	Homo sapiens chromosome 21 segment HS21C101
583	15546		3.7	8.0E-08	AI911352.1	EST_HUMAN	h53c11.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3132212 3' similar to TR:O95722 O95722
1028	13789		0.72	8.0E-08	BE785469.1	EST_HUMAN	h53c11.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3132212 3' similar to TR:O95722 O95722
3532	16288		1.53	8.0E-08	BE785469.1	EST_HUMAN	h53c11.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3132212 3' similar to TR:O95722 O95722
8638	21330	34474	3.05	8.0E-08	AI752367.1	EST_HUMAN	h53c11.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3132212 3' similar to TR:O95722 O95722
8638	21330	34475	3.05	8.0E-08	AI752367.1	EST_HUMAN	h53c11.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3132212 3' similar to TR:O95722 O95722
9527	22180	35364	2.83	8.0E-08	AV970693.1	EST_HUMAN	h53c11.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3132212 3' similar to TR:O95722 O95722
10461	23107	36338	0.47	8.0E-08	AF111167.2	NT	Homo sapiens Jun dimerization protein gene, partial cds; cfos gene, complete cds; and unknown gene
11211	23874		2.1	8.0E-08	AF253417.1	NT	ANKYRIN 1 (ERYTHROCYTE ANKYRIN)
78	12904	25542	2.66	7.0E-08	Q02357	SWISSPROT	ANKYRIN 1 (ERYTHROCYTE ANKYRIN)
1340	14088	26764	13.91	7.0E-08	X04809.1	NT	Rat mRNA for ribosomal protein L31
3563	16318	28965	1.15	7.0E-08	P15305	SWISSPROT	DYNEIN HEAVY CHAIN (DYHC)

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Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3563	16318	28966	1.15	7.0E-08	P15305	SWISSPROT	DYNEIN HEAVY CHAIN (DYHC)
10716	23405		1.67	7.0E-08	A1535743.1	EST_HUMAN	comp3.P11.A5 conorm Homo sapiens cDNA 3'
11672	24267	37589	5.17	7.0E-08	U24070.1	NT	Rattus norvegicus Munc13-1 mRNA, complete cds
12619	16318	28965	2.98	7.0E-08	P15305	SWISSPROT	DYNEIN HEAVY CHAIN (DYHC)
12619	16318	28966	2.98	7.0E-08	P15305	SWISSPROT	DYNEIN HEAVY CHAIN (DYHC)
12690	24975		1.89	7.0E-08	A1131016.1	NT	Homo sapiens SCL gene locus
798	13570	26230	2.88	6.0E-08	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
798	13570	26231	2.88	6.0E-08	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
2363	15085	27824	2.97	6.0E-08	BE144398.1	EST_HUMAN	MRO-HT0168-19199-004-g09 HT0166 Homo sapiens cDNA
3058	19824	28469	0.81	6.0E-08	7682473	NT	Homo sapiens KIAA1074 protein (KIAA1074), mRNA
4222	16963	29588	0.98	6.0E-08	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
7831	20546		0.69	6.0E-08	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
9227	21906		0.56	6.0E-08	AA827075.1	EST_HUMAN	db56c05.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1335368 3' similar to contains MER12.b3 MER12 repetitive element ;
11391	23997	37299	2.24	6.0E-08	P11369	SWISSPROT	RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ; ENDONUCLEASE]
11520	24120		1.33	6.0E-08	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
83	12909	25547	3.72	5.0E-08	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
2229	14957	27697	1.82	5.0E-08	AA493851.1	EST_HUMAN	hh03b09.s1 NCI_CGAP_Tty1 Homo sapiens cDNA clone IMAGE:943193 similar to contains Alu repetitive element;
11914	24477		8.36	5.0E-08	P06681	SWISSPROT	COMPLEMENT C2 PRECURSOR (C3/C5 CONVERTASE)
12059	24599	31085	2.84	5.0E-08	AW851878.1	EST_HUMAN	QV0-CT0225-131099-034-a12 CT0225 Homo sapiens cDNA
1754	14496	27195	0.97	4.0E-08	P25723	SWISSPROT	DORSAL-VENTRAL PATTERNING TOLLOID PROTEIN PRECURSOR
1754	14496	27196	0.97	4.0E-08	P25723	SWISSPROT	DORSAL-VENTRAL PATTERNING TOLLOID PROTEIN PRECURSOR
2888	15655		1.09	4.0E-08	AL079581.1	EST_HUMAN	DKFZp434J0426_r1 434 (synonym: hbs3) Homo sapiens cDNA clone DKFZp434J0426 5'
3894	16644	29284	1.04	4.0E-08	U82668.1	NT	Homo sapiens shox gene, alternatively spliced products, complete cds
6311	19082	32067	1.08	4.0E-08	P52624	SWISSPROT	URIDINE PHOSPHORYLASE (UDRPASE)
8697	21389	34533	0.63	4.0E-08	O15393	SWISSPROT	TRANSMEMBRANE PROTEASE, SERINE 2
9037	21727	34881	1.05	4.0E-08	L42571.1	NT	Cricetulus griseus ribosomal transcription factor (UBF2) mRNA, complete cds
9545	22198		0.71	4.0E-08	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
10228	22876		0.68	4.0E-08	A1016342.1	EST_HUMAN	at78d12.s1 Soares_total_fetus_Nb2HF8_gw Homo sapiens cDNA clone IMAGE:1622903 3'
10284	22932	36147	3.87	4.0E-08	A1050027.1	EST_HUMAN	an22a10.x1 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:1698411 3' similar to contains Alu repetitive element; contains element MER22 repetitive element ;

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit: Accession No.	Top Hit Database Source	Top Hit Descriptor
11009	23681	36939	1.71	4.0E-08	AA393627.1	EST_HUMAN	z176b08.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:728247 5' similar to TR:G505579
11009	23681	36940	1.71	4.0E-08	AA393627.1	EST_HUMAN	G505579 NA/CA,K-EXCHANGER. ;
11031	23702	36989	4.02	4.0E-08	BF692493.1	EST_HUMAN	z176b08.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:728247 5' similar to TR:G505579
11031	23702	36970	4.02	4.0E-08	BF692493.1	EST_HUMAN	G505579 NA/CA,K-EXCHANGER. ;
11919	25334		4.31	4.0E-08	W76159.1	EST_HUMAN	602248024F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4333300 5'
12549	24887		2.18	4.0E-08	AI343353.1	EST_HUMAN	602248024F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4333300 5'
5523	18321	31222	2.22	3.0E-08	BE018348.1	EST_HUMAN	z465g03.r1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:345556 5' similar to contains L1.11 L1 repetitive element ;
6879	17955	30552	4.24	3.0E-08	AI792737.1	EST_HUMAN	1b95a11.x1 NCI_CGAP_Cot6 Homo sapiens cDNA clone IMAGE:2062076 3' similar to contains MER18.53
7439	20116	33205	1.66	3.0E-08	AL163246.2	NT	MER18 MER18 repetitive element ;
							5b79a10.y1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3048570 5' similar to TR:Q9Z158 Q9Z158
							SYNTAXIN 17. ;
							gs76f11.y6 NCI_CGAP_P28 Homo sapiens cDNA clone IMAGE:1944045 5'
							Homo sapiens chromosome 21 segment HS21C046
7649	20313		3.56	3.0E-08	AI436352.1	EST_HUMAN	th93h09.x1 Soares_NSF_F8_gw_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2126273 3' similar to TR:Q13537 Q13537 MER37 TRANSPORTABLE ELEMENT, COMPLETE CONSENSUS SEQUENCE. ;
8788	22449		0.52	3.0E-08	AF055066.1	NT	Homo sapiens MHC class 1 region
10948	23628	36877	1.32	3.0E-08	AI218001.1	EST_HUMAN	qh21a04.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1845284 3'
11566	24165	37477	61.58	3.0E-08	R86279.1	EST_HUMAN	yp12b10.s1 Soares_breast_3NbHBst Homo sapiens cDNA clone IMAGE:187195 3' similar to gb:M34079 TAT
11566	24165	37478	61.58	3.0E-08	R86279.1	EST_HUMAN	BINDING PROTEIN-1 (HUMAN);
11888	24459		2.27	3.0E-08	R18420.1	EST_HUMAN	yp12b10.s1 Soares_breast_3NbHBst Homo sapiens cDNA clone IMAGE:187195 3' similar to gb:M34079 TAT
201	13014		9.03	2.0E-08	AW302996.1	EST_HUMAN	BINDING PROTEIN-1 (HUMAN);
221	13033		9.14	2.0E-08	AA425598.1	EST_HUMAN	yg02f04.r1 Soares_infant_brain_1N1B Homo sapiens cDNA clone IMAGE:30948 5' similar to contains Alu
484	13289	25905	1.01	2.0E-08	AF198349.1	NT	repetitive element;
645	13424	26062	13.62	2.0E-08	AW886438.1	EST_HUMAN	z46807.r1 Soares_fetal_tetus_Nb2HF8_gw Homo sapiens cDNA clone IMAGE:773317 5' similar to contains Alu repetitive element;contains element MER15 repetitive element ;
645	13424	26063	13.62	2.0E-08	AW886438.1	EST_HUMAN	Gallus gallus Dach2 protein (Dach2) mRNA, complete cds
969	13735		24.4	2.0E-08	BE280477.1	EST_HUMAN	MRO-OT0080-240200-001-g08 OT0080 Homo sapiens cDNA
1320	14069	26743	2.38	2.0E-08	AL163247.2	NT	MRO-OT0080-240200-001-g08 OT0080 Homo sapiens cDNA
1734	14476		12.18	2.0E-08	BE734871.1	EST_HUMAN	601156321F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3138863 5'
							Homo sapiens chromosome 21 segment HS21C047
							801570463F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3845189 5'

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1847	14585		4.11	2.0E-08	AW270271.1	EST_HUMAN	xp43f11.x1 NCI CGAP_HN11 Homo sapiens cDNA clone IMAGE:2743149 3'
2545	15260		1.71	2.0E-08	K00216.1	NT	Sheep His-IRNA-GUG
3202	15985	28618	7.94	2.0E-08	O42280	SWISSPROT	WNT-14 PROTEIN PRECURSOR
3202	15985	28619	7.94	2.0E-08	O42280	SWISSPROT	WNT-14 PROTEIN PRECURSOR
3840	18591		1.76	2.0E-08	AW813620.1	EST_HUMAN	RC3-ST0197-181098-012-b03 ST0197 Homo sapiens cDNA
4373	17111		2.48	2.0E-08	AA450040.1	EST_HUMAN	aa26c07.t1 NCI CGAP_GCB1 Homo sapiens cDNA clone IMAGE:814380 5' similar to contains L1, L2 L1 repetitive element;
4903	17630		2.36	2.0E-08	AW572881.1	EST_HUMAN	het17h08.x2 NCI CGAP_CML1 Homo sapiens cDNA clone IMAGE:2919327 3' similar to contains Alu repetitive element;
5549	18346	31255	1.19	2.0E-08	AA813204.1	EST_HUMAN	ab0h11.s1 Soares testis_NHT Homo sapiens cDNA clone 1377189 3'
5742	18534	31457	0.93	2.0E-08	AW088924.1	EST_HUMAN	xd32c04.x1 NCI CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2595462 3' similar to contains MER18.b3
7903	20598	33728	0.92	2.0E-08	P10272	SWISSPROT	MER18 MER18 repetitive element;
8009	20704	33832	1.35	2.0E-08	AA490121.1	EST_HUMAN	POLYPROTEIN [CONTAINS: PROTEASE; REVERSE TRANSCRIPTASE; ENDONUCLEASE]
8983	21673		0.9	2.0E-08	AU139978.1	EST_HUMAN	ab02g06.s1 Stralagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:839674 3'
10416	23062	36281	0.79	2.0E-08	N78097.1	EST_HUMAN	AU139978 PLACE1 Homo sapiens cDNA clone PLACE1011719 5'
10416	23062	36282	0.79	2.0E-08	N78097.1	EST_HUMAN	yw72f02.t1 Soares fetal liver spleen 1NFSL Homo sapiens cDNA clone IMAGE:248283 5' similar to contains LTR1.b3 LTR1 repetitive element;
12184	24668		1.54	2.0E-08	AL163284.2	NT	yw72f02.t1 Soares fetal liver spleen 1NFSL Homo sapiens cDNA clone IMAGE:248283 5' similar to contains LTR1.b3 LTR1 repetitive element;
1499	15571	26931	1.16	1.0E-08	P31792	SWISSPROT	Homo sapiens chromosome 21 segment HS21.C084
1768	14510	27211	1.45	1.0E-08	AF125348.1	NT	POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE; ENDONUCLEASE]
2044	14777		2.31	1.0E-08	BE141959.1	EST_HUMAN	Homo sapiens cavolin 1 (CAV1) gene, exon 3 and partial cds
5512	18310	31211	4.85	1.0E-08	AJ010770.1	NT	PM2-HT0130-150989-001-f12 HT0130 Homo sapiens cDNA
7668	20332	33443	1.26	1.0E-08	P19474	SWISSPROT	Homo sapiens hyperion gene, exons 1-50
7934	20629	33756	0.52	1.0E-08	AL163302.2	NT	52 KD RO PROTEIN (SJOJOREN SYNDROME TYPE A ANTIGEN (SS-A)) (RO(SS-A))
8028	20723	33855	0.64	1.0E-08	AF224669.1	NT	Homo sapiens chromosome 21 segment HS21C102
8028	20723	33856	0.64	1.0E-08	AF224669.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3
8445	21137	34275	1.94	1.0E-08	AJ015304.1	EST_HUMAN	(UBE2D3) genes, complete cds
9104	21792		0.45	1.0E-08	P09593	SWISSPROT	(UBE2D3) genes, complete cds
9105	21793	34956	0.78	1.0E-08	BE072572.1	EST_HUMAN	g35a05.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1618736 3'
							S-ANTIGEN PROTEIN PRECURSOR
							PM2-BT0546-210100-004-d02 BT0546 Homo sapiens cDNA

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8866	22516	35712	1.2	1.0E-08	P79110	SWISSPROT	TRICARBOXYLATE TRANSPORT PROTEIN PRECURSOR (CITRATE TRANSPORT PROTEIN) (CTP)
10453	23089	36330	0.77	1.0E-08	P98063	SWISSPROT	TRICARBOXYLATE CARRIER PROTEIN
11285	23946	37241	4.14	1.0E-08	A040483.1	NT	BONE MORPHOGENETIC PROTEIN 1 PRECURSOR (BMP-1)
12282	24715		2.82	1.0E-08	X51755.1	NT	Homo sapiens major histocompatibility locus class III region
4218	16959	29583	4.65	9.0E-09	AL163279.2	NT	Human lambda-immunoglobulin constant region complex (germline)
4218	16959	29584	4.65	9.0E-09	AL163279.2	NT	Homo sapiens chromosome 21 segment HS21C079
9962	22610		0.52	9.0E-09	T97950.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C079
6390	19159		0.62	8.0E-09	A1270815.1	EST_HUMAN	ye58a12.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:121918 3'
7164	19851	32920	7.68	8.0E-09	A1183500.1	EST_HUMAN	qu86c11.x1 NCL CGAP_Gas4 Homo sapiens cDNA clone IMAGE:1732164 3' similar to repetitive element;
7889	20594	33726	2.65	8.0E-09	AW900159.1	EST_HUMAN	q442e07.x1 Soares fetal heart NBHH19W Homo sapiens cDNA clone IMAGE:1732164 3' similar to contains MSR1.11 MSR1 repetitive element;
8887	21578		2.65	8.0E-09	AA836892.1	EST_HUMAN	CMD-NN1004-100300-273-e08 NN1004 Homo sapiens cDNA
3593	16346		1.73	7.0E-09	D86842.1	NT	qp74d08.s1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1582575 3'
7802	20497		0.61	7.0E-09	BF108755.1	EST_HUMAN	Homo sapiens DNA for 3-ketacyl-CoA thiolase beta-subunit of mitochondrial trifunctional protein, exon 2, 3
7946	20641		0.92	7.0E-09	AA256200.1	EST_HUMAN	7445e10.x1 Soares NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3524443 3' similar to contains MER28 b2 MER29 repetitive element;
8159	21829	34983	2.91	7.0E-09	L09709.1	NT	zr80c05.r1 Soares NHHMPu_S1 Homo sapiens cDNA clone IMAGE:681992 5' similar to contains L1.12 L1 repetitive element;
10083	22731	35946	1.42	7.0E-09	BE254850.1	EST_HUMAN	Human lysosomal membrane glycoprotein-2 (LAMP2) gene, 5' end and flanking region
10244	22892		0.5	7.0E-09	AA058626.1	EST_HUMAN	601111173F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3351834 5'
10571	23266		1.49	7.0E-09	T97950.1	EST_HUMAN	zf58e07.s1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:381156 3' similar to contains L1.12 L1 repetitive element;
2149	14879		0.89	6.0E-09	AL040439.1	EST_HUMAN	ye58a12.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:121918 3'
4922	17680	30263	3.12	6.0E-09	BE169421.1	EST_HUMAN	DKFZp434C0514.J1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434C0514 5'
5296	18101	30760	11.59	6.0E-09	AW195784.1	EST_HUMAN	PM1-H10527-160200-001-P05 HT0527 Homo sapiens cDNA
8475	21187	34311	0.93	6.0E-09	BE161653.1	EST_HUMAN	xn85f03.x1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2701311 3'
9074	21763	34925	1.98	6.0E-09		NT	MR3-HT0446-260300-201-h12 HT0446 Homo sapiens cDNA
10176	22824		3.76	6.0E-09	AF200923.2	NT	Homo sapiens fibroblast growth factor receptor 3 (achondroplasia, thanatophoric dwarfism) (FGFR3) mRNA
10632	23324	36561	1.44	6.0E-09	BF108755.1	EST_HUMAN	7445e10.x1 Soares NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3524443 3' similar to contains MER28 b2 MER29 repetitive element;

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Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11798	24388	37722	1.37	6.0E-09	C01803.1	EST_HUMAN	HUMG50003762 Human adult (K. Okubo) Homo sapiens cDNA
1394	14141	28818	3.27	5.0E-09	BE149284.1	EST_HUMAN	RC2-HT0252-120200-014-h10 HT0252 Homo sapiens cDNA
1845	14583	27298	1.06	5.0E-09	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
6316	19087	32071	1.73	5.0E-09	AA3359454.1	EST_HUMAN	EST68748 Fetal lung II Homo sapiens cDNA 5' end
6748	17917	30581	0.76	5.0E-09	U66059.1	NT	Human germline T-cell receptor beta chain Dopamine-beta-hydroxylase-like, TRY1, TRY2, TRY3, TCRBV27S1P, TCRBV22S1A2N1T, TCRBV9S1A1T, TCRBV7S1A1N2T, TCRBV5S1A1T, TCRBV13S3, TCRBV6S7P, TCRBV7S3A2T, TCRBV13S2A1T, TCRBV9S2A2P, TCRBV7S2A1N4T, TCRBV13S9/13S>
8484	21176	34321	0.48	5.0E-09	P37071	SWISSPROT	OLFACTORY RECEPTOR-LIKE PROTEIN COR5
9955	22643	35855	2.22	5.0E-09	AW709667.1	EST_HUMAN	PM2-UM0053-240300-005-c09 UM0053 Homo sapiens cDNA
508	13292		2.12	4.0E-09	AL163282.2	NT	Homo sapiens chromosome 21 segment HS21C082
944	13710		2.5	4.0E-09	AL163282.2	NT	Homo sapiens chromosome 21 segment HS21C085
1453	14200	26884	2.52	4.0E-09	9558718	NT	Homo sapiens hypothetical protein (AF038169), mRNA
2016	14751	27479	2.31	4.0E-09	AF175325.1	NT	Homo sapiens eukaryotic initiation factor 4A1 (EIF4A1) gene, partial cds
2430	15151	27885	6.07	4.0E-09	AF175325.1	NT	Homo sapiens eukaryotic initiation factor 4A1 (EIF4A1) gene, partial cds
7746	20442	33595	0.59	4.0E-09	AA350878.1	EST_HUMAN	EST66385 Infant brain Homo sapiens cDNA 5' end similar to similar to heat shock protein, 90 kDa
8420	21113	34250	0.62	4.0E-09	AA495747.1	EST_HUMAN	zxd4c06.r1 Soares NIHMPu_S1 Homo sapiens cDNA clone IMAGE:768298 5'
10779	23462	36704	2.06	4.0E-09	T64942.1	EST_HUMAN	ydt1a07.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:68804 3'
11011	23683	36943	1.47	4.0E-09	A1888401.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C009
11061	23731		1.53	4.0E-09	AA195142.1	EST_HUMAN	wm94f10.x1 NCL CGAP_U12 Homo sapiens cDNA clone IMAGE:2443627 3'
2351	15073	27610	4.77	3.0E-09	BE222239.1	EST_HUMAN	z34a12.r1 Soares NIHMPu_S1 Homo sapiens cDNA clone IMAGE:665278 5' similar to gb:L07807
2557	15271	28008	1.2	3.0E-09	BE222239.1	EST_HUMAN	DYNAMIN-1 (HUMAN);
2658	15366	28104	1.13	3.0E-09	P23249	SWISSPROT	hu09e09.x1 NCL CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3166120 3' similar to contains MER18.i3
3323	16083	28733	1.12	3.0E-09	BE222239.1	EST_HUMAN	MER18 repetitive element;
3371	16130		1.08	3.0E-09	AA442272.1	EST_HUMAN	hu09e09.x1 NCL CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3166120 3' similar to contains MER18.i3
4076	16820		0.7	3.0E-09	X16674.1	NT	MER18 repetitive element;
4392	17129	29761	3.42	3.0E-09	AF175325.1	NT	z54a04.r1 Soares testis NIH-T Homo sapiens cDNA clone IMAGE:757422 5'
4476	17211	29836	1.65	3.0E-09	Q9Y3R5	SWISSPROT	H. sapiens PADPRP-I gene for NAD(+) ADP-ribosyltransferase
							Homo sapiens eukaryotic initiation factor 4A1 (EIF4A1) gene, partial cds
							258.1 KDA PROTEIN C21ORF5 (KIAA0933)

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7800	20495	33617	1.19	3.0E-09	BE465780.1	EST_HUMAN	h80a02.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3194090 3' similar to TR:O55091
10147	22795	36009	1.7	3.0E-09	AL163247.2	NT	O55091 IMPACT PROTEIN.
10945	23624	36873	4.8	3.0E-09	BF109943.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C047
10945	23624	36874	4.8	3.0E-09	BF109943.1	EST_HUMAN	717208.x1 Soares NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3527030 3'
794	13586		2.43	2.0E-09	X16674.1	NT	717208.x1 Soares NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3527030 3'
1235	13984	26653	7.99	2.0E-09	AL163284.2	NT	H. sapiens PADPRP-1 gene for NAD(+) ADP-ribosyltransferase
1855	14401		7.46	2.0E-09	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
2326	15051	27787	1.1	2.0E-09	AL118573.1	EST_HUMAN	DKFZp761B1710.J1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761B1710 5'
3918	16666	29306	3.01	2.0E-09	Q9Y3R5	SWISSPROT	258.1 KDA PROTEIN C2TORF5 (KIAA0933)
5076	17795	30411	0.85	2.0E-09	O60241	SWISSPROT	BRAIN-SPECIFIC ANGIOGENESIS INHIBITOR 2 PRECURSOR
5633	18428	31341	0.55	2.0E-09	M23161.1	NT	Human transposon-like element mRNA
6058	18838		0.57	2.0E-09	AI004062.1	EST_HUMAN	ct47b09.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1618897 3'
6582	19599		0.93	2.0E-09	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C049
7351	20032	33110	8.4	2.0E-09	AA461430.1	EST_HUMAN	EST66142 Kidney IX Homo sapiens cDNA 5' and similar to EST containing L1 repeat
7423	20100	33188	0.68	2.0E-09	W28934.1	EST_HUMAN	z63h06.r1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:796187 5' similar to contains Alu repetitive element;
7717	20381	33494	0.62	2.0E-09	AW862126.1	EST_HUMAN	52d11 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA
8612	21304	34447	1.78	2.0E-09	AJ271735.1	NT	MR1-CT0352-240200-105-b08 CT0352 Homo sapiens cDNA
11233	23896	37183	1.62	2.0E-09	AL163246.2	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
12428	13566		22.07	2.0E-09	X16674.1	NT	Homo sapiens chromosome 21 segment HS21C048
12495	25403		2.41	2.0E-09	AA226070.1	EST_HUMAN	H. sapiens PADPRP-1 gene for NAD(+) ADP-ribosyltransferase
12634	24934		1.75	2.0E-09	U82668.1	NT	nc11c02.r1 NCI_CGAP_P1 Homo sapiens cDNA clone IMAGE:1007810 similar to contains Alu repetitive element;
974	13739		0.72	1.0E-09	W78152.1	EST_HUMAN	Homo sapiens shox gene, alternatively spliced products, complete cds
1087	13845	26503	2.01	1.0E-09	5031624	NT	zd79d03.s1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:346853 3' similar to gb.L02932 PEROXISOME PROLIFERATOR ACTIVATED RECEPTOR ALPHA (HUMAN);
1087	13845	26504	2.01	1.0E-09	5031624	NT	Homo sapiens CCAAT-box-binding transcription factor (CBF2) mRNA
1630	14376		1.17	1.0E-09	AJ229041.1	NT	Homo sapiens CCAAT-box-binding transcription factor (CBF2) mRNA
2892	15659	28304	1.59	1.0E-09	U80017.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3
2926	15692	28336	3.25	1.0E-09	M26699.1	NT	Homo sapiens basic transcription factor 2 p44 (btf2p44) gene, partial cds, neuronal apoptosis inhibitory protein (nrip) and survival motor neuron protein (smn) genes, complete cds
2926	15692	28337	3.25	1.0E-09	M26699.1	NT	Homo sapiens nucleolar phosphoprotein B23 (NPM1) mRNA, complete cds
3034	15800	28446	0.7	1.0E-09	BE534440.1	EST_HUMAN	Homo sapiens nucleolar phosphoprotein B23 (NPM1) mRNA, complete cds
							601058902F.1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3445177 5'

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4744	17476						z135b03.s1 Soares_pineal_gland_N3HPG Homo sapiens cDNA clone IMAGE:414029 3' similar to contains
5416	18215	30923	0.4	1.0E-09	AA719297.1	EST_HUMAN	Alu repetitive element; contains element MER22 repetitive element;
6740	18532	31455	0.86	1.0E-09	AL163283.2	NT	Homo sapiens chromosome 21 segment HS21C083
6053	18833	31795	1.89	1.0E-09	U07000.1	NT	Human breakpoint cluster region (BCR) gene, complete cds
8289	20983		3.13	1.0E-09	P26894	SWISSPROT	GIRGLMSPOROZOITE PROTEIN PRECURSOR (GS)
10212	22860	34124	0.85	1.0E-09	AI688474.1	EST_HUMAN	wd39505.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2330481 3' similar to contains
11799	24389		2.92	1.0E-09	AL163283.2	NT	MER25.11 MER25 repetitive element;
12333	25344	30717	1.68	1.0E-09	AL163283.2	NT	Homo sapiens chromosome 21 segment HS21C083
12503	24857		2.25	1.0E-09	11418127	NT	Homo sapiens chromosome 21 segment HS21C083
1286	14036	26707	1.35	1.0E-09	T93178.1	EST_HUMAN	ye24e05.t1 Stralgene lung (#937210) Homo sapiens cDNA clone IMAGE:118688 5'
			3.74	9.0E-10	AW867740.1	EST_HUMAN	MRO-SN0040-050500-002-c07 SN0040 Homo sapiens cDNA
2838	15606	28256	4.41	9.0E-10	AI870071.1	EST_HUMAN	we78h03.x1 Soares_Dieckgraefe_colon_NHCD Homo sapiens cDNA clone IMAGE:2347253 3' similar to
6735	19569	32601	4.78	9.0E-10	AI452982.1	EST_HUMAN	SW_RL29_HUMAN P47914 60S RIBOSOMAL PROTEIN L29 ; contains element PTR5 repetitive element ;
142	12957	25599	13.27	8.0E-10	U63630.2	NT	TR:000372 O00372 PUTATIVE P150 ;
3337	16097	28748	0.88	8.0E-10	BE080748.1	EST_HUMAN	Homo sapiens MCM4 (MCM4) and DNA-PKcs (PRKDC) genes, partial cds
4177	16917	29544	3.17	8.0E-10	AA376832.1	EST_HUMAN	QV1-BT0631-150200-071-01 BT0631 Homo sapiens cDNA
9855	22515		2.44	8.0E-10	U36308.2	EST_HUMAN	EST89564 Small intestine I Homo sapiens cDNA 5' end
685	13460	26107	9.36	7.0E-10		NT	Homo sapiens lens major intrinsic protein (MIP) gene, complete cds
685	13460	26108	9.36	7.0E-10	7706225	NT	Homo sapiens TPA inducible protein (LOC51586) mRNA
1618	14365	27055	2.24	7.0E-10	Q13342	SWISSPROT	LYSP100 PROTEIN (LYMPHOID-RESTRICTED HOMOLOG OF SP100)
2013	14748		3.17	7.0E-10	P08548	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
3086	15278	28491	24.23	7.0E-10	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
2564	15278		2.19	7.0E-10	X00856.1	NT	H.sapiens DHFR gene, exon 3
6092	18870	31836	4.18	7.0E-10	AA345220.1	EST_HUMAN	EST151247 Gall bladder II Homo sapiens cDNA 5' end
7318	19999	33078	1.08	7.0E-10	BF552883.1	EST_HUMAN	IL3-HT0619-110700-209-D12 HT0619 Homo sapiens cDNA
7556	20226		1.48	7.0E-10	P35084	SWISSPROT	DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT
7875	20570	33696	1.6	7.0E-10	AF029701.2	NT	Homo sapiens presentin-1 gene, exons 1 and 2
7875	20570	33697	1.6	7.0E-10	AF029701.2	NT	Homo sapiens presentin-1 gene, exons 1 and 2
10209	22857	36073	1.67	7.0E-10	L08895.1	NT	Homo sapiens MADS/MEF2-family transcription factor (MEF2C) mRNA, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
893	13662	26327	3.5	6.0E-10	AJ408877.1	NT	Homo sapiens ASCI.3 gene, CEGP1 gene, C11orf14 gene, C11orf15 gene, C11orf16 gene and C11orf17 gene
2684	15393	28132	1.21	6.0E-10	AI424405.1	EST_HUMAN	t02d07.x1 NCI_CGAP_P128 Homo sapiens cDNA clone IMAGE:2095021 3'
4689	17423		2.7	6.0E-10	AW853719.1	EST_HUMAN	RC3-C70254-031089-012-g12 C70254 Homo sapiens cDNA
8682	21374	34518	1	6.0E-10	P33730	SWISSPROT	E-SELECTIN PRECURSOR (ENDOTHELIAL LEUKOCYTE ADHESION MOLECULE 1) (ELAM-1)
8682	21374	34519	1	6.0E-10	P33730	SWISSPROT	(LEUKOCYTE-ENDOTHELIAL CELL ADHESION MOLECULE 2) (LECAM2) (CD62E)
9534	22187	35373	0.46	6.0E-10	P98073	SWISSPROT	E-SELECTIN PRECURSOR (ENDOTHELIAL LEUKOCYTE ADHESION MOLECULE 1) (ELAM-1)
11950	24503		2.16	6.0E-10	AW971923.1	EST_HUMAN	(LEUKOCYTE-ENDOTHELIAL CELL ADHESION MOLECULE 2) (LECAM2) (CD62E)
745	13518		7.27	5.0E-10	AL048804.1	EST_HUMAN	ENTEROPEPTIDASE PRECURSOR (ENTEROKINASE)
3468	16224	28878	2.5	5.0E-10	Q01033	SWISSPROT	ENTEROPEPTIDASE PRECURSOR (ENTEROKINASE)
4931	17659	30269	1	5.0E-10	AF181897.1	NT	DKFZp434N219_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434N219 5'
7222	18907		1.51	5.0E-10	BF105159.1	EST_HUMAN	HYPOTHETICAL GENE 48 PROTEIN
9436	22114	35288	1.89	5.0E-10	P34878	SWISSPROT	Homo sapiens WRN (WRN) gene, complete cds
9436	22114	35289	1.89	5.0E-10	P34878	SWISSPROT	601822184F1 NIH_MGC_75 Homo sapiens cDNA clone IMAGE:4042413 5'
109	12930		1.17	4.0E-10	AI221083.1	EST_HUMAN	HYPOTHETICAL 87.9 KD PROTEIN ZK698.8 IN CHROMOSOME III
567	13348	25976	0.74	4.0E-10	AA515260.1	EST_HUMAN	HYPOTHETICAL 87.9 KD PROTEIN ZK698.8 IN CHROMOSOME III
1989	14725	27446	1.31	4.0E-10	AW594709.1	EST_HUMAN	qg09f09.x1 Soares_placenta_8to9weeks_2NbHP808W Homo sapiens cDNA clone IMAGE:1759049 3'
2580	15294	28032	3.73	4.0E-10	AL163303.2	NT	similar to contains LTR8.b2 LTR8 repetitive element;
7076	19767	32831	25.71	4.0E-10	AF224669.1	NT	repetitive element;
10095	22743	35957	0.49	4.0E-10	AW293243.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C103
10343	22990	36208	0.89	4.0E-10	AI267342.1	EST_HUMAN	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3
895	13663	26329	3.55	3.0E-10	N36113.1	EST_HUMAN	UI-H-B12-ah1-a-07-Q-U1.s1 NCI_CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2727061 3'
1329	14078		4.72	3.0E-10	AY005150.1	NT	aq83h11.x1 Stanley Frontal SN pool 2 Homo sapiens cDNA clone IMAGE:2035653
4498	17234	29864	1.04	3.0E-10	AL163203.2	NT	y93206.s1 Soares_melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:2729683 similar to contains L1.11 L1 repetitive element;
4498	17234	29865	1.04	3.0E-10	AL163203.2	NT	Homo sapiens extracellular glycoprotein lactrin, precursor, gene, complete cds
5369	18169	30855	1.24	3.0E-10	N50109.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C003
6110	18887	31896	2.52	3.0E-10	P20350	SWISSPROT	Homo sapiens chromosome 21 segment HS21C003
6298	19032	32007	3.43	3.0E-10	BE302970.1	EST_HUMAN	yz11g08.s1 Soares_multiple_sclerosis_2NbHMSP Homo sapiens cDNA clone IMAGE:282782 3'
							RHOMBOID PROTEIN (VEINLET PROTEIN)
							ba76d08.y1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2906319 5'

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7660	20324	33432	1.42	3.0E-10	AV743302.1	EST_HUMAN	AV743302 CB Homo sapiens cDNA clone CBFBGD08 5'
7660	20324	33433	1.42	3.0E-10	AV743302.1	EST_HUMAN	AV743302 CB Homo sapiens cDNA clone CBFBGD08 5'
8628	21321	34463	1.2	3.0E-10	H87208.1	EST_HUMAN	ys74b12.81 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:220511 3' similar to contains MER29 repetitive element;
8947	21638	34784	1.58	3.0E-10	AW850731.1	EST_HUMAN	IL3-CT0219-160200-064-B06 CT0219 Homo sapiens cDNA
8947	21638	34785	1.58	3.0E-10	AW850731.1	EST_HUMAN	IL3-CT0219-160200-064-B06 CT0219 Homo sapiens cDNA
9240	21919						
10359	23008		0.58	3.0E-10	AF020503.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHT) gene, exon 5
10483	23139		2.37	3.0E-10	T66891.1	EST_HUMAN	ys11e12.11 Stralagens lung (#837210) Homo sapiens cDNA clone IMAGE:80398 5'
12584	24907	31003	1.34	3.0E-10	AA769294.1	EST_HUMAN	nc26g03.s1 NCI CGAP_G0B1 Homo sapiens cDNA clone IMAGE:1289808 3'
34	12862	25479	2.65	3.0E-10	BE179517.1	EST_HUMAN	IL3-HT0618-110500-136-E07 HT0618 Homo sapiens cDNA
34	12862	25480	1.67	2.0E-10	P48988	SWISSPROT	MAJOR CENTROMERE AUTOANTIGEN B (CENTROMERE PROTEIN B) (CENP-B)
1890	14627		1.96	2.0E-10	P48988	SWISSPROT	MAJOR CENTROMERE AUTOANTIGEN B (CENTROMERE PROTEIN B) (CENP-B)
2985	15751		1.04	2.0E-10	U80017.1	NT	Homo sapiens basic transcription factor 2 p44 (btf2p44) gene, partial cds, neuronal apoptosis inhibitory protein (haiip) and survival motor neuron protein (smn) genes, complete cds
5714	18507		2.54	2.0E-10	BF675047.1	EST_HUMAN	602136640F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4273377 5'
					Q28640	SWISSPROT	(HPRG)
6156	18933	31900	1.37	2.0E-10	AF280107.1	NT	Homo sapiens cytochrome P450 polypeptide 43 (CYP3A43) gene, partial cds; cytochrome P450 polypeptide 6 (CYP3A4) and cytochrome P450 polypeptide 7 (CYP3A7) genes, complete cds; and cytochrome P450 polypeptide 5 (CYP3A5) gene, partial cds
7279	19963	33039	6.47	2.0E-10	BE791082.1	EST_HUMAN	601596208F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3940824 5'
7912	20607	33737	0.48	2.0E-10	P26809	SWISSPROT	POL POLYPROTEIN [CONTAINS: PROTEASE; REVERSE TRANSCRIPTASE; RIBONUCLEASE H]
7912	20607	33738	0.48	2.0E-10	P26809	SWISSPROT	POL POLYPROTEIN [CONTAINS: PROTEASE; REVERSE TRANSCRIPTASE; RIBONUCLEASE H]
9202	21871		0.99	2.0E-10	BF434565.1	EST_HUMAN	7078408.x1 NCI CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3642303 3' similar to contains L1.13 L1 repetitive element;
11297	23958		1.37	2.0E-10	AI862153.1	EST_HUMAN	ta10f12.x1 Scores: total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:2043695 3'
1498	14245		1.87	2.0E-10	AI862153.1	EST_HUMAN	MRO-SN0038-290300-001-01 SN0038 Homo sapiens cDNA
1602	14348	27037	3.18	1.0E-10	AW867767.1	EST_HUMAN	AV652123 GLC Homo sapiens cDNA clone GLCXA11 3'
2586	15300		3.16	1.0E-10	AW862001.1	EST_HUMAN	QV0-CT0225-191199-058-a08 CT0225 Homo sapiens cDNA
3491	16247	28901	0.89	1.0E-10	AW832912.1	EST_HUMAN	QV2-TT0003-161199-013-g10 TT0003 Homo sapiens cDNA
3528	16284		0.7	1.0E-10	AL041685.1	EST_HUMAN	DKFZp434N1317_r1_434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434N1317 5'
3825	16284		1.03	1.0E-10	AL041685.1	EST_HUMAN	DKFZp434N1317_r1_434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434N1317 5'
3996	16744		6.19	1.0E-10	AF213884.1	NT	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4108	16851	29477	5.1	1.0E-10	U52111.2	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMK1), creatine transporter (CRTR), CDM protein (CDM), adrenoleukodystrophy protein >
4108	16851	29478	5.1	1.0E-10	U52111.2	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMK1), creatine transporter (CRTR), CDM protein (CDM), adrenoleukodystrophy protein >
4113	16856	29484	1.94	1.0E-10	AB031069.1	NT	Homo sapiens PCCX1 mRNA for protein containing CXXC domain 1, complete cds
4149	16891		1.84	1.0E-10	M30629.1	NT	Human pregnancy-specific glycoprotein beta-1 (SP1) mRNA, last exon
5085	17804		1.51	1.0E-10	A1797745.1	EST_HUMAN	we82704.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2347615 3' similar to contains MER31.11 MER31 repetitive element;
6720	19635	32678	0.66	1.0E-10	AF003528.1	NT	Homo sapiens X-linked acrodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
7375	20055		0.65	1.0E-10	P08548	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
7583	20251	33357	0.55	1.0E-10	AU128584.1	EST_HUMAN	AU128584 NT2RP2 Homo sapiens cDNA clone NT2RP2003751 5'
8138	20832	33996	1.04	1.0E-10	AW408990.1	EST_HUMAN	IB_9A4 Fetal brain library Homo sapiens cDNA
8553	21245		1.07	1.0E-10	AI268340.1	EST_HUMAN	qm04e10.x1 NCL CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1880874 3' similar to contains L1.11 L1 repetitive element;
10102	22750		4.01	1.0E-10	AA081868.1	EST_HUMAN	zn23g06.r1 Stratagene neuroepithelium NT2RAM1 937234 Homo sapiens cDNA clone IMAGE:548314 5'
10831	23513	36754	2.65	1.0E-10	AI036280.1	EST_HUMAN	oy65h03.x1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:1672661 3'
11896	17913		1.71	1.0E-10	X87344.1	NT	Hi.sapiens DMA, DMB, HLA-Z1, IP2, LMP2, TAP1, LMP7, TAP2, DOB, DQ82 and RING8, 9, 13 and 14 genes
255	13063	25702	1.59	9.0E-11	BE145600.1	EST_HUMAN	IL2-HT0203-291089-016-c08 HT0203 Homo sapiens cDNA
2097	14828	27661	6.12	9.0E-11	AL134395.1	EST_HUMAN	DKFZp547D225_r1 547 (synonym: hfb1) Homo sapiens cDNA clone DKFZp547D225 5'
2097	14828	27662	6.12	9.0E-11	AL134395.1	EST_HUMAN	DKFZp547D225_r1 547 (synonym: hfb1) Homo sapiens cDNA clone DKFZp547D225 5'
3378	16137	28785	2.45	9.0E-11	AL134395.1	EST_HUMAN	DKFZp547D225_r1 547 (synonym: hfb1) Homo sapiens cDNA clone DKFZp547D225 5'
3378	16137	28786	2.45	9.0E-11	AL134395.1	EST_HUMAN	DKFZp547D225_r1 547 (synonym: hfb1) Homo sapiens cDNA clone DKFZp547D225 5'
4465	17201	29827	1.03	9.0E-11	AA775985.1	EST_HUMAN	ae7801.s1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:970297 3'
5487	18286		3.83	9.0E-11	BE079780.1	EST_HUMAN	RC6-BT0627-14D200-011-E06 BT0627 Homo sapiens cDNA
10054	22702	35919	1.19	9.0E-11	AA324960.1	EST_HUMAN	EST27872 Cerebellum II Homo sapiens cDNA 5' end
10054	22702	35920	1.19	9.0E-11	AA324960.1	EST_HUMAN	EST27872 Cerebellum II Homo sapiens cDNA 5' end
12258	24703	31080	3.9	9.0E-11	C16635.1	EST_HUMAN	C16635 Clontech human acta polyA+ mRNA (#6572) Homo sapiens cDNA clone GEN-506508 5'
3114	15879		8.33	8.0E-11	H19971.1	EST_HUMAN	yn53f11.s1 Soares adult brain N2b5HB65Y Homo sapiens cDNA clone IMAGE:172173 3' similar to contains L1 repetitive element;

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Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3945	16895	29334	0.7	8.0E-11	AI478617.1	EST_HUMAN	hm54c09.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2161836 3'
4022	16768	29398	4.88	8.0E-11	N23712.1	EST_HUMAN	yw46e06.s1 Weizmann Olfactory Epithelium Homo sapiens cDNA clone IMAGE:255298 3'
6574	18338		0.65	8.0E-11	AW166158.1	EST_HUMAN	x45r11.x1 NCI_CGAP_Brm50 Homo sapiens cDNA clone IMAGE:2621061 3' similar to contains MER10.11
1430	14177	26862	1.75	7.0E-11	AA330842.1	EST_HUMAN	MER10 repetitive element ; EST34392 Embryo, 6 week Homo sapiens cDNA 5' end
3852	16802	29240	1.03	7.0E-11	AJ277546.2	NT	Homo sapiens WEE1 gene for protein kinase and partial ZNF143 gene for zinc finger transcription factor
8398	21089	34224	2.05	7.0E-11	AF163864.1	NT	Homo sapiens SNCA isoform (SNCA) gene, complete cds, alternatively spliced
10129	22777		1.17	7.0E-11	P11369	SWISSPROT	RETROVIRUS-RELATED POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ; ENDONUCLEASE]
403	13188	25837	7.01	6.0E-11	M55270.1	NT	Human matrix Gla protein (MGP) gene, complete cds
403	13188	25838	7.01	6.0E-11	M55270.1	NT	Human matrix Gla protein (MGP) gene, complete cds
6622	18384	32398	0.67	6.0E-11	L44140.1	NT	Homo sapiens chromosome X region from filamin (FLN) gene to glucose-6-phosphate dehydrogenase (G6PD) gene, complete cds's
7583	20261	33369	3.65	6.0E-11	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
8262	20956	34095	7.81	6.0E-11	AV727859.1	EST_HUMAN	AV727859 HTC Homo sapiens cDNA clone HTCASC06 5'
9213	21892	35059	0.62	6.0E-11	BE063509.1	EST_HUMAN	CM0-BT0281-031199-087-a03 BT0281 Homo sapiens cDNA
11	12838	25451	1.49	5.0E-11	AL163283.2	NT	Homo sapiens chromosome 21 segment HS21C083
3359	12838	25451	1.9	5.0E-11	AL163283.2	NT	Homo sapiens chromosome 21 segment HS21C083
4203	16944	29571	1.36	5.0E-11	P48034	SWISSPROT	ALDEHYDE OXIDASE
6423	19191	32187	1.63	5.0E-11	AL163213.2	NT	Homo sapiens chromosome 21 segment HS21C013
7430	20107	33194	14.05	5.0E-11	11416789	NT	Homo sapiens probocadherin beta 3 (PCDH3), mRNA
1380	14127		1.94	4.0E-11	AA436042.1	EST_HUMAN	zu07b12.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:730659 5'
2793	15498	28238	7.14	4.0E-11	BE885900.1	EST_HUMAN	801507531F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3908295 5'
2869	15735	28385	1.16	4.0E-11	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
4576	17311	29939	0.85	4.0E-11	D44688.1	EST_HUMAN	HUMSUPY069 Human brain cDNA Homo sapiens cDNA clone 069
6384	19153	32153	3.2	4.0E-11	P20095	SWISSPROT	PRE-MRNA SPLICING FACTOR RNA HELICASE PRP2
6903	19841	32686	0.82	4.0E-11	AA442630.1	EST_HUMAN	zv59f10.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:757963 5' similar to TR:G1055250
7274	19958		4.5	4.0E-11	AF224689.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3
9295	21982		1.78	4.0E-11	BE149425.1	EST_HUMAN	(UBE2D3) genes, complete cds RC1-HT0256-210100-013-08 HT0256 Homo sapiens cDNA
9582	22215	35402	0.9	4.0E-11	AI609753.1	EST_HUMAN	#82g12.x1 NCI_CGAP_Brm23 Homo sapiens cDNA clone IMAGE:2106830 3' similar to WP:2K353.1 CE00385 ;

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Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12462	24830	31029	1.47	4.0E-11	11545732	NT	Homo sapiens SH3-domain binding protein 1 (SH3BP1), mRNA
1475	14222	26908	2.8	3.0E-11	6679077	NT	Mus musculus expressed in non-metastatic cells 2, protein (NM23B) (Nme2), mRNA
4243	16984		1.04	3.0E-11	AA309248.1	EST_HUMAN	EST180120 Liver, hepatocellular carcinoma Homo sapiens cDNA 5' end
940	13707	26372	1.97	2.0E-11	AI150502.1	EST_HUMAN	qf36c04.x1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1752102 3' similar to contains MER10.13
1162	13916	26580	3.99	2.0E-11	R24807.1	EST_HUMAN	y943e12.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:35144 5'
1182	13916	26581	3.99	2.0E-11	R24807.1	EST_HUMAN	y943e12.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:35144 5'
1608	14354	27042	4.86	2.0E-11	L17432.1	NT	Gallus gallus rho-globin, beta-H globin, beta-A globin, epsilon-globin, and olfactory receptor-like protein
1608	14354	27043	4.86	2.0E-11	L17432.1	NT	Gallus gallus rho-globin, beta-H globin, beta-A globin, epsilon-globin, and olfactory receptor-like protein
1612	14359	27048	1.21	2.0E-11	AI126371.1	EST_HUMAN	qc51c10.x1 Soares pregnant_uterus_NHPU Homo sapiens cDNA clone IMAGE:1713138 3' similar to
3191	15954	28607	7.58	2.0E-11	P10263	SWISSPROT	qbl02832 PEROXISOME PROLIFERATOR ACTIVATED RECEPTOR ALPHA (HUMAN); contains L1.t1
3320	16080	28730	1.11	2.0E-11	AI478617.1	EST_HUMAN	L1 repetitive element; RETROVIRUS-RELATED GAG POLYPROTEIN (VERSION 1)
3356	16116	28771	0.93	2.0E-11	Q10473	SWISSPROT	hm54c09.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2161836 3'
3488	16244		1.01	2.0E-11	AF020503.1	NT	POLYPEPTIDE N-ACETYL GALACTOSAMINYLTRANSFERASE (PROTEIN-UDP
4409	17146		0.68	2.0E-11	BE065537.1	EST_HUMAN	ACETYL GALACTOSAMINYLTRANSFERASE (UDP-GALNAC:POLYPEPTIDE, N-
4587	17302		0.72	2.0E-11	AL163227.2	NT	ACETYL GALACTOSAMINYLTRANSFERASE (GALNAC-T1)
4882	17609		1.77	2.0E-11	BE062558.1	EST_HUMAN	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHIT) gene, exon 5
6044	18824	31785	1.02	2.0E-11	AW877806.1	EST_HUMAN	RC3-BT0316-170200-014-e05 BT0316 Homo sapiens cDNA
6218	18992	31968	1.87	2.0E-11	AA561028.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C027
7095	19784	32850	0.59	2.0E-11	BF592945.1	EST_HUMAN	QV2-BT0258-261099-014-a01 BT0258 Homo sapiens cDNA
7782	20477		0.56	2.0E-11	P37072	SWISSPROT	QV2-PT0073-280300-108-h08 PT0073 Homo sapiens cDNA
9123	21811		1.14	2.0E-11	AF029308.1	NT	nc83h05.r1 NCI_CGAP_GC1 Homo sapiens cDNA clone IMAGE:767433 5' similar to SW:PR16_YEAST
10184	22832	36046	5.44	2.0E-11	Q13606	SWISSPROT	P15938 PRE-MRNA SPLICING FACTOR RNA HELICASE PRP16 ;
10413	23059	36277	1.12	2.0E-11	AW885874.1	EST_HUMAN	7i97c03.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:3442565 3'
10413	23059	36278	1.12	2.0E-11	AW885874.1	EST_HUMAN	OLFACTORY RECEPTOR-LIKE PROTEIN COR6
							Homo sapiens chromosome 9 duplication of the T cell receptor beta locus and hypoxanthine gene families
							OLFACTORY RECEPTOR 5f1 (OLFACTORY RECEPTOR-LIKE PROTEIN OLF1)
							RC4-OT0072-170400-013-c11 OT0072 Homo sapiens cDNA
							RC4-OT0072-170400-013-c11 OT0072 Homo sapiens cDNA

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11056	23726	36997	1.48	2.0E-11	AA035369.1	EST_HUMAN	z27g02.s1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:471794 3'
11056	23726	36998	1.48	2.0E-11	AA035369.1	EST_HUMAN	z27g02.s1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:471794 3'
11090	23760	37035	1.57	2.0E-11	AA281956.1	EST_HUMAN	zs18b04.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:685519 5'
12017	25332		1.54	2.0E-11	AA704195.1	EST_HUMAN	z77e03.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:460924 3'
12048	24567		3.54	2.0E-11	AW842143.1	EST_HUMAN	RCO-CN0027-210100-011-c01 CN0027 Homo sapiens cDNA
12073	24586	31123	1.87	2.0E-11	BF377859.1	EST_HUMAN	CM2-TN0140-070900-372-g01 TN0140 Homo sapiens cDNA
12332	24748		2.67	2.0E-11	D25217.2	NT	Homo sapiens mRNA for KIAA0027 protein, partial cds
12479	24840		3.14	2.0E-11	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
12781	25035		3.37	2.0E-11	11417968	NT	Homo sapiens SEC14 (S. cerevisiae)-like 2 (SEC14L2), mRNA
661	13437	26078	1.34	1.0E-11	AJ131016.1	NT	Homo sapiens SCL gene locus
1195	13947	26611	3.35	1.0E-11	AL163279.2	NT	Homo sapiens chromosome 21 segment HS21C078
1485	14232		2.36	1.0E-11	AF119914.1	NT	Homo sapiens PRO3078 mRNA, complete cds
2030	14765	27494	1.13	1.0E-11	P16258	SWISSPROT	OXYSTEROL-BINDING PROTEIN
2122	14853	27582	2.91	1.0E-11	AF000573.1	NT	Homo sapiens homogenisate 1,2-dioxygenase gene, complete cds
3490	16246	28900	1.2	1.0E-11	BE004315.1	EST_HUMAN	CM0-SN0105-170300-292-d12 BN0105 Homo sapiens cDNA
5249	18055	30683	16.93	1.0E-11	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
5741	18533	31456	0.63	1.0E-11	BF222646.1	EST_HUMAN	7b57d01.x1 NCI_CGAP_P128 Homo sapiens cDNA clone IMAGE:3649945 3' similar to contains MER10.b3
8101	20795	33928	3.15	1.0E-11	4885546	NT	MER10 repetitive element
8480	21172	34317	5.44	1.0E-11	R13174.1	EST_HUMAN	Homo sapiens PHD finger protein 2 (PHF2) mRNA
8946	21637	34782	1.89	1.0E-11	BF365119.1	EST_HUMAN	y73d08.r1 Soares_infant_brain_1N1B Homo sapiens cDNA clone IMAGE:28166 5'
8946	21637	34783	1.89	1.0E-11	BF365119.1	EST_HUMAN	QV4-NN1149-250900-423-a03 NN1149 Homo sapiens cDNA
11257	23918	37212	1.62	1.0E-11	BF680078.1	EST_HUMAN	QV4-NN1149-250900-423-a03 NN1149 Homo sapiens cDNA
9697	22348	35542	1.07	9.0E-12	AL163300.2	NT	802154807F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4295977 5'
9697	22348	35543	1.07	9.0E-12	AL163300.2	NT	Homo sapiens chromosome 21 segment HS21C100
9237	21916		0.93	8.0E-12	BE074720.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C100
12125	24617		3.91	8.0E-12	AJ271736.1	NT	IL6-BT0578-130300-036-G12 BT0578 Homo sapiens cDNA
4813	17348	29882	1.16	7.0E-12	Q05904	SWISSPROT	Homo sapiens Xq pseudautosomal region; segment 2/2
11322	24013	37316	9.59	7.0E-12	AA704735.1	EST_HUMAN	34 KD SPICULE MATRIX PROTEIN PRECURSOR (LSM34)
3535	16231		0.71	6.0E-12	AV730554.1	EST_HUMAN	z23g01.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:451152 3'
4314	17053	26678	8.52	6.0E-12	AA732516.1	EST_HUMAN	AV730554 HTF Homo sapiens cDNA clone HTFAWF08 5'
6295	18068	32051	0.77	6.0E-12	AF020503.1	NT	nz88f1.1.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1302673 3' similar to contains Alu repetitive element
							Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHT) gene, exon 5

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Table 4

Single Exon Probes Expressed In Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8894	21585	34723	1.04	6.0E-12	AF003249.1	NT	Morone saxatilis myosin heavy chain FM3A (FM3A) mRNA, complete cds
9374	21949		1.87	6.0E-12	AA847898.1	EST_HUMAN	cd10g11.1 s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1387588 similar to contains MER28.12
1020	13780	26442	3.52	5.0E-12	T06573.1	EST_HUMAN	MER29 repetitive element
3385	16144	28801	1.81	5.0E-12	BE047779.1	EST_HUMAN	EST04462 Fetal brain, Strategene (cat#936206) Homo sapiens cDNA clone HFBDV33
3713	16466	29104	5.03	5.0E-12	AJ271736.1	NT	IZ42605.y1 NCI_CGAP_Bms2 Homo sapiens cDNA clone IMAGE:2201217 5'
5931	18715	31671	8.41	5.0E-12	AL163278.2	NT	Homo sapiens Xq pseudautosomal region, segment 2/2
5931	18715	31672	6.41	5.0E-12	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
6399	19168	32167	11.33	5.0E-12	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
6933	19424	32439	0.94	5.0E-12	AL040739.1	EST_HUMAN	EST386850 MAGE resequences, MAGN Homo sapiens cDNA
6942	19424	32439	1.16	5.0E-12	AL040739.1	EST_HUMAN	DKFZp434B1815_s1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434B1815 3'
8128	20822	33959	1.33	5.0E-12	AA033745.1	EST_HUMAN	DKFZp434B1815_s1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434B1815 3'
8566	21258		0.55	5.0E-12	AW887037.1	EST_HUMAN	z01g12.s1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:375718 3' similar to contains
8893	21584		0.54	5.0E-12	AL079581.1	EST_HUMAN	L1.13 L1 repetitive element
9006	21696	34847	2.93	5.0E-12	AJ271735.1	NT	RC1-O10086-220300-011-b07 OT0086 Homo sapiens cDNA
9323	21990	35161	0.96	5.0E-12	P34982	SWISSPROT	DKFZp434J0426_r1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434J0426 5'
10175	22823		4.45	5.0E-12	AL163303.2	NT	Homo sapiens Xq pseudautosomal region, segment 1/2
10262	22910	36120	0.76	5.0E-12	AL163302.2	NT	OLFACTORY RECEPTOR 1D2 (OLFACTORY RECEPTOR-LIKE PROTEIN HGMP07E) (OLFACTORY RECEPTOR 17-4) (OR17-4)
10468	23114	36344	0.44	5.0E-12	6978754	NT	Homo sapiens chromosome 21 segment HS21C103
237	13047	25686	4.2	4.0E-12	AA700326.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C102
238	13047	25686	4.03	4.0E-12	AA700326.1	EST_HUMAN	Rattus norvegicus Deleted in colorectal cancer (rat homolog) (Dcc), mRNA
4577	17312	29940	0.8	4.0E-12	AI689984.1	EST_HUMAN	z74g11.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:460676 3'
7519	20180		0.72	4.0E-12	BF445140.1	EST_HUMAN	z74g11.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:460676 3'
8141	20835		3.2	4.0E-12	AF109907.1	NT	b26h05.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2270745 3' similar to TR:Q13539 Q13539
8587	21279	34418	0.87	4.0E-12	AB042815.1	NT	MARINER TRANSPOSASE
11019	23691	36954	4.2	4.0E-12	AJ229043.1	NT	med21b03.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3368077 3' similar to contains MER7.b2
12375	24774		2.76	4.0E-12	U78027.1	NT	MER7 repetitive element
							Homo sapiens S164 gene, partial cds; PS1 and hypothetical protein genes, complete cds; and S171 gene, partial cds
							Bos taurus Mtn2 mRNA for mitochondrial carrier homolog 2, complete cds
							Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22, segment 3/3
							Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44L) and FTP3 (FTP3) genes, complete cds

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
602	13380	26011	4.27	3.0E-12	AW341883.1	EST_HUMAN	h13401.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2909377 3' similar to TR:O14517 O14517 SMRP ;
602	13380	26012	4.27	3.0E-12	AW341883.1	EST_HUMAN	h13401.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2909377 3' similar to TR:O14517 O14517 SMRP ;
5084	17803	30421	0.81	3.0E-12	AL163288.2	NT	Homo sapiens chromosome 21 segment HS21C068
5365	18167	30853	1.52	3.0E-12	AF111168.2	NT	Homo sapiens serine palmitoyl transferase, subunit II gene, complete cds; and unknown genes
7654	20318		0.63	3.0E-12	AW854328.1	EST_HUMAN	RC3-CT0255-031093-011-h02 CT0255 Homo sapiens cDNA
8273	20867	34109	0.51	3.0E-12	O35453	SWISSPROT	SERINE PROTEASE HEPSIN
9004	21694	34844	0.52	3.0E-12	O35453	SWISSPROT	SERINE PROTEASE HEPSIN
10551	23247	36483	3.03	3.0E-12	U37672.1	NT	Human prostate specific antigen gene, 5' flanking region
10551	23247	36484	3.03	3.0E-12	U37672.1	NT	Human prostate specific antigen gene, 5' flanking region
1649	14395	27084	1.39	2.0E-12	AW802131.1	EST_HUMAN	IL5-UM0071-120-000-065-a05 UM0071 Homo sapiens cDNA
4094	18838	29462	0.91	2.0E-12	J01884.1	NT	Rat USA small nuclear RNA
4094	18836	29463	0.81	2.0E-12	J01884.1	NT	Rat USA small nuclear RNA
4387	17124		2.03	2.0E-12	BE063509.1	EST_HUMAN	CM0-BT0281-031199-087-a03 BT0281 Homo sapiens cDNA
4840	17570	30192	1.18	2.0E-12	O70306	SWISSPROT	TBX15 PROTEIN (T-BOX PROTEIN 15)
4840	17570	30193	1.18	2.0E-12	O70306	SWISSPROT	TBX15 PROTEIN (T-BOX PROTEIN 15)
5169	17978	30491	0.77	2.0E-12	P11369	SWISSPROT	RETROVIRUS-RELATED POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ; ENDONUCLEASE]
6385	19154		2.8	2.0E-12	AW971857.1	EST_HUMAN	EST333946 MAGI resequences, MAGI Homo sapiens cDNA
7075	19766	32830	3.74	2.0E-12	T08169.1	EST_HUMAN	EST06060 Infant Brain, Benito Soares Homo sapiens cDNA clone HIBBA13 5' end
7244	19928	33005	1.02	2.0E-12	BE173035.1	EST_HUMAN	MR0-HT0559-200400-015-a08 HT0559 Homo sapiens cDNA
7558	20228	33331	2.2	2.0E-12	11422229	NT	Homo sapiens Ac-like transposable element (ALTE), mRNA
9208	22087		1.84	2.0E-12	AF198864.1	NT	Homo sapiens putative BPES syndrome breakpoint region protein gene, complete cds
9865	22535		11.12	2.0E-12	BE165980.1	EST_HUMAN	MR3-HT0487-150200-113-g01 HT0487 Homo sapiens cDNA
10412	23088	36276	0.87	2.0E-12	AI334130.1	EST_HUMAN	qq0702.x1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:1931835 3' similar to TR:Q13538
12032	24557		2.81	2.0E-12	AL163283.2	NT	Q13538 ORF2: FUNCTION UNKNOWN ;
12223	24680		2.5	2.0E-12	11418248	NT	Homo sapiens chromosome 21 segment HS21C083
119	12938	25579	2.21	1.0E-12	AW627674.1	EST_HUMAN	hh50a09.x1 NCL_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2970040 3' similar to contains MER18.1 MER18 repetitive element ;
1980	14716		1.39	1.0E-12	AI871726.1	EST_HUMAN	wm51f07.x1 NCL_CGAP_U2 Homo sapiens cDNA clone IMAGE:2439493 3' similar to contains L1.b3 L1 repetitive element ;
3087	15833	28476	1.29	1.0E-12	AF000991.1	NT	Homo sapiens testis-specific Testis Transcript Y.2 (TTY2) mRNA, partial cds

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Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3067	15833	28477	1.29	1.0E-12	AF000991.1	NT	Homo sapiens testis-specific Testis Transcript Y 2 (TTY2) mRNA, partial cds
3855	16605	29242	26.43	1.0E-12	AU132248.1	EST_HUMAN	AU132248 NT2RP3 Homo sapiens cDNA clone NT2RP3004070 5'
3855	16605	29243	26.43	1.0E-12	AU132248.1	EST_HUMAN	AU132248 NT2RP3 Homo sapiens cDNA clone NT2RP3004070 5'
5877	18683		2.25	1.0E-12	U82828.1	NT	Homo sapiens ataxia telangiectasia (ATM) gene, complete cds
5950	18732		1.93	1.0E-12	Q9Y2G7	SWISSPROT	HYPOPHOSPHATASE 1 (HPP1) gene, complete cds
6438	19206	32202					Mus musculus WNT-2 gene, partial cds; putative ankyrin-related protein and cystic fibrosis transmembrane conductance regulator (CFTR) genes, section 1 of 2 of the complete cds, and unknown gene
7016	19708	32764	0.62	1.0E-12	AF229843.1	NT	Homo sapiens putative BPES syndrome breakpoint region protein gene, complete cds
			2.07	1.0E-12	AF196964.1	NT	gbM19503 LINE-1 REVERSE TRANSCRIPTASE HOMOLOG (HUMAN); contains MER10.11 MER10 repetitive element;
7050	19741	32802	11.32	1.0E-12	A1248533.1	EST_HUMAN	gbM19503 LINE-1 REVERSE TRANSCRIPTASE HOMOLOG (HUMAN); contains MER10.11 MER10 repetitive element;
7050	19741	32803	11.32	1.0E-12	A1248533.1	EST_HUMAN	gbM19503 LINE-1 REVERSE TRANSCRIPTASE HOMOLOG (HUMAN); contains MER10.11 MER10 repetitive element;
8606	21298	34442	1.16	1.0E-12	AA782323.1	EST_HUMAN	ac26405.s1 Stragene ovary (#937217) Homo sapiens cDNA clone IMAGE:857577 3'
11273	23934		1.72	1.0E-12	AW488478.1	EST_HUMAN	he38107.x1 NCL CGAP_CML1 Homo sapiens cDNA clone IMAGE:2921317 3' similar to contains element
11942	24497	37809	4.54	1.0E-12	AW962164.1	EST_HUMAN	EST374237 IMAGE resequences, MAGG Homo sapiens cDNA
12150	24637		1.52	1.0E-12	A1738592.1	EST_HUMAN	w33108.x1 NCL CGAP_Co16 Homo sapiens cDNA clone IMAGE:2392095 3'
12294	25308		2.92	1.0E-12	AL163298.2	NT	Homo sapiens chromosome 21 segment HS21C088
3618	16371		1	8.0E-13	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
3927	16677	29320	0.96	9.0E-13	AB029900.1	NT	Homo sapiens CST gene for cerebroside sulfotransferase, exon 1, 2, 3, 4, 5
8501	22154		2.67	9.0E-13	N89653.1	EST_HUMAN	za26606.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:283651 3'
700	13475	26123	7.37	8.0E-13	U29185.1	NT	Homo sapiens prion protein (PrP) gene, complete cds
700	13475	26124	7.37	8.0E-13	U29185.1	NT	Homo sapiens prion protein (PrP) gene, complete cds
1830	14669	27281	2.94	8.0E-13	U80017.1	NT	Homo sapiens basic transcription factor 2 p44 (btf2p44) gene, partial cds, neuronal apoptosis inhibitory protein (naip) and survival motor neuron protein (smn) genes, complete cds
8011	20706	33834	0.76	8.0E-13	A1884398.1	EST_HUMAN	wn31109.x1 NCL CGAP_U14 Homo sapiens cDNA clone IMAGE:2437601 3'
8011	20706	33835	0.76	8.0E-13	A1884398.1	EST_HUMAN	wn31109.x1 NCL CGAP_U14 Homo sapiens cDNA clone IMAGE:2437601 3'
10046	22694		3.08	8.0E-13	U78027.1	NT	Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44L) and FTP3 (FTP3) genes, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11779	24370	37701	1.67	8.0E-13	U66080.1	NT	Human germline T-cell receptor beta chain TCRBV13S1, TCRBV6S8A2T, TCRBV6S9A3N2T, TCRBV13S6A2T, TCRBV6S9P, TCRBV6S3A2T, TCRBV13S8P, TCRBV6S3A1N1T, TCRBV5S2, TCRBV6S6A2T, TCRBV6S7P, TCRBV13S4, TCRBV6S2A1N1T, TCRBV6S4A2T, TCRBV6S4A1, TCRBV23S1A2T, TCRBV12S
7718	20382	33495	0.71	7.0E-13	A1884388.1	EST_HUMAN	wm31h09.x1 NCI CGAP_U14 Homo sapiens cDNA clone IMAGE:2437601 3'
7718	20382	33496	0.71	7.0E-13	A1884388.1	EST_HUMAN	wm31h09.x1 NCI CGAP_U14 Homo sapiens cDNA clone IMAGE:2437601 3'
8133	20827		0.56	7.0E-13	Q95155	SWISSPROT	OLFACTORY RECEPTOR-LIKE PROTEIN OLF2
12404	24788		3.05	7.0E-13	BE778223.1	EST_HUMAN	601463285F1 NIH_MGC 67 Homo sapiens cDNA clone IMAGE:3866613 5'
12617	24823		1.37	7.0E-13	Q10473	SWISSPROT	POLYPEPTIDE N-ACETYL GALACTOSAMINYL TRANSFERASE (PROTEIN UDP ACETYL GALACTOSAMINYL TRANSFERASE) (UDP-GALNAc:POLYPEPTIDE, N-ACETYL GALACTOSAMINYL TRANSFERASE) (GALNAc-T1)
2094	14825	27558	6.75	6.0E-13	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C007
3316	16076		0.74	5.0E-13	R78338.1	EST_HUMAN	y82704.1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:145759 5'
3392	18151		1.54	5.0E-13	AA435773.1	EST_HUMAN	z177a12.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:728350 3' similar to contains Alu repetitive element; contains element MER22 repetitive element;
6777	19621	32548	0.84	5.0E-13	P08983	SWISSPROT	GAP_JUNCTION BETA-1 PROTEIN (CONNEXIN 30) (CX30)
10767	23451	36893	2.72	5.0E-13	P07313	SWISSPROT	MYOSIN LIGHT CHAIN KINASE, SKELETAL MUSCLE (MLCK)
1860	14598		2.23	4.0E-13	AW378614.1	EST_HUMAN	PM2-HT0224-221089-001-e11 HT0224 Homo sapiens cDNA
2462	15180		1.67	4.0E-13	AF003529.1	NT	Homo sapiens glypican 3 (GPC3) gene, partial cds and flanking repeat regions
5499	18297	31195	5.51	4.0E-13	BE169131.1	EST_HUMAN	PM3-HT0520-230200-002-c08 HT0520 Homo sapiens cDNA
7105	19793	32858	1.05	4.0E-13	AB037750.1	NT	Homo sapiens mRNA for KIAA1329 protein, partial cds
7512	20183	33277	0.94	4.0E-13	AA431520.1	EST_HUMAN	z1776g12.r1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:782182 5' similar to TR.G452763 G452763 COR1 MRNA.
7620	20286		1.07	4.0E-13	N44291.1	EST_HUMAN	y93g05.r1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:273080 5' similar to PIR.A32995
8740	21432	34577	1.07	4.0E-13	AL043810.1	EST_HUMAN	A32995 (complex sterility protein - mouse);
9402	22064	35235	0.45	4.0E-13	AA076807.1	EST_HUMAN	DKFZp434A0128_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434A0128 5'
9919	22588	35764	4.94	4.0E-13	A1298831.1	EST_HUMAN	7B04H11 Chromosome 7 Fetal Brain cDNA Library Homo sapiens cDNA clone 7B04H11
11120	23789	37066	2.09	4.0E-13	AA435819.1	EST_HUMAN	q132405.x1 NCI CGAP_U14 Homo sapiens cDNA clone IMAGE:1899845 3' similar to contains Alu repetitive element;
11120	23789	37067	2.09	4.0E-13	AA435819.1	EST_HUMAN	z1776g10.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:728514 3'
175	12987		4.94	3.0E-13	AF003528.1	NT	z1776g10.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:728514 3'
845	13615		1.62	3.0E-13	AA430310.1	EST_HUMAN	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
							z1768g08.r1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:781406 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2370	15092	27831	1.26	3.0E-13	AJ271738.1	NT	Homo sapiens Xq pseudautosomal region, segment 2/2
2483	15201		2.47	3.0E-13	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
2669	15379	28117	2.91	3.0E-13	BF372962.1	EST_HUMAN	GM3-FT10100-140700-242-108 FT10100 Homo sapiens cDNA
3182	15945		2.97	3.0E-13	AA745844.1	EST_HUMAN	cbt18402.s1 NCI CGAP Kids Homo sapiens cDNA clone IMAGE:1324035 3'
5452	18251	31140	0.59	3.0E-13	AA134017.1	EST_HUMAN	z188h10.1 Stralagene lung carcinoma 937218 Homo sapiens cDNA clone IMAGE:565315 5' similar to contains THR.12 THR repetitive element;
5452	18251	31141	0.59	3.0E-13	AA134017.1	EST_HUMAN	z188h10.1 Stralagene lung carcinoma 937218 Homo sapiens cDNA clone IMAGE:565315 5' similar to contains THR.12 THR repetitive element;
5902	18687	31635	0.62	3.0E-13	AW005639.1	EST_HUMAN	wz88c02.x1 NCI CGAP Brn25 Homo sapiens cDNA clone IMAGE:2565880 3' similar to TR:O75139
7783	20478	33603	7.67	3.0E-13	U52111.2	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRTR), CDM protein (CDM), adrenoleukodystrophy protein >
7975	20670	33792	0.6	3.0E-13	AA352487.1	EST_HUMAN	EST60487 Activated T-cells XX Homo sapiens cDNA 5' end similar to similar to serine protease P100, Ra-reactive factor
7975	20670	33793	0.6	3.0E-13	AA352487.1	EST_HUMAN	EST60487 Activated T-cells XX Homo sapiens cDNA 5' end similar to similar to serine protease P100, Ra-reactive factor
10098	22746	35961	0.72	3.0E-13	AW935487.1	EST_HUMAN	RC2-DT0007-110100-014-g10 DT0007 Homo sapiens cDNA
10575	23270		3.61	3.0E-13	A1064768.1	EST_HUMAN	HA0536 Human fetal liver cDNA library Homo sapiens cDNA
10975	23651	36904	3.96	3.0E-13	BE063508.1	EST_HUMAN	CMO-BT0281-031199-087-a03 BT0281 Homo sapiens cDNA
11588	24197	37517	2.29	3.0E-13	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
145	12960	25602	3.42	2.0E-13	U52111.2	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRTR), CDM protein (CDM), adrenoleukodystrophy protein >
232	13043	25683	2.05	2.0E-13	U23639.1	NT	Danio rerio fibroblast growth factor receptor 4 mRNA, complete cds
1247	13986	26663	7.98	2.0E-13	AF239710.1	NT	Homo sapiens DNA polymerase delta small subunit (POLD2) gene, exons 1 through 11 and complete cds
3005	15771	28419	0.9	2.0E-13	8924119	NT	Homo sapiens hypothetical protein PRO2130 (PRO2130), mRNA
3005	15771	28420	0.9	2.0E-13	8924119	NT	Homo sapiens hypothetical protein PRO2130 (PRO2130), mRNA
3275	16036	28686	1.13	2.0E-13	BF431698.1	EST_HUMAN	bab7605.x1 Soares NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE: 3'
3498	18254	28908	1.11	2.0E-13	AF109907.1	NT	Homo sapiens S164 gene, partial cds; PS1 and hypothetical protein genes, complete cds, and S171 gene, partial cds
4088	18831		1.34	2.0E-13	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6032	18812	31772	4.7	2.0E-13	Q06852	SWISSPROT	CELL SURFACE GLYCOPROTEIN 1 PRECURSOR (OUTER LAYER PROTEIN B) (S-LAYER PROTEIN 1)
6113	18890		0.58	2.0E-13	X79417.1	NT	S.scrofa rps12 mRNA for ribosomal protein S12
6717	19032	32875	7.15	2.0E-13	X16912.1	NT	Human PFKL gene for liver-type B-phosphofructokinase (EC 2.7.1.11) exon 2
6954	19436	32451	0.65	2.0E-13	10835072	NT	Homo sapiens N-myristoyltransferase 1 (NMT1), mRNA
6954	19436	32452	0.65	2.0E-13	10835072	NT	Homo sapiens N-myristoyltransferase 1 (NMT1), mRNA
10355	23002	36219	3.87	2.0E-13	5031896	NT	Homo sapiens mab-21 (C. elegans)-like 1 (MAB21L1) mRNA
12105	24602		3.48	2.0E-13	AW892155.1	EST_HUMAN	CGM0-NN0001-100300-274-e11 NN0001 Homo sapiens cDNA
285	13091	25732	1.52	1.0E-13	S74129.1	NT	FGF-1-fibroblast growth factor 1 [human, kidney, Genomic, 342 nt, segment 2 of 2]
868	13637	26307	5.64	1.0E-13	AJ007973.1	NT	Homo sapiens LGMD2B gene
1313	14061	26736	1.08	1.0E-13	X87344.1	NT	H.sapiens DMA, DMB, HLA-Z1, JPP2, LMP2, TAP1, LMP7, TAP2, DOB, DOB2 and RING8, 9, 13 and 14 genes
2015	14750	27478	2.13	1.0E-13	AA720574.1	EST_HUMAN	nw21802.s1 NCI_CGAP_GCB0 Homo sapiens cDNA clone IMAGE:1241138 3' similar to contains THR13
4553	17286	25917	1.64	1.0E-13	BF340987.1	EST_HUMAN	THR1 repetitive element;
7810	20505	33628	0.78	1.0E-13	AA577812.1	EST_HUMAN	602038009F1 NCI_CGAP_Bm64 Homo sapiens cDNA clone IMAGE:4185866 5'
7810	20505	33627	0.78	1.0E-13	AA577812.1	EST_HUMAN	nm24401.s1 NCI_CGAP_Gas1 Homo sapiens cDNA clone IMAGE:1084801 3' similar to contains Alu repetitive element; contains element MER24 repetitive element;
9890	22638		0.79	1.0E-13	O15481	EST_HUMAN	nm24401.s1 NCI_CGAP_Gas1 Homo sapiens cDNA clone IMAGE:1084801 3' similar to contains Alu repetitive element; contains element MER24 repetitive element;
10199	22847	36063	0.53	1.0E-13	AF300701.1	SWISSPROT	MELANOMA-ASSOCIATED ANTIGEN B4 (MAGE-B4 ANTIGEN)
11352	24042	37345	11.1	1.0E-13	BF108755.1	EST_HUMAN	Mus musculus osteoblastic protein tyrosine phosphatase mRNA, complete cds
11934	24492		2.26	1.0E-13	AV715377.1	EST_HUMAN	745610.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3524443 3' similar to contains MER29 b2 MER29 repetitive element;
12563	24893		2.12	1.0E-13	AJ271735.1	NT	AV715377 DOB Homo sapiens cDNA clone DCBAIE03 5'
324	13125	25781	1.81	9.0E-14	AA781159.1	EST_HUMAN	Homo sapiens Xq pseudautosomal region; segment 1/2
325	13126	25782	3.05	9.0E-14	AA781159.1	EST_HUMAN	aj24c01.s1 Soares_testis_NHT Homo sapiens cDNA clone 1391232 3' similar to contains MER19.11 MER19 repetitive element;
2504	15221		3.66	9.0E-14	AW661577.1	EST_HUMAN	aj24c01.s1 Soares_testis_NHT Homo sapiens cDNA clone 1391232 3' similar to contains MER19.11 MER19 repetitive element;
2599	15313	28050	1.18	9.0E-14	AJ133127.1	NT	RC4-CT0322-080100-013-d09 C10322 Homo sapiens cDNA
2599	15313	28051	1.18	9.0E-14	AJ133127.1	NT	Homo sapiens mRNA for sodium-glucose cotransporter (SGLT2 gene)
2758	15463	28206	2.6	9.0E-14	AB038162.1	NT	Homo sapiens mRNA for sodium-glucose cotransporter (SGLT2 gene)
3109	15874	28513	3.96	9.0E-14	AW513298.1	EST_HUMAN	Homo sapiens TFF gene cluster for trefoil factor, complete cds
							xc64h05.x1 NCI_CGAP_U11 Homo sapiens cDNA clone IMAGE:2707833 3'

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3232	13125	25761	0.84	9.0E-14	AA781159.1	EST_HUMAN	el24c01.s1 Soares_testis_NHT Homo sapiens cDNA clone 1391232 3' similar to contains MER18.11 MER19
3778	16530	29169	6.85	9.0E-14	D14547.1	NT	repetitive element;
4707	17439	30071	1.66	9.0E-14	AJ002153.1	NT	Human DNA, SINE repetitive element
3489	16245		1.27	8.0E-14	BE468263.1	EST_HUMAN	Sagittinus oedipus gene for seminal vesicle secreted protein semenogelin I
3937	16687		2.67	8.0E-14	R76269.1	EST_HUMAN	hz71c09.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3213424 3'
9348	20419	33539	15.04	8.0E-14	X89211.1	NT	W72603.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:144796 3'
9460	22010	35180	3.68	8.0E-14	AA218316.1	EST_HUMAN	H.sapiens DNA for endogenous retroviral like element
11410	24059		1.72	8.0E-14	BE062558.1	EST_HUMAN	zq17c10.s1 Strategene fetal retina 937202 Homo sapiens cDNA clone IMAGE:629870 3'
12302	24727	31056	2.48	8.0E-14	AI688118.1	EST_HUMAN	QV2-BT0258-281098-014-401 BT0258 Homo sapiens cDNA
1625	15574		4.77	7.0E-14	AW151673.1	EST_HUMAN	wc92b08.x1 NCI_CGAP_C63 Homo sapiens cDNA clone IMAGE:2328143 3'
8818	21510		10.57	7.0E-14	AL163285.2	NT	xi87e10.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2623146 3' similar to contains MER10.12
358	13186	25797	14.14	6.0E-14	AF020503.1	NT	repetitive element;
9722	22373	35572	2.6	6.0E-14	AF020503.1	NT	Homo sapiens chromosome 21 segment HS21C085
9722	22373	35573	2.6	6.0E-14	AF020503.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHT) gene, exon 5
604	13382	28014	5.46	5.0E-14	Q63120	SWISSPROT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHT) gene, exon 5
4993	17716	30322	1.41	5.0E-14	AW073791.1	EST_HUMAN	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHT) gene, exon 5
5446	18245	31133	5.77	5.0E-14	P08547	SWISSPROT	CANALICULAR MULTISPECIFIC ORGANIC ANION TRANSPORTER 1 (MULTIDRUG RESISTANCE-ASSOCIATED PROTEIN 2) (CANALICULAR MULTIDRUG RESISTANCE PROTEIN)
1101	18560		2.18	4.0E-14	P04928	SWISSPROT	x603b05.x1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2575185 3' similar to contains L1.12 L1
1870	14608	27319	5.9	4.0E-14	AJ007973.1	NT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
3735	16489		0.87	4.0E-14	AA046602.1	EST_HUMAN	S-ANTIGEN PROTEIN PRECURSOR
4259	17000	29630	1.05	4.0E-14	N46328.1	EST_HUMAN	Homo sapiens LGMD2B gene
7858	20563		0.59	4.0E-14	X87344.1	NT	z67a06.r1 Soares_pregant_uterus_NHRPU Homo sapiens cDNA clone IMAGE:467858 5'
12626	25414		7.02	4.0E-14	AI886224.1	EST_HUMAN	w73c12.s1 Soares_multiple_sclerosis_2NbHMSP Homo sapiens cDNA clone IMAGE:279180 3' similar to contains L1.13 L1 repetitive element;
930	13697	26361	1.88	3.0E-14	X85466.1	NT	H.sapiens DNA, DMB, HLA-Z1, IPP2, LMP2, LMP7, TAP1, LMP7, TAP2, DOB, DOB2 and RING8, B, 13 and 14 genes
							wm08c03.x1 NCI_CGAP_Ut4 Homo sapiens cDNA clone IMAGE:2436332 3' similar to contains Alu
							repetitive element;
							R.norvegicus mRNA for CPG2 protein

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4870	17597	30220	0.92	3.0E-14	AW265354.1	EST_HUMAN	xp45f12.x1 NCI_CGAP_HN11 Homo sapiens cDNA clone IMAGE:2743343 3' similar to contains Alu repetitive element; contains element MER9 repetitive element;
4873	17600	30222	0.97	3.0E-14	7656864	NT	Homo sapiens a disintegrin and metalloproteinase domain 29 (ADAM29), mRNA
6635	19397	32411	1.49	3.0E-14	AI420786.1	EST_HUMAN	te91c12.x1 NCI_CGAP_P128 Homo sapiens cDNA clone IMAGE:2094070 3' similar to TR:O00519 O00519 FATTY ACID AMIDE HYDROLASE.
6635	19397	32412	1.49	3.0E-14	AI420786.1	EST_HUMAN	te91c12.x1 NCI_CGAP_P128 Homo sapiens cDNA clone IMAGE:2094070 3' similar to TR:O00519 O00519 FATTY ACID AMIDE HYDROLASE.
6744	25099		0.62	3.0E-14	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
8686	21378	34522	0.87	3.0E-14	N42165.1	EST_HUMAN	y07b10.r1 Soares melanocyte 2NBHM Homo sapiens cDNA clone IMAGE:270623 5'
10914	23594	36840	1.28	3.0E-14	BE888016.1	EST_HUMAN	601511530F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3913087 5'
11201	17597	30220	7.19	3.0E-14	AW265354.1	EST_HUMAN	xp45f12.x1 NCI_CGAP_HN11 Homo sapiens cDNA clone IMAGE:2743343 3' similar to contains Alu repetitive element; contains element MER9 repetitive element;
12539	25282		1.68	3.0E-14	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
381	13168	25811	3.71	2.0E-14	AJ271736.1	NT	Homo sapiens Xq pseudautosomal region; segment 2/2
381	13168	25812	3.71	2.0E-14	AJ271736.1	NT	Homo sapiens Xq pseudautosomal region; segment 2/2
674	15548	26091	9.05	2.0E-14	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
2387	15108		1.49	2.0E-14	AW372868.1	EST_HUMAN	RC6-BT0377-091299-031-D12 BT0377 Homo sapiens cDNA
2467	15185		2.15	2.0E-14	7657529	NT	Homo sapiens thalidomide tumor deletion region protein 1 (RTDR1), mRNA
2529	15245	27983	1.19	2.0E-14	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
2542	15256		1.14	2.0E-14	BE222432.1	EST_HUMAN	h90g10.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3180738 3' similar to contains Alu repetitive element; contains OFR.t1 OFR repetitive element;
2681	15390		0.95	2.0E-14	P08548	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
5437	18236	30950	0.8	2.0E-14	BF380661.1	EST_HUMAN	IL2-UT0072-240800-142-D07 UT0072 Homo sapiens cDNA
5533	18331	31236	0.92	2.0E-14	AI312351.1	EST_HUMAN	ta78h01.x2 NCI_CGAP_HSC2 Homo sapiens cDNA clone IMAGE:2050225 3' similar to contains L1.13 L1 repetitive element;
5634	18429	31342	3.42	2.0E-14	U01317.1	NT	Human beta globin region on chromosome 11
6784	19528		0.91	2.0E-14	BE000550.1	EST_HUMAN	RC3-BN0072-240200-011-a08 BN0072 Homo sapiens cDNA
6984	19677	32724	0.62	2.0E-14	4585709	NT	Homo sapiens a disintegrin and metalloproteinase domain 11 (ADAM11) mRNA
7186	19871	32945	1.25	2.0E-14	P56163	SWISSPROT	ZINC-FINGER PROTEIN NEURO-D4
7407	20084	33167	22.12	2.0E-14	BE158761.1	EST_HUMAN	IL2-HT0397-071299-024-D04 HT0397 Homo sapiens cDNA
7407	20084	33168	22.12	2.0E-14	BE158761.1	EST_HUMAN	IL2-HT0397-071299-024-D04 HT0397 Homo sapiens cDNA
9817	22468	35671	0.57	2.0E-14	AI978786.1	EST_HUMAN	wr50g10.x1 NCI_CGAP_U11 Homo sapiens cDNA clone IMAGE:2492034 3' similar to contains Alu repetitive element;
10317	22964	36181	0.53	2.0E-14	AV741648.1	EST_HUMAN	AV741648 CB Homo sapiens cDNA clone CBFBBF04 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10679	23370	36612	4.88	2.0E-14	AW139800.1	EST_HUMAN	U1-H-BIT-adv-a-10-0-U1 s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2718234 3'
11591	24190	37507	1.29	2.0E-14	AW089689.1	EST_HUMAN	xc36f02.x1 NCI_CGAP_Co20 Homo sapiens cDNA clone IMAGE:2586363 3' similar to contains MER1 t3
12538	25284		2.29	2.0E-14	AF008191.1	NT	MER1 repetitive element;
1045	13804	26463	1.86	1.0E-14	AL163246.2	NT	Homo sapiens putative G6 protein (GR6) gene, complete cds
1385	14132	26805	6.41	1.0E-14	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C046
1385	14132	26806	6.41	1.0E-14	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C068
1994	14730	27452	12.44	1.0E-14	L44140.1	NT	Homo sapiens chromosome X region from filamin (FLN) gene to glucose-6-phosphate dehydrogenase (G6PD) gene, complete cds
2182	14911	27643	4.55	1.0E-14	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
2409	15130	27868	3.56	1.0E-14	AF001689.1	NT	Homo sapiens ribosomal protein L23A (RPL23A) gene, complete cds
2945	15711	28363	1.79	1.0E-14	P08227	SWISSPROT	HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PFHRP-II)
3185	15928	28576	5.42	1.0E-14	BF335227.1	EST_HUMAN	RC2-CT0432-310700-013-a09_1 CT0432 Homo sapiens cDNA
3165	15928	28577	5.42	1.0E-14	BF335227.1	EST_HUMAN	RC2-CT0432-310700-013-a09_1 CT0432 Homo sapiens cDNA
3868	16616	29255	1.67	1.0E-14	AA682894.1	EST_HUMAN	ae89c12 s1 Striatogene schizo brain S11 Homo sapiens cDNA
4440	17176	29802	1.91	1.0E-14	AW275852.1	EST_HUMAN	xq39h10.x1 NCI_CGAP_Lu28 Homo sapiens cDNA clone IMAGE:2753059 3'
5719	18511	31432	2.42	1.0E-14	AF126145.1	NT	Bos taurus xenobiotic/medium-chain fatty acid:CoA ligase form XL-III mRNA, nuclear mRNA encoding mitochondrial protein, complete cds
6576	25095	32351	11.5	1.0E-14	11437160	NT	Homo sapiens prolamin (mouse)-like 1 (PROML1), mRNA
6576	25095	32352	11.5	1.0E-14	11437160	NT	Homo sapiens prolamin (mouse)-like 1 (PROML1), mRNA
11818	15928	28576	3.05	1.0E-14	BF335227.1	EST_HUMAN	RC2-CT0432-310700-013-a09_1 CT0432 Homo sapiens cDNA
11818	15928	28577	3.05	1.0E-14	BF335227.1	EST_HUMAN	RC2-CT0432-310700-013-a09_1 CT0432 Homo sapiens cDNA
1570	14317	27002	2.06	9.0E-15	7427522	NT	Homo sapiens protein tyrosine phosphatase, receptor type, T (PTPRT), mRNA
2170	14899						Homo sapiens transcription factor (GHM enhancer 3, JM11 protein, JM5 protein, T54 protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synaptophysin genes, complete cds; and L-type calcium channel a)
7395	20074	33152	1.43	9.0E-15	AF196779.1	NT	
7915	20610	33740	4.51	9.0E-15	P21416	SWISSPROT	GAG POLYPEPTIDE [CONTAINS: CORE PROTEINS P15, P12, P30, P10]
12718	24891		1.08	9.0E-15	BE903559.1	EST_HUMAN	60167750F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3960156 5'
2814	13253		2.36	9.0E-15	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
7081	19771	32836	0.91	8.0E-15	BE261482.1	EST_HUMAN	601148632F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:3164023 5'
			1.14	7.0E-15	BF035327.1	EST_HUMAN	60145853F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3862086 5'
10334	22981						xn77d02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2700483 3' similar to contains THR.12 THR repetitive element;
973	13738	28403	3.07	7.0E-15	AW241958.1	EST_HUMAN	Homo sapiens Xq pseudautosomal region; segment 2/2
			8.64	6.0E-15	AJ271736.1	NT	

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5829	18618	31549	1.02	6.0E-15	X73482.1	NT	O.aries mRNA for hair keratin cysteine-rich protein
5829	18618	31550	1.02	6.0E-15	X73482.1	NT	O.aries mRNA for hair keratin cysteine-rich protein
407	13186	25834	6.63	5.0E-15	AL163208.2	NT	Homo sapiens chromosome 21 segment HS21G008
2764	15489	28212	1.38	5.0E-15	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RAR gene, and sodium phosphate transporter (NPT3) gene, complete cds
3461	16217		1.03	5.0E-15	AV268817.1	EST_HUMAN	UHLBW0-ajb-g-10-0-U1.s1 NCI_CGAP_Sub6 Homo sapiens cDNA clone IMAGE:2731219 3'
10574	23269		2.4	5.0E-15	AV730056.1	EST_HUMAN	AV730056 HTF Homo sapiens cDNA clone HTFAVE08 5'
418	12829	25442	2.85	4.0E-15	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
6567	19332	32339	0.76	4.0E-15	AB007970.1	NT	Homo sapiens mRNA, chromosome 1 specific transcript KIAA0501
10984	20392	33505	3.08	4.0E-15	AJ130894.1	NT	Homo sapiens mRNA for transcription factor
10994	20392	33506	3.08	4.0E-15	AJ130894.1	NT	Homo sapiens mRNA for transcription factor
4192	16833		7.06	3.0E-15	N89452.1	EST_HUMAN	LY1142F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone LY1142 5' similar to ANFCARDIODILATIN
4872	17599		0.79	3.0E-15	P92485	SWISSPROT	NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 5
6716	19631		1.33	3.0E-15	Q64625	SWISSPROT	GLUTATHIONE PEROXIDASE RY2D1 PRECURSOR (ODORANT-METABOLIZING PROTEIN RY2D1)
7179	19665	32937	2.9	3.0E-15	M27685.1	NT	Mus musculus ultra high sulfur keratin gene, complete cds
7179	19665	32938	2.9	3.0E-15	M27685.1	NT	Mus musculus ultra high sulfur keratin gene, complete cds
9825	22476		2.51	3.0E-15	AA807128.1	EST_HUMAN	oc36a07.s1 NCI_CGAP_G0B1 Homo sapiens cDNA clone IMAGE:1351764 3' similar to contains MER19.H
10694	23385	36825	2.47	3.0E-15	AB028898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
12310	25315		1.81	3.0E-15	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region, segment 1/2
12814	25056		1.35	3.0E-15	AW877214.1	EST_HUMAN	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
243	13052	25692	3.8	2.0E-15	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
359	13157	25798	3.99	2.0E-15	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
359	13157	25799	3.99	2.0E-15	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
3500	16256	28910	0.71	2.0E-15	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
3500	16256	28911	0.71	2.0E-15	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4049	16794	29423	1.08	2.0E-15	AW238499.1	EST_HUMAN	xp26h01.x1 NCI_CGAP_HN10 Homo sapiens cDNA clone IMAGE:2741521 3' similar to contains L1.13 L1 repetitive element ;
4580	17315		2.46	2.0E-15	AI806335.1	EST_HUMAN	wf07f06.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2349923 3' similar to TR:Q61043
6089	18867	31833	0.88	2.0E-15	BE562352.1	EST_HUMAN	Q61043 NINEIN ;
6089	18867	31834	0.88	2.0E-15	BE562352.1	EST_HUMAN	601344253F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3677268 5'
7014	19706		1.5	2.0E-15	AJ400877.1	NT	601344253F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3677268 5'
7171	19857	32929	2.82	2.0E-15	AA704195.1	EST_HUMAN	Homo sapiens ASCL3 gene, CEGP1 gene, C11orf14 gene, C11orf15 gene, C11orf16 gene and C11orf17 gene
7294	19977	33054	5.18	2.0E-15	W05084.1	EST_HUMAN	z177e03.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:400924 3'
8804	21496	34642	2.86	2.0E-15	D14547.1	NT	WP:F44F4.8 CE02227 TRANSPOSASE ;
8971	21661	34811	1	2.0E-15	AA397758.1	EST_HUMAN	Human DNA, SINE repetitive element
8971	21661	34812	1	2.0E-15	AA397758.1	EST_HUMAN	z177g08.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:728414 5'
9304	21971	35145	1.23	2.0E-15	AW378465.1	EST_HUMAN	z177g08.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:728414 5'
9304	21971	35146	1.23	2.0E-15	AW378465.1	EST_HUMAN	GM0-HT0244-201099-078-e12 HT0244 Homo sapiens cDNA
10742	23426		5.56	2.0E-15	AJ271735.1	NT	GM0-HT0244-201099-078-e12 HT0244 Homo sapiens cDNA
12451	25338		2.04	2.0E-15	U82828.1	NT	Homo sapiens Xq pseudautosomal region: segment 1/2
12653	16256	28910	3.34	2.0E-15	AF223391.1	NT	Homo sapiens ataxia telangiectasia (ATM) gene, complete cds
12653	16256	28911	3.34	2.0E-15	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
2777	15482		2.39	1.0E-15	AI889984.1	EST_HUMAN	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
3011	15777	28427	1.35	1.0E-15	BE043584.1	EST_HUMAN	bx26h05.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2270745 3' similar to TR:Q13539 Q13539 MARINER TRANSPOSASE ;
3139	15903	28548	1.29	1.0E-15	P08347	SWISSPROT	hk40e02.y1 NCI_CGAP_Ov34 Homo sapiens cDNA clone IMAGE:2899162 5'
5138	17656		0.97	1.0E-15	AW021431.1	EST_HUMAN	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
6279	19052	32030	1.74	1.0E-15	T95763.1	EST_HUMAN	d123e06.y1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:2484202 5'
6909	19647		2.12	1.0E-15	BE074217.1	EST_HUMAN	ye40e10.s1 Soares_fetal_liver_spleen_1NFLS Homo sapiens cDNA clone IMAGE:120234 3' similar to contains MERB repetitive element ;
8131	20825	33961	0.86	1.0E-15	AL163280.2	NT	QV3-B10569-270100-074-g05 BT0569 Homo sapiens cDNA
8319	21012	34149	4.56	1.0E-15	AI200976.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C080
8319	21012	34150	4.56	1.0E-15	AI200976.1	EST_HUMAN	qf68h06.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1755227 3'
8937	21628	34170	0.67	1.0E-15	AL163207.2	NT	qf68h06.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1755227 3'
							Homo sapiens chromosome 21 segment HS21C007

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8940	21631	34774	1.78	1.0E-15	4507208	NT	Homo sapiens spermidine synthase (SRM) mRNA
9146	21877	35042	0.87	1.0E-15	Q39575	SWISSPROT	DYNEIN GAMMA CHAIN, FLAGELLAR OUTER ARM
9532	22185	35370	0.94	1.0E-15	AA864653.1	EST_HUMAN	ch37c03.s1 NCI_CGAP_Kid6 Homo sapiens cDNA clone IMAGE:1459972 3' similar to contains L1.13 L1
10720	23409	36851	3.6	1.0E-15	AF044083.1	NT	repetitive element:
12722	25148	30896	4.72	1.0E-15	AI783944.1	EST_HUMAN	Homo sapiens major histocompatibility locus class III region
4469	17204	29830	0.98	9.0E-16	4503168	NT	element.
10915	23595	36841	2.04	9.0E-16	F08688.1	EST_HUMAN	Homo sapiens cut (Drosophila)-like 1 (COAT displacement protein) (CUTL1) mRNA
11696	24291	37615	1.46	9.0E-16	AI244341.1	EST_HUMAN	q176a02.x1 NCI_CGAP_Kid3 Homo sapiens cDNA clone c-23705
11696	24291	37616	1.46	9.0E-16	AI244341.1	EST_HUMAN	MER10 repetitive element:
5615	18411	31324	0.71	7.0E-16	4885120	EST_HUMAN	q176a02.x1 NCI_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1865354 3' similar to contains MER10.13
7241	19926	33001	1.49	7.0E-16	O88807	SWISSPROT	MER10 repetitive element:
7241	19926	33002	1.49	7.0E-16	O88807	SWISSPROT	Homo sapiens chemokine (C-C motif) receptor 8 (CCR8) mRNA
12675	25237		1.98	7.0E-16	T94149.1	EST_HUMAN	PROTEIN-ARGININE DEIMINASE TYPE IV (PEPTIDYLARGININE DEIMINASE IV) (PAD-R4)
2137	14857		8.38	6.0E-16	AW972611.1	EST_HUMAN	PROTEIN-ARGININE DEIMINASE TYPE IV (PEPTIDYLARGININE DEIMINASE IV) (PAD-R4)
1476	14223	26909	1.08	5.0E-16	AJ251154.1	NT	ye28c12.11 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:119082 5'
2687	15396	28134	2.17	5.0E-16	AA992176.1	EST_HUMAN	EST384702 IMAGE sequences, MAGL Homo sapiens cDNA
9854	22802	35806	0.54	5.0E-16	AL163246.2	NT	Mus musculus olfactory receptor cluster: OR37A, OR37B, OR37C, OR37E genes and OR37D pseudogene
11504	24105	37418	3.6	5.0E-16	BF217398.1	EST_HUMAN	contains element L1 repetitive element:
12737	25018		14.19	5.0E-16	11418127	NT	Homo sapiens chromosome 21 segment HS21C046
2233	14961		1.81	4.0E-16	AB001523.1	NT	601885734F1 NIH_MGC 57 Homo sapiens cDNA clone IMAGE:4104129 5'
2378	15100	27839	1.77	4.0E-16	AW797168.1	EST_HUMAN	Homo sapiens GTP binding protein 1 (GTPBP1), mRNA
2378	15100	27840	1.77	4.0E-16	AW797168.1	EST_HUMAN	Homo sapiens gene for TMEM1 and PWP2, complete and partial cds
3450	16208	28856	3.58	4.0E-16	Q16863	SWISSPROT	QV1-UM0036-200300-115-g02 UM0036 Homo sapiens cDNA
4121	16863	29489	5.02	4.0E-16	BE083875.1	EST_HUMAN	QV1-UM0036-200300-115-g02 UM0036 Homo sapiens cDNA
4121	16863	29490	5.02	4.0E-16	BE083875.1	EST_HUMAN	MYELIN-OLIGODENDROCYTE GLYCOPROTEIN PRECURSOR
7612	20278	33386	46.62	4.0E-16	AL163284.2	NT	PM4-BT0650-010400-002-g09 BT0650 Homo sapiens cDNA
							PM4-BT0650-010400-002-g09 BT0650 Homo sapiens cDNA
							Homo sapiens chromosome 21 segment HS21C084

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Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9195	21865	35029	1.04	4.0E-16	11423191	NT	Homo sapiens hypothetical protein FLJ10024 (FLJ10024), mRNA
11182	23847	37133	1.51	4.0E-16	AV730030.1	EST_HUMAN	AV730030 HTF Homo sapiens cDNA clone HTFAWA03 5'
11851	24435	37778	1.44	4.0E-16	Q62832	SWISSPROT	FOLLISTATIN-RELATED PROTEIN PRECURSOR
12014	24847		2.04	4.0E-16	P08548	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
12109	24805	31087	2.51	4.0E-16	6912459	NT	Homo sapiens Grb2-associated binder 2 (KIAA0571), mRNA
130	12845	25589	2.03	3.0E-16	AW022862.1	EST_HUMAN	dlf45c01.yt Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:2486376 5'
130	12945	25589	2.03	3.0E-16	AW022862.1	EST_HUMAN	dlf45c01.yt Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:2486376 5'
453	13239		1.5	3.0E-16	AL048445.1	EST_HUMAN	DKFZp434P037.1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434P037 5'
463	13248		1.5	3.0E-16	AF135446.1	NT	Homo sapiens TSX (TSX) pseudogene, exon 5
1435	14182	26867	1.38	3.0E-16	Q28983	SWISSPROT	ZONADHESIN PRECURSOR
2875	15741	28388	3.76	3.0E-16	P03200	SWISSPROT	ENVELOPE GLYCOPROTEIN GP340 (MEMBRANE ANTIGEN) (MA) [CONTAINS: GLYCOPROTEIN GP220]
3913	16663	28304	19.63	3.0E-16	T08169.1	EST_HUMAN	EST06060 Infant Brain, Bonto Soares Homo sapiens cDNA clone HIBBA13 5' end
3939	16689		0.95	3.0E-16	U03887.1	NT	Human BXP20 gene
5196	18004		0.98	3.0E-16	AA077225.1	EST_HUMAN	7B10F02 Chromosome 7 Fetal Brain cDNA Library Homo sapiens cDNA clone 7B10F02
5529	18327	31230	1.78	3.0E-16	AF003529.1	NT	Homo sapiens glypican 3 (GPC3) gene, partial cds and flanking repeat regions
8556	21248	34387	4.28	3.0E-16	A002836.1	EST_HUMAN	am98h05.s1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:1084185 3' similar to contains THR.b2 THR repetitive element
9790	22441		0.89	3.0E-16	BF690617.1	EST_HUMAN	602246538FT NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4332032 5'
10019	22687	35883	5.57	3.0E-16	L78810.1	NT	Homo sapiens ADP/ATP carrier protein (ANT-2) gene, complete cds
951	13717		1.2	2.0E-16	AL163279.2	NT	Homo sapiens chromosome 21 segment HS21C079
2385	15108		0.91	2.0E-16	AA621761.1	EST_HUMAN	af06d04.s1 Soares testis NHT Homo sapiens cDNA clone IMAGE:1030855 3'
2694	16403		1.06	2.0E-16	J03061.1	NT	Human SSAN-related endogenous retroviral LTR-like element
4157	16897	29526	1.16	2.0E-16	X89211.1	NT	H. sapiens DNA for endogenous retroviral LTR-like element
4447	17183	29807	0.96	2.0E-16	A1208733.1	EST_HUMAN	q956f03.x1 Soares testis NHT Homo sapiens cDNA clone IMAGE:1839197 3' similar to contains MER29.13
5104	17822	30439	0.78	2.0E-16	BE081178.1	EST_HUMAN	MER29 repetitive element
6642	19404	32419	0.99	2.0E-16	Q31125	SWISSPROT	RC3-BT0048-131199-003-H12 BT0046 Homo sapiens cDNA HISTIDINE-RICH PROTEIN KE4
7615	20281	33369	0.75	2.0E-16	A1470723.1	EST_HUMAN	lji18e11.x1 NCI CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2141708 3' similar to contains element MER33 repetitive element
7887	20562	33699	2.14	2.0E-16	A1732637.1	EST_HUMAN	nz47f06.x5 NCI CGAP_P12 Homo sapiens cDNA clone IMAGE:1280947 similar to TR:O54849 O54849
8058	20752	33883	0.57	2.0E-16	BE686026.1	EST_HUMAN	HYPOTHETICAL 42.9 KD PROTEIN. [2] TR:O08905 contains MER7.11 MER7 repetitive element
							7f82109.x1 NCI CGAP_P28 Homo sapiens cDNA clone IMAGE:3303521 3'

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8058	20752	33884	0.57	2.0E-16	BE88028.1	EST_HUMAN	782109.x1 NCL CGAP_P28 Homo sapiens cDNA clone IMAGE:3303521 3'
8425	21118	34256	0.81	2.0E-16	AW877214.1	EST_HUMAN	CM4-PT0034-180200-506-a01 PT0034 Homo sapiens cDNA
8425	21118	34257	0.81	2.0E-16	AW877214.1	EST_HUMAN	CM4-PT0034-180200-506-a01 PT0034 Homo sapiens cDNA
180	12892	25630	1.84	1.0E-16	AF200719.1	NT	Homo sapiens pituitary tumor transforming gene protein (PTTG) gene, complete cds
373	13198						af39g11.s1 Soares_tbal_fetus_Nb2HF8_gw Homo sapiens cDNA clone IMAGE:1034084 3' similar to contains OFR 12 OFR repetitive element;
1963	14699	27414	2.37	1.0E-16	AA628592.1	EST_HUMAN	QV0-BN0148-070700-283-a10 BN0148 Homo sapiens cDNA
5635	18430	31343	0.75	1.0E-16	BF327942.1	EST_HUMAN	Homo sapiens SNCA isoform (SNCA) gene, complete cds, alternatively spliced
6341	19111		27.85	1.0E-16	AF163864.1	NT	Homo sapiens CCR8 chemokine receptor (CMKBR8) gene, complete cds
6479	19246	32246	3.39	1.0E-16	Q02779	SWISSPROT	MITOGEN-ACTIVATED PROTEIN KINASE KINASE 10 (MIXED LINEAGE KINASE 2) (PROTEIN KINASE MST)
7453	19111		7.15	1.0E-16	U45983.1	NT	Homo sapiens CCR8 chemokine receptor (CMKBR8) gene, complete cds
9183	21863	35018	1.07	1.0E-16	AW875651.1	EST_HUMAN	QV2-PT0012-040400-124-a05 PT0012 Homo sapiens cDNA
3722	16475	29112	2.11	9.0E-17	AW900048.1	EST_HUMAN	CM1-NN1003-200300-153-a01 NN1003 Homo sapiens cDNA
6624	19386		2.2	9.0E-17	A1322984.1	EST_HUMAN	tg22x11.x1 NCL CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2108524 3' similar to contains MER28.12 MER28 repetitive element;
8007	20702		4.75	9.0E-17	AW150257.1	EST_HUMAN	xg49g12.x1 NCL CGAP_U11 Homo sapiens cDNA clone IMAGE:2630950 3' similar to contains OFR 12 OFR repetitive element;
10124	22772		2.47	9.0E-17	AF200719.1	NT	Homo sapiens pituitary tumor transforming gene protein (PTTG) gene, complete cds
897	13757		1.77	8.0E-17	AW880701.1	EST_HUMAN	QV0-OT0032-080300-155-d01 OT0032 Homo sapiens cDNA
3872	16622		0.87	8.0E-17	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
5496	25069	31193	3.7	8.0E-17	BE172081.1	EST_HUMAN	MR0-HT0559-060300-003-a04 HT0559 Homo sapiens cDNA
7175	19861		1.94	8.0E-17	AV730759.1	EST_HUMAN	AV730759 HTF Homo sapiens cDNA clone HTFAQB07 5'
1441	14188		3.44	7.0E-17	6753097	NT	Mus musculus apolipoprotein B editing complex 2 (ApoBec2), mRNA
5240	18046		3.3	7.0E-17	AF216650.1	NT	Homo sapiens putative MTAP (MTAP) mRNA, partial cds, alternatively spliced
6588	19351	32365	8.05	7.0E-17	AF229843.1	NT	Mus musculus WNT-2 gene, partial cds; putative ankyrin-related protein and cystic fibrosis transmembrane conductance regulator (CFTR) genes, section 1 of 2 of the complete cds; and unknown gene
198	13011	25653	8	6.0E-17	AW983880.1	EST_HUMAN	RC1-HN0003-220300-021-b04 HN0003 Homo sapiens cDNA
6221	18995	31971	1.64	6.0E-17	AW682772.1	EST_HUMAN	hi81d04.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2978695 3' similar to contains L1.12 L1 repetitive element;
10190	22838	35053	0.46	6.0E-17	P20138	SWISSPROT	MYELOID CELL SURFACE ANTIGEN CD33 PRECURSOR (GP87)
412	12823	25438	2.97	5.0E-17	TF64110.1	EST_HUMAN	yc05h08.r1 Stralagene lung (#637210) Homo sapiens cDNA clone IMAGE:79839 5'
7486	20158	33250	2.09	5.0E-17	T81043.1	EST_HUMAN	yd28b04.r1 Soares fetal liver spleen (NFL-S Homo sapiens cDNA clone IMAGE:109327 5'

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3626	16379	28020	0.89	4.0E-17	AA643697.1	EST_HUMAN	nl96a05.s1 NCI_CGAP_Co10 Homo sapiens cDNA clone IMAGE:1058528 3'
9262	22016	35184	1.07	4.0E-17	AW129165.1	EST_HUMAN	x20604.x1 NCI_CGAP_Kld8 Homo sapiens cDNA clone IMAGE:2618622 3' similar to contains Alu repetitive element; contains MER19.b1 MER19 repetitive element;
11475	24076	37386	2.64	4.0E-17	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
12027	24555		1.75	4.0E-17	AI073546.1	EST_HUMAN	ov45a04.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1640286 3' similar to TR:Q16530
1477	14224		1.14	3.0E-17	D14547.1	NT	Q16530 PMS3 mRNA ; contains MER10.12 MER10 repetitive element ;
2091	14822	27554	1.85	3.0E-17	AW119123.1	EST_HUMAN	Human DNA, SINE repetitive element
3188	16951		1.18	3.0E-17	P35410	SWISSPROT	xd88c09.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2604784 3'
3633	16386	28026	1.34	3.0E-17	BE326522.1	EST_HUMAN	MAS-RELATED G PROTEIN-COUPLED RECEPTOR MRG
3633	16386	29027	1.34	3.0E-17	BE326522.1	EST_HUMAN	hw05b04.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3181989 3'
4970	17695		1.89	3.0E-17	BF511266.1	EST_HUMAN	hw05b04.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3181989 3'
8168	20860	33992	5.16	3.0E-17	N68451.1	EST_HUMAN	UHH-B14-eqj-c-06-0-UJ.s1 NCI_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3085043 3'
9601	22254	35439	6.58	3.0E-17	AB026898.1	NT	z14b02.s1 Soares_fetal_liver_spleen_1NFLS Homo sapiens cDNA clone IMAGE:292491 3' similar to contains PTR5.13 PTR5 repetitive element ;
10279	22927	36140	0.64	3.0E-17	BF327012.1	EST_HUMAN	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
10279	22927	36141	0.64	3.0E-17	BF327012.1	EST_HUMAN	QV3-BN0047-270700-283-at12 BN0047 Homo sapiens cDNA
11894	24532		3.65	3.0E-17	11417966	NT	QV3-BN0047-270700-283-at12 BN0047 Homo sapiens cDNA
12764	25023		1.44	3.0E-17	AV720204.1	EST_HUMAN	Homo sapiens SEC14 (S. cerevisiae)-like 2 (SEC14L2), mRNA
343	13144	25782	3	2.0E-17	AI270080.1	EST_HUMAN	AV720204 GLC Homo sapiens cDNA clone GLCDF08 5'
344	13144	25782	2.17	2.0E-17	AI270080.1	EST_HUMAN	q163a06.x1 NCI_CGAP_Eso2 Homo sapiens cDNA clone IMAGE:1959922 3' similar to contains Alu repetitive element;
967	13733		1.84	2.0E-17	AA722932.1	EST_HUMAN	q163a06.x1 NCI_CGAP_Eso2 Homo sapiens cDNA clone IMAGE:1959922 3' similar to contains Alu repetitive element;
2448	15167	27904	2.21	2.0E-17	Q28993	SWISSPROT	z981404.s1 Soares_fetal_heart_NBHH19W Homo sapiens cDNA clone IMAGE:399751 3'
2448	15167	27905	2.21	2.0E-17	Q28993	SWISSPROT	ZONADHESIN PRECURSOR
2930	15996	28343	6.64	2.0E-17	P12036	SWISSPROT	ZONADHESIN PRECURSOR
5282	18087	30745	1.88	2.0E-17	M27685.1	NT	NEUROFILAMENT TRIPLET H PROTEIN (200 KDA NEUROFILAMENT PROTEIN) (NEUROFILAMENT HEAVY POLYPEPTIDE) (NF-H)
5282	18087	30746	1.88	2.0E-17	M27685.1	NT	Mus musculus ultra high sulfur keratin gene, complete cds
6171	18948		2.04	2.0E-17	AF055096.1	NT	Mus musculus ultra high sulfur keratin gene, complete cds
6398	19167		1.16	2.0E-17	AL134881.1	EST_HUMAN	Homo sapiens MHC class 1 region
7982	20677	33802	1.12	2.0E-17	Q95156	SWISSPROT	DKFZp762j0610_r1 762 (synonym: hme2) Homo sapiens cDNA clone DKFZp762j0610 5'
							OLFACTORY RECEPTOR-LIKE PROTEIN OLF3

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8366	21049	34188	1	2.0E-17	AA300640.1	EST_HUMAN	EST13504 Testis tumor Homo sapiens cDNA 5' end similar to glycogenin
9769	22420	35628	2.81	2.0E-17	BE298988.1	EST_HUMAN	6009448907.1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2960615 5'
9804	22455	35657	3.22	2.0E-17	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
9804	22455	35658	3.22	2.0E-17	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
10159	22807	36025	4.82	2.0E-17	D13391.1	NT	Human CYP19 gene for aromatase cytochrome P-450, promoter region (containing two cis-acting transcriptional regulatory elements)
10278	22826	36138	0.73	2.0E-17	P98063	SWISSPROT	BONE MORPHOGENETIC PROTEIN 1 PRECURSOR (BMP-1)
10278	22826	36139	0.73	2.0E-17	P98063	SWISSPROT	BONE MORPHOGENETIC PROTEIN 1 PRECURSOR (BMP-1)
10307	22954	36169	0.49	2.0E-17	A1798902.1	EST_HUMAN	we94b04.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2348719 3'
10307	22954	36170	0.49	2.0E-17	A1798902.1	EST_HUMAN	we94b04.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2348719 3'
733	13507	26164	3.86	1.0E-17	P08183	SWISSPROT	MULTIDRUG RESISTANCE PROTEIN 1 (P-GLYCOPROTEIN 1)
1703	14446		1.26	1.0E-17	AJ271736.1	NT	Homo sapiens Xq pseudautosomal region; segment 2/2
1761	14503	27204	2.73	1.0E-17	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C007
2109	14840	27571	2.35	1.0E-17	P02461	SWISSPROT	COLLAGEN ALPHA 1(III) CHAIN PRECURSOR
2335	15059	27795	2.06	1.0E-17	U79410.1	NT	Homo sapiens thrombospondin 2 (THBS2) gene, promoter region and exons 1A and 1B
3554	18309		1.3	1.0E-17	AF224669.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3
4116	18858		7.37	1.0E-17	R09942.1	EST_HUMAN	(UBE2D3) genes, complete cds
6366	19136		0.69	1.0E-17	AW468488.1	EST_HUMAN	he38a05.x1 NCI_CGAP_CML1 Homo sapiens cDNA clone IMAGE:128388 5'
6555	19320	32327	2.04	1.0E-17	A1185642.1	EST_HUMAN	repetitive element: contains LTR8.1 LTR8 repetitive element;
6555	19320	32328	2.04	1.0E-17	A1185642.1	EST_HUMAN	qe65b05.x1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:1743825 3'
6999	19682	32730	0.93	1.0E-17	Q16831	SWISSPROT	qe65b05.x1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:1743825 3'
8490	21182	34324	1.33	1.0E-17	BE062744.1	EST_HUMAN	URIDINE PHOSPHORYLASE (UDRPASE)
9907	22556	35751	0.88	1.0E-17	AW995338.1	EST_HUMAN	QV0-BT0263-101299-072-407 BT0263 Homo sapiens cDNA
11394	24000	37304	2.09	1.0E-17	Q28824	SWISSPROT	QV3-BN0046-220300-129-c10 BN0046 Homo sapiens cDNA
11792	24325	37649	2.47	1.0E-17	AA453647.1	EST_HUMAN	MYOSIN LIGHT CHAIN KINASE, SMOOTH MUSCLE (MLCK) [CONTAINS: TELOKIN]
2474	15182	27632	0.95	9.0E-18	AA174078.1	EST_HUMAN	z448f05.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:795489 3' similar to TR:G1263081
9398	22080		3.31	9.0E-18	A172167.1	EST_HUMAN	G1263081 MARINER TRANSPOSASE;
3766	16518	29156	1.52	8.0E-18		NT	zp18g12.s1 Striatogene fetal retina 937202 Homo sapiens cDNA clone IMAGE:2148389 3'
					4758977	NT	q66a03.x1 Soares_NSF_F8_gw_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2148389 3'
						NT	Homo sapiens protein tyrosine phosphatase, non-receptor type substrate 1 (PTPNS1) mRNA
339	13140	25776	16.92	7.0E-18	AW316976.1	EST_HUMAN	xx10b04.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2837071 3' similar to gb:L20868 60S

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Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
339	13140	25777	16.92	7.0E-18	AW316976.1	EST_HUMAN	xx10b04.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2837071 3' similar to gb.L20868 60S
7343	20024	33100	1.33	7.0E-18	AW887542.1	EST_HUMAN	RIBOSOMAL PROTEIN L4 (HUMAN);
12492	13140	25778	3.41	7.0E-18	AW316976.1	EST_HUMAN	xx10b04.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2837071 3' similar to gb.L20868 60S
12492	13140	25777	3.41	7.0E-18	AW316976.1	EST_HUMAN	RIBOSOMAL PROTEIN L4 (HUMAN);
3289	19050	28698	1	6.0E-18	X71791.2	NT	RIBOSOMAL PROTEIN L4 (HUMAN);
4698	17432		3.02	6.0E-18	P52181	SWISSPROT	Rattus norvegicus partial Gdn/Pn-1 gene for glia-derived nexin/protease nexin I, enhancer region
8148	20842		2.84	6.0E-18	11428155	NT	PROTEIN-GLUTAMINE GAMMA-GLUTAMYLTRANSFERASE (TISSUE TRANSGLUTAMINASE)
8248	20940	34077	0.72	6.0E-18	AL163210.2	NT	Homo sapiens similar to high-mobility group (nucleosome chromosomal) protein 4 (H. sapiens) (LOC63446), mRNA
11079	23749	37024	1.61	6.0E-18	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C010
11300	23980	37260	1.74	6.0E-18	X87344.1	NT	Homo sapiens chromosome 21 segment HS21C046
12241	24692	31076	3.29	6.0E-18	U87928.1	NT	H. sapiens DMA, DMB, HLA-Z1, IPP2, LMP2, TAP1, LMP7, TAP2, DOB, DQB2 and RING8, 9, 13 and 14 genes
1125	13881	26541	21.7	5.0E-18	AI280214.1	EST_HUMAN	Human aconitase hydratase (ACO2) gene, exon 4
5047	17766	30384	0.98	5.0E-18	D61517.1	EST_HUMAN	qm65g11.x1 Soares_placenta_86c9weeks_2NbhHP89W Homo sapiens cDNA clone IMAGE:1893668 3' similar to contains Alu repetitive element
5181	17899	30622	1.2	5.0E-18	AF087913.1	NT	HUM411F05B Clontech human fetal brain polyA+ mRNA (#6535) Homo sapiens cDNA clone GEN-411F05 5'
8820	21312	34454	6.25	5.0E-18	BE143312.1	EST_HUMAN	Human endogenous retrovirus HERV-P-T47D
10899	23579	36828	3.47	5.0E-18	10242378	NT	MR0-HT0161-221099-002-c06 HT0161 Homo sapiens cDNA
10899	23579	36829	3.47	5.0E-18	10242378	NT	Homo sapiens lymphocyte activation-associated protein (LOC51088), mRNA
12368	24770		3.4	5.0E-18	AW867182.1	EST_HUMAN	Homo sapiens lymphocyte activation-associated protein (LOC51088), mRNA
12695	24978		4.16	5.0E-18	AV650547.1	EST_HUMAN	MR1-SN0035-060400-001-g11 SN0035 Homo sapiens cDNA
121	12539	25580	1.37	4.0E-18	BE044076.1	EST_HUMAN	AV650547 GLC Homo sapiens cDNA clone GLCCGA02 3'
121	12639	25581	1.37	4.0E-18	BE044076.1	EST_HUMAN	h036h04.x1 NCI_CGAP_U11 Homo sapiens cDNA clone IMAGE:3039511 3' similar to contains MER29.b3
1711	14454	27153	1.19	4.0E-18	AA621814.1	EST_HUMAN	h036h04.x1 NCI_CGAP_U11 Homo sapiens cDNA clone IMAGE:3039511 3' similar to contains MER29.b3
1882	14619		1.12	4.0E-18	A1738592.1	EST_HUMAN	h036h04.x1 NCI_CGAP_U11 Homo sapiens cDNA clone IMAGE:3039511 3' similar to contains MER29.b3
							KERATIN, TYPE I CYTOSKELETAL 18 (HUMAN);
							w033h08.x1 NCI_CGAP_C016 Homo sapiens cDNA clone IMAGE:2392095 3'

Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2198	14927	27662	1.33	4.0E-18	Q06430	SWISSPROT	N-ACETYLGLUCOSAMINIDE BETA-1,6-N-ACETYLGLUCOSAMINYLTRANSFERASE (N-ACETYLGLUCOSAMINYLTRANSFERASE) (I-BRANCHING ENZYME) (IGNT)
2198	14927	27663	1.33	4.0E-18	Q06430	SWISSPROT	N-ACETYLGLUCOSAMINIDE BETA-1,6-N-ACETYLGLUCOSAMINYLTRANSFERASE (N-ACETYLGLUCOSAMINYLTRANSFERASE) (I-BRANCHING ENZYME) (IGNT)
3772	16524	29162	0.88	4.0E-18	A1581586.1	EST_HUMAN	ar93b06.x1 Barstead cdon HP1RB7 Homo sapiens cDNA clone IMAGE:2173139 3' similar to contains Alu repetitive element;
5279	18084	30740	2.24	4.0E-18	A1017565.1	EST_HUMAN	ou23a06.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1627138 3'
5279	18084	30741	2.24	4.0E-18	A1017565.1	EST_HUMAN	ou23a06.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1627138 3'
7746	20441		0.63	4.0E-18	AA746811.1	EST_HUMAN	nv64a08.s1 NCI_CGAP_Alv1 Homo sapiens cDNA clone IMAGE:1266998 similar to contains L1.12 L1 repetitive element;
10927	23607	36858	8.76	4.0E-18	AA371807.1	EST_HUMAN	EST83633 Pituitary gland, subcloned (prolactin/growth hormone) II Homo sapiens cDNA 5' end similar to EST containing O family repeat
829	13598	26270	1.68	3.0E-18	AA814196.1	EST_HUMAN	gb23h11.s1 NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1324581 3' similar to SW:RSS_HUMAN
909	13678	26340	3.47	3.0E-18	BE086634.1	EST_HUMAN	P46782 40S RIBOSOMAL PROTEIN S5.
3931	16681	29322	1.47	3.0E-18	AL163247.2	NT	CMO-BT0690-210300-298-g07 BT0690 Homo sapiens cDNA
6730	19584	32696	5.64	3.0E-18	BE001671.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C047
10844	23526	36769	1.61	3.0E-18	BF218650.1	EST_HUMAN	PMO-BN0081-100300-001-b08 BN0081 Homo sapiens cDNA
12497	24852		6.14	3.0E-18	AW022015.1	EST_HUMAN	d331h12.y1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:4103652 5'
244	13053	26693	4.42	2.0E-18	AW836820.1	EST_HUMAN	QV1-L1T0036-150200-070-e07 L1T0036 Homo sapiens cDNA
1130	13886		62.93	2.0E-18	BE256097.1	EST_HUMAN	601114352F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3355044 5'
5326	18129		3.19	2.0E-18	AA868610.1	EST_HUMAN	ak53a07.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1409852 3' similar to TR:O14577
5419	18218	30927	3.68	2.0E-18	D14547.1	NT	O14577 BAC CLONE RG114A06 FROM 7Q31, COMPLETE SEQUENCE.
5419	18218	30928	3.68	2.0E-18	D14547.1	NT	Human DNA, SINE repetitive element
5768	18579		1.68	2.0E-18	BF347229.1	EST_HUMAN	602021164F1 NCI_CGAP_Bm87 Homo sapiens cDNA clone IMAGE:4156670 5'
6073	18852	31817	0.77	2.0E-18	X60459.1	NT	Human IFNAR gene for interferon alpha/beta receptor
6073	18852	31818	0.77	2.0E-18	X60459.1	NT	Human IFNAR gene for interferon alpha/beta receptor
6185	18962	31935	1.04	2.0E-18	BF352940.1	EST_HUMAN	IL3-HT0619-220700-222-C12 HT0619 Homo sapiens cDNA
6226	19000	31977	5.18	2.0E-18	AW665853.1	EST_HUMAN	h194g01.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2879984 3' similar to contains
7336	20018	33096	0.81	2.0E-18	AA457619.1	EST_HUMAN	aa89d11.r1 Stralagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:838485 5' similar to
8047	20741	33873	0.47	2.0E-18	BE439524.1	EST_HUMAN	TR:G61634 G61634 POLYPEPTIDE PR77 ;
							HTM1-160F1 HTM1 Homo sapiens cDNA

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Single Exon Probes Expressed In Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9947	22595	35798	1.66	2.0E-18	AW151673.1	EST_HUMAN	x167e10.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2623146 3' similar to contains MER10.12
9947	22595	35799	1.66	2.0E-18	AW151673.1	EST_HUMAN	x167e10.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2623146 3' similar to contains MER10.12
10894	23574	36824	2	2.0E-18	AW470791.1	EST_HUMAN	hs33d06.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2875489 3' similar to contains THR.b3
11736	24329	37653	3.91	2.0E-18	AW151299.1	EST_HUMAN	xg47d09.x1 NCI_CGAP_U11 Homo sapiens cDNA clone IMAGE:2630728 3' similar to contains MER8.b2
12174	13886		1.45	2.0E-18	BE256097.1	EST_HUMAN	MER8 repetitive element;
4382	17119		1.02	1.0E-18	T95406.1	EST_HUMAN	601114352F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3355044 5'
5271	18077	30707	3.63	1.0E-18	AV653405.1	EST_HUMAN	ye43g05.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:120536 5' similar to contains L1 repetitive element;
5483	18282	31180	2.94	1.0E-18	D00099.1	NT	AV653405 GLC Homo sapiens cDNA clone GLCDE11 3'
5483	18282	31181	2.94	1.0E-18	D00099.1	NT	Homo sapiens mRNA for Na,K-ATPase alpha-subunit, complete cds
6363	19133	32126	1.53	1.0E-18	AL163280.2	NT	Homo sapiens mRNA for Na,K-ATPase alpha-subunit, complete cds
8341	21034	34171	1.43	1.0E-18	A1148288.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C080
9799	22450	35653	4.22	1.0E-18	U91328.1	NT	oz69d09.x1 Soares senescent fibroblasts_NbHSF Homo sapiens cDNA clone IMAGE:1680593 3' similar to contains L1.t1 L1 repetitive element;
12130	24621	31092	4.23	1.0E-18	AF003529.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RqRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
532	13316	25952	5.34	9.0E-19	AA281861.1	EST_HUMAN	Homo sapiens glycican 3 (GPC3) gene, partial cds and flanking repeat regions
533	13316	25952	3.24	9.0E-19	AA281861.1	EST_HUMAN	z111d06.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:712811 5' similar to contains MER19.12
7747	20443		4.47	9.0E-19	F08688.1	EST_HUMAN	MER19 repetitive element;
8568	21280	34419	2.54	9.0E-19	AL163203.2	NT	HSC23F051 normalized infant brain cDNA Homo sapiens cDNA clone c-23f05
8568	21280	34420	2.54	9.0E-19	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
11072	23742	37016	4.82	9.0E-19	AB032669.1	NT	Homo sapiens chromosome 21 segment HS21C003
11901	13316	25952	1.88	9.0E-19	AA281861.1	EST_HUMAN	Homo sapiens mRNA for KIAA1143 protein, partial cds
1026	13786		1.25	8.0E-19	AW974902.1	EST_HUMAN	z111d06.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:712811 5' similar to contains MER19.12
4372	17110		1.04	8.0E-19	P08548	SWISSPROT	MER19 repetitive element;
8048	20742	33874	0.92	8.0E-19	BE186936.1	EST_HUMAN	EST387007 IMAGE resequences, MAGN Homo sapiens cDNA
							LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
							MRO-HT0404-210200-007-g06 HT0404 Homo sapiens cDNA

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Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2242	14970	27708	1.51	7.0E-19	4758139	NT	Homo sapiens DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 6 (RNA helicase, 54kD) (DDX6) mRNA
6364	19134	32129	2.34	7.0E-19	AF092090.1	NT	Rattus norvegicus qp151 mRNA, partial cds
7189	19885	32959	0.8	7.0E-19	P28444	SWISSPROT	BETA CRYSTALLIN A2
8911	22560	35756	0.51	7.0E-19	AI344951.1	EST_HUMAN	U01c08.x1 NCI_CGAP_Lu26 Homo sapiens cDNA clone IMAGE:2052302 3'
12036	25397		2.05	7.0E-19	AA705684.1	EST_HUMAN	260501.st Soares_fetal_liver_spleen_TNFS_S1 Homo sapiens cDNA clone IMAGE:435145 3'
3761	16513		1.34	6.0E-19	AW852830.1	EST_HUMAN	PMD-CT0248-131099-001-g01 CT0248 Homo sapiens cDNA
4430	17166	29796	1.36	6.0E-19	P34986	SWISSPROT	OLFACTORY RECEPTOR 6 (M60)
4747	17479		1.3	6.0E-19	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region, segment 1/2
4967	17692	30301	1.04	6.0E-19	AL120817.1	EST_HUMAN	DKFZ762F192.1 762 (synonym: hmel2) Homo sapiens cDNA clone DKFZ762F192 5'
5767	18558	31485	5.36	5.0E-19	Q00193	SWISSPROT	ZONA PELLUCIDA SPERM-BINDING PROTEIN B PRECURSOR (ZONA PELLUCIDA GLYCOPROTEIN ZP-X) (RC55)
10324	22971	36191	1.03	5.0E-19	AJ297699.1	NT	Homo sapiens partial IL-12RB1 gene for IL-12 receptor beta1 chain, exon 14
11525	24125	37431	7.45	5.0E-19	AW183725.1	EST_HUMAN	X87b02.X1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2684171 3' similar to contains element MSR1 repetitive element ;
541	13324	25956	1.86	4.0E-19	AB007970.1	NT	Homo sapiens mRNA, chromosome 1 specific transcript KIAA0501
2689	15398	28136	1.02	4.0E-19	BF607362.1	EST_HUMAN	602130910F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4287674 5'
5311	18115	30773	0.97	4.0E-19	AF224669.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D) genes, complete cds
3833	16594	29219	1.04	3.0E-19	Q26997	SWISSPROT	BETA-2 ADRENERGIC RECEPTOR
3833	16594	29220	1.04	3.0E-19	Q26997	SWISSPROT	BETA-2 ADRENERGIC RECEPTOR
4253	16994	29622	0.89	3.0E-19	O43900	SWISSPROT	LIM-ONLY PROTEIN 6 (TRIPLE LIM DOMAIN PROTEIN 6)
4253	16994	29623	0.89	3.0E-19	O43900	SWISSPROT	LIM-ONLY PROTEIN 6 (TRIPLE LIM DOMAIN PROTEIN 6)
4413	17150	29777	1.12	3.0E-19	AV708136.1	EST_HUMAN	AV708136 ADC Homo sapiens cDNA clone ADCANA11 5'
5198	18006		0.64	3.0E-19	AF223467.1	NT	Homo sapiens NPD008 protein (NPD008) mRNA, complete cds
7283	19968		2.79	3.0E-19	11432214	NT	Homo sapiens similar to aldo-keto reductase family 1, member B11 (aldose reductase-like) (H. sapiens) (LOC63222), mRNA
9359	20430	33548	1.15	3.0E-19	X99885.1	NT	M.musculus mRNA for TPOR33 protein
12264	24709		23.34	3.0E-19	AF165520.1	NT	Homo sapiens phorbol 1 protein (PBI) mRNA, complete cds
2565	15279	28017	21.33	2.0E-19	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
4411	17148		1.03	2.0E-19	AI311783.1	EST_HUMAN	q091e02.x1 NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1915898 3' similar to TR:Q69336 Q69386 POL/ENV GENE ;
5963	18745	31706	0.57	2.0E-19	AV731382.1	EST_HUMAN	AV731382 HTF Homo sapiens cDNA clone HTFAZC06 5'

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7238	19923	32988	0.93	2.0E-19	7657286	NT	Mus musculus keratin-associated protein 9-1 (Krtap9-1), mRNA
8228	20922	34061	8.08	2.0E-19	AA012854.1	EST_HUMAN	ze34c09.r1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:360880 5'
9809	22460	35686	0.68	2.0E-19	Q85155	SWISSPROT	OLFACTORY RECEPTOR-LIKE PROTEIN OLF2
11829	24413	37750	1.33	2.0E-19	BF330867.1	EST_HUMAN	RC3-BT0333-250800-114-04 BT0333 Homo sapiens cDNA
11829	24413	37751	1.33	2.0E-19	BF330867.1	EST_HUMAN	RC3-BT0333-250800-114-04 BT0333 Homo sapiens cDNA
469	13255		1.87	1.0E-19	BE408611.1	EST_HUMAN	607304129F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3638310 5'
2161	14891	27626	1.58	1.0E-19	H30795.1	EST_HUMAN	y079g07.r1 Soares adult brain N2b4HB55Y Homo sapiens cDNA clone IMAGE:184188 5' similar to contains
2723	15430		2.37	1.0E-19	D38044.1	NT	MER10 repetitive element;
2851	15619		4.95	1.0E-19	4758977	NT	Human gene for Ahr-receptor, exon 7-9
3398	16154	28806	1.2	1.0E-19	AA834967.1	EST_HUMAN	aj49b12.s1 Soares, testes_NHT Homo sapiens cDNA clone IMAGE:1393631 3' similar to contains MER37.12
5983	18764	31728	2.38	1.0E-19	U12166.1	NT	MER37 repetitive element;
6114	25419		0.83	1.0E-19	AA595527.1	EST_HUMAN	Oryctolagus cuniculus sodium/dicarboxylate cotransporter mRNA, partial cds
7528	20199	33293	0.86	1.0E-19	U08813.1	NT	nh22d03.s1 NCL_CGAP_P1 Homo sapiens cDNA clone IMAGE:953083 similar to contains L1.11 L1
7528	20199	33294	0.86	1.0E-19	U08813.1	NT	Oryctolagus cuniculus Na+/glucose cotransporter-related protein mRNA, complete cds
7695	25118		0.93	1.0E-19	AF200719.1	NT	Oryctolagus cuniculus Na+/glucose cotransporter-related protein mRNA, complete cds
8348	21042	34179	1.75	1.0E-19	M64657.1	NT	Homo sapiens pituitary tumor transforming gene protein (PTTG) gene, complete cds
8640	21332		2.64	1.0E-19	T99920.1	EST_HUMAN	Rabbit phosphorylase kinase beta subunit mRNA, complete cds
9849	22301		0.46	1.0E-19	U60822.1	NT	y072b02.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:123243 5' similar to contains
10087	22735	35950	23.03	1.0E-19	AW812259.1	EST_HUMAN	OFK repetitive element;
10087	22745	35950	1.46	1.0E-19	N44631.1	EST_HUMAN	Human dystrophin (DMD) gene, exons 7, 8 and 9, and partial cds
11760	24351	37683	1.55	1.0E-19	U93163.1	NT	RC0-ST0174-191099-031-b05 ST0174 Homo sapiens cDNA
6549	19314	32319	2.56	8.0E-20	7657286	NT	y071e09.r1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:272872 5'
6549	19314	32320	2.56	8.0E-20	7657286	NT	Homo sapiens IMAGE-B2 (IMAGE-B2), IMAGE-B3 (IMAGE-B3), IMAGE-B4 (IMAGE-B4), and IMAGE-B1
7418	20095	33180	1.34	8.0E-20	A1221371.1	EST_HUMAN	(IMAGE-B1) genes, complete cds
7418	20095	33181	1.34	8.0E-20	A1221371.1	EST_HUMAN	Mus musculus keratin-associated protein 9-1 (Krtap9-1), mRNA
3270	18031	28682	1.41	7.0E-20	BF326455.1	EST_HUMAN	qg86f09.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1842089 3'
6898	17972	30529	6.29	7.0E-20	AL138120.1	EST_HUMAN	qg86f09.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1842089 3'
8394	21087	34222	12.48	7.0E-20	AA557657.1	EST_HUMAN	PM4-AN0096-050900-003-a04 AN0096 Homo sapiens cDNA
							DKFZp547D092 t1 547 (synonym: hibr1) Homo sapiens cDNA clone DKFZp547D092 5'
							n48c04.s1 NCL_CGAP_P1 Homo sapiens cDNA clone IMAGE:1043718 similar to contains MER29.b2
							MER29 repetitive element;

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Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8394	21087	34223	12.48	7.0E-20	AA557657.1	EST_HUMAN	nl46c04.s1 NCI_CGAP_P14 Homo sapiens cDNA clone IMAGE:1043718 similar to contains MER29.b2
11714	24308		1.95	7.0E-20	6912833	NT	MER29 repetitive element;
3543	16298	28949	3.52	6.0E-20	P39188	SWISSPROT	Homo sapiens ribosomal protein L13a (RPL13A), mRNA
4239	16980	28605	3.33	6.0E-20	BE622434.1	EST_HUMAN	ALU SUBFAMILY J SEQUENCE CONTAMINATION WARNING ENTRY
4556	17291		1.18	5.0E-20	AV725123.1	EST_HUMAN	601441231F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3916231 5'
7015	19707	32763	1.07	5.0E-20	AF075301.1	EST_HUMAN	AV725123 HTC Homo sapiens cDNA clone HT08TA01 5'
7846	20541	33668	5.28	5.0E-20	W90525.1	EST_HUMAN	AF075301 Human fetal liver cDNA library Homo sapiens cDNA clone HA0250
7846	20541	33669	5.28	5.0E-20	W90525.1	EST_HUMAN	zh78d08.s1 Scores_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:418191 3' similar to
8002	20697	33825	0.7	5.0E-20	BE165980.1	EST_HUMAN	zh78d08.s1 Scores_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:418191 3' similar to
8734	21426	34572	2.54	5.0E-20	AB028174.1	NT	contains MER30.1f1 MER30 repetitive element;
8734	21426	34573	2.54	5.0E-20	AB028174.1	NT	MR3-H10487-130200-113-g01 HT0487 Homo sapiens cDNA
9345	20416		0.94	5.0E-20	O60809	SWISSPROT	Mus musculus MMAN-g mRNA, complete cds
1616	14363	27054	1.34	4.0E-20	AL163247.2	NT	Mus musculus MMAN-g mRNA, complete cds
5562	18359		0.8	4.0E-20	Q99880	SWISSPROT	HYPOTHETICAL PROTEIN DJ845024.1
7826	20521		5.15	4.0E-20	A1874362.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C047
10396	23042	36259	1.33	4.0E-20	AW937489.1	EST_HUMAN	HISTONE H2B C (H2B/C)
2135	14865	27595	1.02	3.0E-20	U03888.1	NT	1264g03.x1 NCI_CGAP_Ov35 Homo sapiens cDNA clone IMAGE:22833396 3'
4185	16928	29557	1.29	3.0E-20	P23273	SWISSPROT	QV3-DT0043-080200-080-c04 DT0043 Homo sapiens cDNA
							Human BXP21 gene
4582	17317	29944	1.05	3.0E-20	AA037618.1	EST_HUMAN	OLFACTORY RECEPTOR-LIKE PROTEIN114
8833	21525		2.95	3.0E-20	D14547.1	NT	z436b12.s1 Scores_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:484895 3' similar to
10219	22867	36078	0.63	3.0E-20	BF185284.1	EST_HUMAN	contains L1.13 L1 repetitive element;
10561	23257		1.87	3.0E-20	P11369	SWISSPROT	Human DNA_SINE repetitive element
11496	24097	37408	1.5	3.0E-20	A1284244.1	EST_HUMAN	601843561F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4064343 5'
11496	24097	37409	1.5	3.0E-20	A1284244.1	EST_HUMAN	RETROVIRUS-RELATED POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ;
12051	24569	31118	2.65	3.0E-20	BE888422.1	EST_HUMAN	ENDONUCLEASE
811	13582		3.12	2.0E-20	AW303868.1	EST_HUMAN	q170d02.x1 NCI_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1864803 3' similar to contains Alu repetitive element;
							q170d02.x1 NCI_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1864803 3' similar to contains Alu repetitive element;
							q170d02.x1 NCI_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1864803 3' similar to contains Alu repetitive element;
							601514180F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3915522 5'
							x24e10.x1 NCI_CGAP_U14 Homo sapiens cDNA clone IMAGE:2761098 3' similar to SW:RS5_MOUSE
							P97461 40S RIBOSOMAL PROTEIN S6 ;

Table 4

Single Exon Probes Expressed In Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1089	13847	26505	3.37	2.0E-20	AA516335.1	EST_HUMAN	ng69h09.s1 NCI_CGAP_Lip2 Homo sapiens cDNA clone IMAGE:940097 similar to TR:G1224066
1089	13847	26506	3.37	2.0E-20	AA516335.1	EST_HUMAN	G1224066 ORF2: FUNCTION UNKNOWN ; ng69h09.s1 NCI_CGAP_Lip2 Homo sapiens cDNA clone IMAGE:940097 similar to TR:G1224066
2820	13582		2.38	2.0E-20	AW303888.1	EST_HUMAN	G1224066 ORF2: FUNCTION UNKNOWN ; xr24e10.x1 NCI_CGAP_U4 Homo sapiens cDNA clone IMAGE:2761068 3' similar to SW:RS5_MOUSE
4883	17620	30238	4.97	2.0E-20	Q28983	SWISSPROT	P97481 40S RIBOSOMAL PROTEIN S8 ;
4883	17620	30239	4.97	2.0E-20	Q28983	SWISSPROT	ZONADHESIN PRECURSOR
5057	17786		5.98	2.0E-20	5174538	NT	ZONADHESIN PRECURSOR
8017	20712	33843	0.81	2.0E-20	AA309457.1	EST_HUMAN	Homo sapiens malate dehydrogenase 1, NAD (soluble) (MDH1) mRNA
9089	21778	34942	8.6	2.0E-20	D10083.1	NT	EST180326 Liver III Homo sapiens cDNA 5' end
9089	21778	34943	8.6	2.0E-20	D10083.1	NT	Homo sapiens RGH1 gene, retrovirus-like element
12426	25141	30895	2.03	2.0E-20	H58371.1	EST_HUMAN	Homo sapiens RGH1 gene, retrovirus-like element
12815	25057		1.39	2.0E-20	11437152	NT	CHR220310 Chromosome 22 exon Homo sapiens cDNA clone G22_391 5'
2007	15525	27468	3.71	1.0E-20	AA281961.1	EST_HUMAN	Homo sapiens heparin-binding growth factor binding protein (HBP17), mRNA
4406	17143	29772	1	1.0E-20	BF115158.1	EST_HUMAN	z11408.r1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3135155 3' similar to contains L1.12 L1
5794	19538	32566	0.75	1.0E-20	AF049567.1	EST_HUMAN	repetitive element ; hr84h06.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:745694 similar to contains L1.12 L1
9061	21750	34909	2.04	1.0E-20	11418491	NT	AF049567 Human activated dendritic cell mRNA Homo sapiens cDNA clone GA05
11541	24141	37450	2.62	1.0E-20	AF223391.1	NT	Homo sapiens Autosomal Highly Conserved Protein (AHCP), mRNA
12171	24851		1.73	1.0E-20	AA420453.1	EST_HUMAN	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
2913	15679		0.98	9.0E-21	AJ003514.1	EST_HUMAN	repetitive element ;
11804	24469		2.52	9.0E-21	AW98189.1	EST_HUMAN	repetitive element ;
8711	21403		2.15	8.0E-21	AW674891.1	EST_HUMAN	RC3-NN0068-090500-021-503 NN0068 Homo sapiens cDNA
11528	24126	37432	3.52	8.0E-21	AA809411.1	EST_HUMAN	b530a02.y1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:2984714 5' similar to SW:NIAM_HUMAN
12064	24579		4.49	8.0E-21	O21330	SWISSPROT	O95168 NADH-JUBIQUINONE OXIDOREDUCTASE ASH1 SUBUNIT PRECURSOR ;
2061	14793	27518	1.62	7.0E-21	P15900	SWISSPROT	cb71f08.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1336835 3'
2061	14793	27519	1.62	7.0E-21	P15900	SWISSPROT	ATP SYNTHASE A CHAIN (PROTEIN 6)
3689	18442	29083	0.89	7.0E-21	AL163300.2	NT	LAMININ BETA-2 CHAIN PRECURSOR (S-LAMININ) (LAMININ CHAIN B3)
4228	16969		5.58	7.0E-21	AA048502.1	EST_HUMAN	LAMININ BETA-2 CHAIN PRECURSOR (S-LAMININ) (LAMININ CHAIN B3)
							Homo sapiens chromosome 21 segment HS21C100
							z67a08.r1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:487858 5'

Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6340	19110	32100	0.79	7.0E-21	AL163218.2	NT	Homo sapiens chromosome 21 segment HS21C018
8287	20981	34121	1.53	7.0E-21	AJ277557.1	NT	Homo sapiens dNT-2 gene for mitochondrial 5(3')-deoxyribonucleotidase (dNT-2 gene), exons 1-5
8576	21268	34407	10.76	7.0E-21	D14718.1	NT	Human chromosomal protein HMG1 related gene
10013	22661	35877	0.86	7.0E-21	AW856922.1	EST_HUMAN	RCO-C10301-271199-031-F03 C10301 Homo sapiens cDNA
10594	23288	36525	2.19	7.0E-21	AA723404.1	EST_HUMAN	zg73d03.s1 Soares_fetal_heart_NBHH19W Homo sapiens cDNA clone IMAGE:398981 3' similar to gb:M14338 VITAMIN K-DEPENDENT PROTEIN S PRECURSOR (HUMAN);contains THR.13 OFR repetitive element;
11234	23897	37184	1.75	7.0E-21	7706668	NT	Homo sapiens PTD013 protein (PTD013), mRNA
4083	16827	29454	0.83	6.0E-21	BE408611.1	EST_HUMAN	601304125F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3638310 5'
9034	21724	26334	0.6	6.0E-21	BE162737.1	EST_HUMAN	PM1-H1T0454-080100-002-H09 HT0454 Homo sapiens cDNA
903	13670	26334	0.7	5.0E-21	5902031	NT	Homo sapiens protein tyrosine phosphatase, non-receptor type 21 (PTPN21), mRNA
4330	17069	29697	2.91	5.0E-21	BE968839.1	EST_HUMAN	601649871F1 NIH_MGC_74 Homo sapiens cDNA clone IMAGE:3933880 5'
4749	17481	30112	5.56	5.0E-21	4885474	NT	Homo sapiens melanoma antigen, family C, 1 (MAGEC1), mRNA
6665	19582		0.9	5.0E-21	AW440864.1	EST_HUMAN	he05e10.x1 NCL_CGAP_CML7 Homo sapiens cDNA clone IMAGE:2918154 3'
6917	19654	32700	0.86	5.0E-21	BE856505.1	EST_HUMAN	783d11.x1 NCL_CGAP_P28 Homo sapiens cDNA clone IMAGE:3303573 3' similar to contains OFR.11 OFR repetitive element;
10474	23120	36349	0.44	5.0E-21	Q91690	SWISSPROT	ZINC FINGER PROTEIN GLI1 (GLI-1)
10474	23120	36350	0.44	5.0E-21	Q91690	SWISSPROT	ZINC FINGER PROTEIN GLI1 (GLI-1)
11988	24527		2.83	5.0E-21	AA399374.1	EST_HUMAN	zt72e04.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:727878 5'
1727	14469	27168	1.81	4.0E-21	AA970713.1	EST_HUMAN	cc86e08.s1 NCL_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1573094 3' similar to TR:Q16630 Q16630 PMS3 MRNA, contains OFR.11 OFR repetitive element;
6772	19516	32544	3.27	4.0E-21	AB019576.1	NT	Rattus norvegicus mRNA for rTIM, complete cds
9680	22332	35527	0.63	4.0E-21	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NP73) gene, complete cds
9705	22358	35552	0.7	4.0E-21	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
1829	14968	27280	0.94	3.0E-21	AA218891.1	EST_HUMAN	zq15d06.s1 Straigene fetal retina 937202 Homo sapiens cDNA clone IMAGE:628771 3'
2272	14998	27736	1.24	3.0E-21	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
3078	15843	28485	4.31	3.0E-21	AJ007973.1	NT	Homo sapiens LGMD2B gene
5412	18211	30919	0.68	3.0E-21	AJ277557.1	NT	Homo sapiens dNT-2 gene for mitochondrial 5(3')-deoxyribonucleotidase (dNT-2 gene), exons 1-5
5412	18211	30920	0.68	3.0E-21	AJ277557.1	NT	Homo sapiens dNT-2 gene for mitochondrial 5(3')-deoxyribonucleotidase (dNT-2 gene), exons 1-5

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5652	18447		0.65	3.0E-21	AV661044.1	EST_HUMAN	AV661044 GLC Homo sapiens cDNA clone GLCGOAT0 3'
6086	18864		2.3	3.0E-21	BF184739.1	EST_HUMAN	601844465F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4084945 5'
6989	19451	32489	7.69	3.0E-21	BF381093.1	EST_HUMAN	RC1-OT0083-100800-019-g08 OT0083 Homo sapiens cDNA
9592	22245	35429	1.15	3.0E-21	AW897760.1	EST_HUMAN	CM1-NN0063-280400-203-h08 NN0063 Homo sapiens cDNA
12533	25327	30714	2.88	3.0E-21	AL163213.2	NT	Homo sapiens chromosome 21 segment HS21C013
141	12956		17.18	2.0E-21	BE163247.1	EST_HUMAN	QV3-HT0458-170200-090-g12 HT0458 Homo sapiens cDNA
914	13881	26342	1.85	2.0E-21	AB007857.2	NT	Homo sapiens mRNA for KIAA0397 protein, partial cds
914	13881	26343	1.85	2.0E-21	AB007857.2	NT	Homo sapiens mRNA for KIAA0397 protein, partial cds
1192	13944		2.75	2.0E-21	BE064410.1	EST_HUMAN	RC4-BT0311-141199-011-h06 BT0311 Homo sapiens cDNA
2844	15354	28098	1.98	2.0E-21	Q28983	SWISSPROT	ZONADHESIN PRECURSOR
2844	15354	28099	1.98	2.0E-21	Q28983	SWISSPROT	ZONADHESIN PRECURSOR
5398	18198	30890	1.64	2.0E-21	A1624592.1	EST_HUMAN	ts3003.x1 NCL_CGAP_Par11 Homo sapiens cDNA clone IMAGE:2230109 3' similar to TR:Q99854 Q99854
5489	18288	31184	0.68	2.0E-21	AA027211.1	EST_HUMAN	HYPOTHETICAL 51.1 KD PROTEIN ;
5489	18288	31185	0.68	2.0E-21	AA027211.1	EST_HUMAN	ze97a12.r1 Soares_fetal_heart_NbH19W Homo sapiens cDNA clone IMAGE:366910 5'
8170	20884	33998	0.5	2.0E-21	AJ010770.1	NT	ze97a12.r1 Soares_fetal_heart_NbH19W Homo sapiens cDNA clone IMAGE:366910 5'
8261	20955	34094	6.16	2.0E-21	BE141785.1	EST_HUMAN	Homo sapiens hyperion gene, exons 1-50
8722	21414	34557	3.74	2.0E-21	AU136779.1	EST_HUMAN	QV0-HT0103-091199-050-g11 HT0103 Homo sapiens cDNA
10991	23665		1.55	2.0E-21	BE350127.1	EST_HUMAN	AU136779 PLACE1 Homo sapiens cDNA clone PLACE1005052 5'
11289	23950	37246	1.3	2.0E-21	BE973829.1	EST_HUMAN	h09g01.x1 NCL_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3148256 3' similar to contains MER29.b3
11289	23950	37247	1.3	2.0E-21	BE973829.1	EST_HUMAN	MER29 repetitive element ;
12272	24712		9.87	2.0E-21	AF176815.1	NT	601680636F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3951008 5'
1233	13982	26652	1.6	1.0E-21	AA557657.1	EST_HUMAN	601680636F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3951008 5'
1381	14128		2.62	1.0E-21	A1601264.1	EST_HUMAN	Homo sapiens putative 8-hydroxyguanine DNA glycosylase gene, complete cds
6396	19165		2.74	1.0E-21	AL079752.1	EST_HUMAN	n46c04.s1 NCL_CGAP_P14 Homo sapiens cDNA clone IMAGE:1043718 similar to contains MER29.b2
7092	19781	32847	6.6	1.0E-21	A1223104.1	EST_HUMAN	MER29 repetitive element ;
10484	23130		1.07	1.0E-21	5730038	NT	ar88d12.x1 Barstead cdon HPLRB7 Homo sapiens cDNA clone IMAGE:2152343 3'
4377	17114	29747	5.65	9.0E-22	A1702438.1	EST_HUMAN	DKFZp434l0830_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434l0830 5'
8502	21194	34338	1.27	9.0E-22	AL163201.2	NT	qg47e05.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1838336 3' similar to gb:1M84241 QM
8502	21194	34337	1.27	9.0E-22	AL163201.2	NT	PROTEIN (HUMAN) ;
							Homo sapiens SET domain and mariner transposase fusion gene (SETMAR) mRNA
							b294a03.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2296204 3' similar to TR:Q15408 Q15408
							NEUTRAL PROTEASE LARGE SUBUNIT ;
							Homo sapiens chromosome 21 segment HS21C001
							Homo sapiens chromosome 21 segment HS21C001

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10691	23382	36622	2.63	9.0E-22	AV761874.1	EST_HUMAN	AV761874 MDS Homo sapiens cDNA clone MDSCG305 5'
11707	24302	37627	1.34	9.0E-22	AU140358.1	EST_HUMAN	AU140358 PLACE2 Homo sapiens cDNA clone PLACE2000394 5'
929	13696		5.55	8.0E-22	BE144748.1	EST_HUMAN	CMO-H10179-281099-076-H05 HT0179 Homo sapiens cDNA
7797	20492		3.72	8.0E-22	AA046502.1	EST_HUMAN	zk67a06.t1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:487858 5'
650	13428	26067	5.92	7.0E-22	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C048
4250	16991	29616	2.21	7.0E-22	Q81838	SWISSPROT	ALPHA-2-MACROGLOBULIN PRECURSOR (ALPHA2M)
4977	17700	30307	0.99	7.0E-22	AB008881.1	NT	Homo sapiens gene for activin receptor type IIB, complete cds
8590	21282		1.38	7.0E-22	AF151054.1	NT	Homo sapiens HSPC220 mRNA, complete cds
8731	21423	34568	3.56	7.0E-22	M7690.1	EST_HUMAN	EST00736 Fetal brain, Stratagene (cat#9336206) Homo sapiens cDNA clone HFBFCF07
9502	22155	35335	2.04	7.0E-22	AF009660.1	NT	Homo sapiens T cell receptor beta locus, TORBV7S3A2 to TORBV12S2 region
4038	16783	29413	0.98	6.0E-22	AA405040.1	EST_HUMAN	zu66d10.t1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:742867 5'
8140	20834		1.33	6.0E-22	AW028123.1	EST_HUMAN	wx05g07.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2542812 3'
6424	19192	32188	3.78	6.0E-22	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
10217	22865	36077	7.83	5.0E-22	U60822.1	NT	Human dystrophin (DMD) gene, exons 7, 8 and 9, and partial cds
12499	24854		2.22	5.0E-22	BF476511.1	EST_HUMAN	naa27b06.x1 NCI_CGAP_P128 Homo sapiens cDNA clone IMAGE:3255988 3' similar to contains Alu repetitive element;
3627	16380		0.85	4.0E-22	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region, segment 1/2
8004	20699	33827	0.45	4.0E-22	AV703223.1	EST_HUMAN	AV703223 ADB Homo sapiens cDNA clone ADBAUE12 5'
8312	25428		3.11	4.0E-22	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
10623	23316	36556	2.47	4.0E-22	BF218030.1	EST_HUMAN	G01882813F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4095434 5'
12657	24957		2.06	4.0E-22	AL163208.2	NT	Homo sapiens chromosome 21 segment HS21C009
939	13706		1.58	3.0E-22	A1469879.1	EST_HUMAN	tm14h10.x1 NCI_CGAP_Cot14 Homo sapiens cDNA clone IMAGE:2156611 3' similar to gb:L19593 HIGH AFFINITY INTERLEUKIN-8 RECEPTOR B (HUMAN); contains L1, L1 repetitive element;
2575	15289	28026	0.92	3.0E-22	A1859038.1	EST_HUMAN	w166b04.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2429839 3' similar to SW:RL21_HUMAN
3662	16415		1.46	3.0E-22	D14718.1	NT	P46778 60S RIBOSOMAL PROTEIN L21;
4748	17480	30111	2.6	3.0E-22	A1090125.1	EST_HUMAN	Human chromosomal protein HMG1 related gene
8129	20823		0.8	3.0E-22	BE156613.1	EST_HUMAN	qb28c07.x1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:1697580 3' similar to contains MER12.12 MER12 repetitive element;
8134	20828	33963	2.46	3.0E-22	BE089841.1	EST_HUMAN	QV0-H10368-090200-099-f12 HT0368 Homo sapiens cDNA
8258	20952	34088	0.97	3.0E-22	X60660.1	NT	RC5-B10707-150300-021-H10 BT0707 Homo sapiens cDNA
8258	20952	34089	0.97	3.0E-22	X60660.1	NT	R. rattus RY2G5 mRNA for a potential ligand-binding protein
1946	14681		2.29	2.0E-22	N24942.1	EST_HUMAN	R. rattus RY2G5 mRNA for a potential ligand-binding protein
2528	15242	27981	2.15	2.0E-22	P24916	SWISSPROT	yv73405.s1 Soares_melanocyte_2NHM Homo sapiens cDNA clone IMAGE:267369 3'
							IMMEDIATE EARLY GENE 13 PROTEIN PRECURSOR

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Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3414	16172	28821	4.41	2.0E-22	8394043	NT	Homo sapiens protein kinase, AMP-activated, gamma 3 non-catalytic subunit (PRKAG3), mRNA
4200	16941	29567	1.17	2.0E-22	AW817794.1	EST_HUMAN	PM1-ST0282-261199-001-d12 ST0282 Homo sapiens cDNA
5761	25075	31476	1.18	2.0E-22	W39456.1	EST_HUMAN	zc20f01.r1 Soares_senescent_fibroblasts_NbHSF Homo sapiens cDNA clone IMAGE:322873 5' similar to
6084	18862	31828	3.58	2.0E-22	BF092116.1	EST_HUMAN	gb:X72308 MONOCYTE CHEMOTACTIC PROTEIN 3 PRECURSOR (HUMAN);
9802	22255	35440	1.53	2.0E-22	AI276522.1	EST_HUMAN	RCO-TN0078-150900-025-h12 TN0078 Homo sapiens cDNA
9696	22347	35540	0.69	2.0E-22	AA715315.1	EST_HUMAN	q176h06.x1 Soares_NbHMPu_S1 Homo sapiens cDNA clone IMAGE:1878299 3' similar to contains
9696	22347	35541	0.69	2.0E-22	AA715315.1	EST_HUMAN	MER29.i3 MER29 repetitive element ;
11761	24352	37684	1.88	2.0E-22	AA715315.1	EST_HUMAN	nv04h11.s1 NCI_CGAP_P122 Homo sapiens cDNA clone IMAGE:1219269 3'
11872	24946	30983	3.71	2.0E-22	AL163280.2	NT	ha24f04.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:1219269 3'
1871	14609	27320	1.79	1.0E-22	AW866517.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C080
2588	15302	28038	1.1	1.0E-22	U50871.1	NT	PM4-SN0020-010400-009-h02 SN0020 Homo sapiens cDNA
3405	16163	28814	1.37	1.0E-22	D14547.1	NT	Human familial Alzheimer's disease (STM2) gene, complete cds
7641	20306	33415	0.89	1.0E-22	BE084667.1	EST_HUMAN	Human DNA, SINE repetitive element
10451	23097	36328	0.79	1.0E-22	AI365435.1	EST_HUMAN	MRO-BT0659-220200-002-h07 BT0659 Homo sapiens cDNA
10451	23097	36329	0.79	1.0E-22	AI365435.1	EST_HUMAN	qz09b07.x1 NCI_CGAP_GLL1 Homo sapiens cDNA clone IMAGE:2020981 3' similar to contains MER29.b2
12704	24984	28959	5.89	9.0E-23	AF802801.1	EST_HUMAN	MER29 repetitive element ;
3557	16312	28959	0.79	8.0E-23	AF198349.1	EST_HUMAN	IL2-JM0076-070400-061-F11 UM0076 Homo sapiens cDNA
3305	16065	36895	2.55	7.0E-23	AV647246.1	EST_HUMAN	Gallus gallus Dach2 protein (Dach2) mRNA, complete cds
10966	23842	36895	4.16	7.0E-23	5031862	NT	AV647246 GLC Homo sapiens cDNA clone GLCAWC07 3'
3427	16184	29601	1.72	6.0E-23	AF199333.1	NT	Homo sapiens Not56 (D, melanogaster)-like protein (NOT56L) mRNA
4235	16976	29601	1.39	6.0E-23	AL163249.2	NT	Rattus norvegicus RIM1B (Rim1B) mRNA, complete cds
12005	24540	31105	1.5	6.0E-23	AF224689.1	NT	Homo sapiens chromosome 21 segment HS21C049
12005	24540	31106	1.5	6.0E-23	AF224689.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3
12192	24663	31067	3.28	6.0E-23	AI209130.1	EST_HUMAN	(UBE2D3) genes, complete cds
5358	18160	30844	4.09	5.0E-23	U82671.2	NT	qg59c03.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1839480 3' similar to
							SW:MV10_MOUSE_P23249 PROTEIN MOV-10 ;
							Homo sapiens chromosome Xq28 melanoma antigen family A2a (MAGEA2A), melanoma antigen family A12 (MAGEA12), melanoma antigen family A2b (MAGEA2B), melanoma antigen family A3 (MAGEA3), caltractin (CALT), NAD(P)H dehydrogenase-like protein (NSDHL), and LI>

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6145	25086	31893	3.93	5.0E-23	AF179818.1	NT	Pongo pygmaeus olfactory receptor (PPY116) gene, partial cds
7337	25088	31893	3.37	5.0E-23	AF179818.1	NT	Pongo pygmaeus olfactory receptor (PPY116) gene, partial cds
6347	19117	32106	1.34	3.0E-23	AL163227.2	NT	Homo sapiens chromosome 21 segment HS21C027
6347	19117	32107	1.34	3.0E-23	AL163227.2	NT	Homo sapiens chromosome 21 segment HS21C027
7738	20434	33556	4.1	3.0E-23	AA130165.1	EST_HUMAN	z135g09.r1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:503968 5' similar to contains MER29.12 MER29 repetitive element ;
9148	21879	35045	2.88	3.0E-23	Z70664.1	NT	Human endogenous retroviral element HC2
9148	21879	35046	2.98	3.0E-23	Z70664.1	NT	Human endogenous retroviral element HC2
10216	22863		1.18	3.0E-23	AW897927.1	EST_HUMAN	RC3-NN0066-270400-011-h01 NN0066 Homo sapiens cDNA
651	13429	26098	4.25	2.0E-23	AJ289890.1	NT	Homo sapiens KIA0851 gene (partial), XT3 gene and LZTFL1 gene
1120	15520		3.87	2.0E-23	M55270.1	NT	Human matrix Gla protein (MGP) gene, complete cds
2798	15503	28243	1.98	2.0E-23	P22105	SWISSPROT	TENASCIN-X PRECURSOR (TN-X) (HEXABRACHION-LIKE)
2798	15503	28244	1.98	2.0E-23	P22105	SWISSPROT	TENASCIN-X PRECURSOR (TN-X) (HEXABRACHION-LIKE)
3364	16123		1.46	2.0E-23	AI201458.1	EST_HUMAN	qs73f11.x1 NCI_CGAP_P28 Homo sapiens cDNA clone IMAGE:1943757 3' similar to TR:Q13537 Q13537
3705	18458		3.35	2.0E-23	BE185980.1	EST_HUMAN	MR3-NT0487-150200-113-g01 HT0487 Homo sapiens cDNA
3958	16707	29346	3.65	2.0E-23	H59931.1	EST_HUMAN	Y16a02.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:205418 5'
3958	16707	29347	3.66	2.0E-23	H59931.1	EST_HUMAN	Y16a02.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:205418 5'
7772	20468		4.3	2.0E-23	AF280107.1	NT	Homo sapiens cytochrome P450 polypeptide 43 (CYP3A4) gene, partial cds; cytochrome P450 polypeptide 4 (CYP3A4) and cytochrome P450 polypeptide 7 (CYP3A7) genes, complete cds; and cytochrome P450 polypeptide 5 (CYP3A5) gene, partial cds
8742	21434	34579	1.21	2.0E-23	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
11991	24530		2.45	2.0E-23	M32658.1	NT	Human alcohol dehydrogenase gamma subunit (ADH3) gene, exon 1
12508	24860		2.87	2.0E-23	AF009660.1	NT	Homo sapiens T cell receptor beta locus, TCRBV7S3A2 to TCRBV12S2 region
4492	17228	28857	1.1	1.0E-23	AL163252.2	NT	Homo sapiens chromosome 21 segment HS21C052
4714	17446		5.56	1.0E-23	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
5620	19382		3.28	1.0E-23	BE379471.1	EST_HUMAN	60123645F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3608653 5'
8254	20948	34085	4.6	1.0E-23	AA448097.1	EST_HUMAN	zw62c06.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:3636254 5'
10570	23286	36503	2.05	1.0E-23	BE409643.1	EST_HUMAN	601301762F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3636254 5'
10570	23285	36504	2.05	1.0E-23	BE409643.1	EST_HUMAN	601301762F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3636254 5'
539	13322		1.84	9.0E-24	AA663213.1	EST_HUMAN	ab75a08.s1 Stragene fetal retina 837202 Homo sapiens cDNA clone IMAGE:852758 3' similar to TR:E19822 E19822 CA PROTEIN ;
6357	19127	32121	1.53	8.0E-24	11422027	NT	Homo sapiens capping protein (actin filament) muscle Z-line, alpha 2 (CAPZA2), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3653	16603		1.49	7.0E-24	AW937854.1	EST_HUMAN	QV0-DT0047-170200-122-a06 DT0047 Homo sapiens cDNA
5087	17806		0.95	7.0E-24	AL039498.1	EST_HUMAN	DKFZp434A2311_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434A2311 5'
10536	23233		1.33	7.0E-24	AW303317.1	EST_HUMAN	xv17f03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2813405 3' similar to contains Alu repetitive element; contains MER19.12 MER19 repetitive element;
690	13465		2.72	6.0E-24	AB001421.1	NT	Macaca fasciata mRNA for Testis-Specific Protein Y (TSPY), complete cds
818	13589	26256	11.74	6.0E-24	AL163249.2	NT	Homo sapiens chromosome 21 segment HS21C049
3953	16703	28342	7.9	5.0E-24	AJ229043.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22, segment 3/3
7657	20321	33430	0.58	5.0E-24	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
11595	24194	37513	1.45	5.0E-24	AW514229.1	EST_HUMAN	hd24b03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2810413 3' similar to TR:OB4851
5840	18628	31563	3.85	4.0E-24	AA594178.1	EST_HUMAN	O94851 KIAA0750 PROTEIN ;
8581	21273	34411	1.35	4.0E-24	AW813711.1	EST_HUMAN	nn31h05.s1 NCL_OGAP_Gas1 Homo sapiens cDNA clone IMAGE:1085529 3' similar to SW.POL_MLVRK
11133	23801	37078	1.95	4.0E-24	BE544822.1	EST_HUMAN	P31785 POL POLYPROTEIN ;
12361	24765	31062	4.89	4.0E-24	AB029016.1	NT	RC3-ST0197-130100-014-06 ST0197 Homo sapiens cDNA
12595	24951	30986	1.77	4.0E-24	11418318	NT	601078812F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3464498 5'
8322	21015		2.85	3.0E-24	AW614871.1	EST_HUMAN	Homo sapiens mRNA for KIAA1093 protein, partial cds
8377	21070		1.57	3.0E-24	AW92076.1	EST_HUMAN	Homo sapiens G-2 and S-phase expressed 1 (GTSE1), mRNA
9365	21940	35114	4.33	3.0E-24	AL163252.2	NT	hh86c08.x1 NCL_OGAP_GU1 Homo sapiens cDNA clone IMAGE:2967950 3' similar to contains MER29.b2
12438	24808	31045	1.41	3.0E-24	BF127762.1	EST_HUMAN	MER29 repetitive element ;
2346	15069	27806	2.72	2.0E-24	AA167538.1	EST_HUMAN	EST374149 IMAGE resequences, MAGG Homo sapiens cDNA
3779	16531		1.01	2.0E-24	AW898189.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C052
7374	20054	33135	0.81	2.0E-24	AF086824.1	NT	601810449FT NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4053396 5'
7379	20059	33138	0.65	2.0E-24	AJ003536.1	EST_HUMAN	zp1109.r1 Stratagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:609161 5'
8639	21331	34476	3.26	2.0E-24	AL119158.1	EST_HUMAN	RC3-NN0068-090500-021-b03 NN0068 Homo sapiens cDNA
8676	21368		0.98	2.0E-24	H69214.1	EST_HUMAN	Mus musculus rhodrac-interacting citron kinase (Crik) mRNA, complete cds
9754	22405	35611	0.94	2.0E-24	AI521759.1	EST_HUMAN	AJ003536 Selected chromosome 21 cDNA library Homo sapiens cDNA clone MPIpl12-5H13
9754	22405	35612	0.94	2.0E-24	AI521759.1	EST_HUMAN	DKFZp761L1712_r1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761L1712 5'
11825	24409	37744	1.31	2.0E-24	AW688552.1	EST_HUMAN	y92b09.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:212729 5' similar to contains MER28 repetitive element ;
11825	24409	37745	1.31	2.0E-24	AW688552.1	EST_HUMAN	h77a09.x1 NCL_OGAP_Kid11 Homo sapiens cDNA clone IMAGE:2138008 3'
12281	25377		7.44	2.0E-24	M28877.1	NT	h77a09.x1 NCL_OGAP_Kid11 Homo sapiens cDNA clone IMAGE:2138008 3'

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1691	14435	27131	2.69	1.0E-24	7706340	NT	Homo sapiens CGI-127 protein (LOC51646), mRNA
2679	15388		1.63	1.0E-24	AW620184.1	EST_HUMAN	QV0-ST0284-100400-185-c10 ST0284 Homo sapiens cDNA
3020	15786	28433	1.49	1.0E-24	DB8423.1	NT	Mus musculus mRNA for HGT, keratin, partial cds
4237	16978		1.71	1.0E-24	AF143313.1	NT	Homo sapiens PTEN (PTEN) gene, exon 2
7447	20123	33214	4.32	1.0E-24	AF163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
7630	20296	33404	0.81	1.0E-24	BE144526.1	EST_HUMAN	MRO-HT0166-271199-005-d08 HT0166 Homo sapiens cDNA
7845	20540	33667	2.09	1.0E-24	AW801164.1	EST_HUMAN	CXMO-NN1010-130300-281-d07 NN1010 Homo sapiens cDNA
11699	24294	37619	1.31	9.0E-25	7706707	NT	Homo sapiens putative secreted protein (SIG11), mRNA
4939	17667	30275	2.33	7.0E-25	AA483944.1	EST_HUMAN	ne92e10.s1 NCL_CGAP_Kid1 Homo sapiens cDNA clone IMAGE:911754 similar to contains MER1.b2
8117	20811	33946	6.59	7.0E-25	AA468646.1	EST_HUMAN	ne06a09.s1 NCL_CGAP_Co3 Homo sapiens cDNA clone IMAGE:880408 3' similar to contains THR.b2 THR repetitive element;
11701	24296	37622	3.28	7.0E-25	AA583540.1	EST_HUMAN	m25h06.s1 NCL_CGAP_P1 Homo sapiens cDNA clone IMAGE:914843 similar to SW:R14A_YEAST
6893	17969		4.9	6.0E-25	W87823.1	EST_HUMAN	P36105 PROBABLE 60S RIBOSOMAL PROTEIN L14EA. ;
7622	20288	33397	8.34	6.0E-25	7305360	NT	zh55f07.r1 Soares fetal liver spleen 1NFLS_s1 Homo sapiens cDNA clone IMAGE:416989 5'
1647	14393	27083	1.18	5.0E-25	AW850271.1	EST_HUMAN	IL3-CT0219-161189-031-D04 CT0219 Homo sapiens cDNA
11286	23947	37242	2.44	5.0E-25	AW979107.1	EST_HUMAN	EST391217 MAGC resequences, MAGP Homo sapiens cDNA
1429	14176	28661	2.25	4.0E-25	T98107.1	EST_HUMAN	ye56h04.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:121783 5'
3397	16155		3.04	4.0E-25	AW887671.1	EST_HUMAN	PM3-OT0093-280200-001-g07 OT0093 Homo sapiens cDNA
4282	17021		2.93	4.0E-25	BE170957.1	EST_HUMAN	QV3-HT0543-140400-149-s11 HT0543 Homo sapiens cDNA
3314	16074	28724	3.98	3.0E-25	8923321	NT	Homo sapiens hypothetical protein FLJ20344 (FLJ20344), mRNA
3314	16074	28725	3.98	3.0E-25	8923321	NT	Homo sapiens hypothetical protein FLJ20344 (FLJ20344), mRNA
4837	17588	30190	0.75	3.0E-25	P28622	SWISSPROT	KALLISTATIN PRECURSOR (KALLIKREIN INHIBITOR) (PROTEASE INHIBITOR 4)
6518	19284	32288	0.6	3.0E-25	AA603590.1	EST_HUMAN	np27b02.s1 NCL_CGAP_P22 Homo sapiens cDNA clone IMAGE:1117515 3' similar to gb:M61866 ZINC
8235	20928	34065	4.86	3.0E-25	AL163210.2	NT	FINGER PROTEIN 85 (HUMAN);
10959	23635	36886	1.99	3.0E-25	AA579013.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C010
1326	14075	26749	2.94	2.0E-25	5032158	NT	np30h10.s1 NCL_CGAP_P1 Homo sapiens cDNA clone IMAGE:915331 similar to contains L1.t1 L1 repetitive element ;
2306	15031	27768	6.42	2.0E-25	BE888016.1	EST_HUMAN	Homo sapiens transducin (beta)-like 1 (TBL1) mRNA
2835	15259	27967	3.67	2.0E-25	P17008	SWISSPROT	601511530F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3913087 5'
4167	16907	28535	1.76	2.0E-25	P17008	SWISSPROT	40S RIBOSOMAL PROTEIN S16
4167	16907	28536	1.76	2.0E-25	P17008	SWISSPROT	40S RIBOSOMAL PROTEIN S16

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9665	22317	35514	1.94	2.0E-25	AL449573.1	EST_HUMAN	AL449573 Homo sapiens Testis (Stavrides GS) Homo sapiens cDNA
355	13153	25794	1.03	1.0E-25	AL040229.1	EST_HUMAN	DKFZp434H0313_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434H0313 5'
1228	13976		2.02	1.0E-25	9635487	NT	Human endogenous retrovirus, complete genome
2435	15158	27890	1.03	1.0E-25	Q06055	SWISSPROT	ATP SYNTHASE LIPID-BINDING PROTEIN P2 PRECURSOR (ATPASE PROTEIN 9) (SUBUNIT C)
4806	17537	30160	2.84	1.0E-25	BE162737.1	EST_HUMAN	PM1-HT0454-080100-002-h09 HT0454 Homo sapiens cDNA
6472	19239		0.79	1.0E-25	AA189080.1	EST_HUMAN	zq45b06.s1 Stratagene HNT neuron (#837233) Homo sapiens cDNA clone IMAGE:632627 3' similar to contains Alu repetitive element;
6699	25100	32657	3.14	1.0E-25	AA582690.1	EST_HUMAN	nm54h11.s1 NCI CGAP_Kid6 Homo sapiens cDNA clone IMAGE:1087749 3'
7814	20509	33633	4.03	1.0E-25	AA709078.1	EST_HUMAN	z86g04.s1 Soares_fetal_heart_Nbr-H119W Homo sapiens cDNA clone IMAGE:384822 3' similar to contains PTR5.t3 PTR5 repetitive element;
9446	22123	35302	0.75	1.0E-25	X60660.1	NT	R.rattus RY2G5 mRNA for a potential ligand-binding protein
9446	22123	35303	0.75	1.0E-25	X60660.1	NT	R.rattus RY2G5 mRNA for a potential ligand-binding protein
10890	23570	36821	3.08	1.0E-25	U93163.1	NT	Homo sapiens IMAGE-B2 (MAGE-B2), MAGE-B3 (MAGE-B3), MAGE-B4 (MAGE-B4), and MAGE-B1 (MAGE-B1) genes, complete cds
12768	25024		2.18	1.0E-25	X51755.1	NT	Human lambda-immunoglobulin constant region complex (germline)
2487	15204	27945	1.41	9.0E-26	AL163218.2	NT	Homo sapiens chromosome 21 segment HS21C018
5607	18403		1.99	8.0E-26	D14547.1	NT	Human DNA, SINE repetitive element
1571	14318	27003	1.72	7.0E-26	AF003528.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
3962	16711	28351	1.23	7.0E-26	X89211.1	NT	H. sapiens DNA for endogenous retroviral like element
4138	16880	29508	2.27	7.0E-26	AW340153.1	EST_HUMAN	hd02e12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2908366 3'
5551	18348	31257	0.62	7.0E-26	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
11669	24284		8.45	7.0E-26	AA115895.1	EST_HUMAN	zn30408.r1 Stratagene neuroepithelium NT2RAMI 937234 Homo sapiens cDNA clone IMAGE:548943 5' similar to gb:M14938 VITAMIN K-DEPENDENT PROTEIN S PRECURSOR (HUMAN);
12547	24885		1.64	7.0E-26	AW954559.1	EST_HUMAN	EST:366629 MAGE resequences, MAGE Homo sapiens cDNA
2222	14950	27689	2.04	6.0E-26	AF029308.1	NT	Homo sapiens chromosome 9 duplication of the T cell receptor beta locus and tyrosinogen gene families
3341	16100	28752	0.95	6.0E-26	AA208131.1	EST_HUMAN	zq52h04.r1 Stratagene neuroepithelium (#837231) Homo sapiens cDNA clone IMAGE:645271 5'
10432	23078	36301	0.68	6.0E-26	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
10432	23078	36302	0.68	6.0E-26	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
11683	24278	37600	2.03	6.0E-26	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
1154	13909	26572	3.61	5.0E-26	AI708235.1	EST_HUMAN	as38h03.x1 Barstead aorta HPLR86 Homo sapiens cDNA clone IMAGE:2319519 3' similar to WP:F49C12.11 CE03371;

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1154	13909	26573	3.61	5.0E-26	AI708235.1	EST_HUMAN	es38h08.x1 Barstead aorta HPLRB6 Homo sapiens cDNA clone IMAGE:2319519 3' similar to WP:F49C12.11 CE03371;
1535	14282		1.4	4.0E-26	AA329548.1	EST_HUMAN	EST33446 Embryo, 12 week II Homo sapiens cDNA 5' and
9312	21979		3.72	4.0E-26	7657670	NT	Homo sapiens upstream binding transcription factor, RNA polymerase I (UBTF), mRNA
10558	23254	38491	2.75	4.0E-26	BE266187.1	EST_HUMAN	601191345F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3535210 5'
1753	14485	27194	1.21	3.0E-26	D14547.1	NT	Human DNA, SINE repetitive element
1898	14732	27464	1.31	3.0E-26	AL045855.2	EST_HUMAN	DKFZp434066.t1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434066 5'
2025	14760		3.15	3.0E-26	AA115895.1	EST_HUMAN	zn30d08.r1 Stratagene neuroepithelium NT2RAMI 937234 Homo sapiens cDNA clone IMAGE:548943 5' similar to gb:MI14338 VITAMIN K-DEPENDENT PROTEIN S PRECURSOR (HUMAN);
3760	16512	29148	1.04	3.0E-26	AA152464.1	EST_HUMAN	zc30f10.r1 Stratagene colon (#837204) Homo sapiens cDNA clone IMAGE:588427 5' similar to TR:G695374
3760	16512	29148	1.04	3.0E-26	AA152464.1	EST_HUMAN	zc30f10.r1 Stratagene colon (#837204) Homo sapiens cDNA clone IMAGE:588427 5' similar to TR:G695374
6811	19472	32495	1.78	3.0E-26	BF245458.1	EST_HUMAN	G695374 THYROID RECEPTOR INTERACTOR;
10626	23319	37468	1.42	3.0E-26	AF036405.1	NT	Homo sapiens MLL (MLL) gene, exons 1-3, and partial cds
11559	24168	37468	1.83	3.0E-26	AW875651.1	EST_HUMAN	QV2-PT0012-040400-124-e05 PT0012 Homo sapiens cDNA
11559	24168	37468	1.83	3.0E-26	AW875651.1	EST_HUMAN	QV2-PT0012-040400-124-e05 PT0012 Homo sapiens cDNA
11602	24201	37523	6.56	3.0E-26	AA583173.1	EST_HUMAN	nn37d05.s1 NCI_CGAP_GC5 Homo sapiens cDNA clone IMAGE:1086057 3' similar to contains OFF.t1
11858	24442	37783	1.36	3.0E-26	AF228925.1	NT	OFI repetitive element;
12724	24995		2.52	3.0E-26	AW073434.1	EST_HUMAN	Mus musculus harmonin isoform b3 (Ush1c) mRNA, complete cds, alternatively spliced
666	13442	26083	6.76	2.0E-26	AL163282.2	NT	MER30 repetitive element;
1861	14599		3.07	2.0E-26	AL038099.2	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C082
3225	15988	28642	5.89	2.0E-26	X88694.1	NT	DKFZp566L171.s1 566 (synonym: lfrkd2) Homo sapiens cDNA clone DKFZp566L171 3'
5147	17868		1.09	2.0E-26	AF073482.1	NT	M.musculus mRNA for astrocytic phosphoprotein, PEA-15
10653	23344		2.7	2.0E-26	D87675.1	NT	Homo sapiens myotubularin related protein 7 mRNA, partial cds
11180	23846	37132	3	2.0E-26	AI801412.1	EST_HUMAN	to89a01.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2185416 3' similar to contains Alu
11395	24001		2.45	2.0E-26	AF055086.1	NT	repetitive element/contains element MER20 MER20 repetitive element;
12106	24603		1.57	2.0E-26	AB037899.1	NT	Homo sapiens MHC class 1 region
133	12948	26591	5.18	1.0E-26	BE170371.1	EST_HUMAN	Homo sapiens mRNA for KIAA1438 protein, partial cds
2040	14774	27503	1.37	1.0E-26	AL039383.2	EST_HUMAN	QV4-HT0538-020300-123-e02 HT0538 Homo sapiens cDNA
2693	15402		9.04	1.0E-26	AF261085.1	NT	DKFZp434H1910.t1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434H1910 5'
							Homo sapiens glyceraldehyde-3-phosphate dehydrogenase (GADPH) mRNA, complete cds

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Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6740	19574		3.05	1.0E-28	BE165980.1	EST_HUMAN	MR3-HT0487-150200-113-g01 HT0487 Homo sapiens cDNA
10809	23492		2.21	1.0E-26	AL038487.1	EST_HUMAN	DKFZp566C2146 J1 566 (synonym: hfkd2) Homo sapiens cDNA clone DKFZp566C2146 5'
12348	23395		3.53	1.0E-26	H55093.1	EST_HUMAN	CHR220032 Chromosome 22 exon Homo sapiens cDNA clone C22_45 5'
7484	20156		1.11	9.0E-27	BF371227.1	EST_HUMAN	RC8-FN0138-110800-022-A02 FN0138 Homo sapiens cDNA
9203	22082		4.14	9.0E-27	U93163.1	NT	Homo sapiens IMAGE-B2 (IMAGE-B2), IMAGE-B3 (IMAGE-B3), IMAGE-B4 (IMAGE-B4), and IMAGE-B1 (IMAGE-B1) genes, complete cds
11875	24454		5.72	9.0E-27	BF445558.1	EST_HUMAN	nao03c07.x1 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:3253644 3' similar to contains OFR.11
10	12837	25450	3.83	8.0E-27	AI831482.1	EST_HUMAN	wj49c04.x1 NCI_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2406150 3' similar to contains THR.b2
544	13327		4.33	8.0E-27	AL163227.2	NT	THR repetitive element ;
1395	14142	26819	59.39	8.0E-27	AW162737.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS210027
1395	14142	26820	59.39	8.0E-27	AW162737.1	EST_HUMAN	au87h08.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2783295 3' similar to gb:K00558
2164	14893	27628	1.37	8.0E-27	AW864776.1	EST_HUMAN	TUBULIN ALPHA-1 CHAIN (HUMAN);
3180	15943	28594	1.81	8.0E-27	P12236	SWISSPROT	au87h08.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2783295 3' similar to gb:K00558
3348	18107	28762	0.81	8.0E-27	AF181897.1	NT	TUBULIN ALPHA-1 CHAIN (HUMAN);
5608	18404	31317	1.02	8.0E-27	AV732214.1	EST_HUMAN	PM2-SN0018-220300-002-g07 SN0018 Homo sapiens cDNA
6881	17957		2.53	8.0E-27	BE926580.1	EST_HUMAN	ADP.ATP CARRIER PROTEIN, LIVER ISOFORM T2 (ADP/ATP TRANSLOCASE 3) (ADENINE
6947	19429	32444	2.29	8.0E-27	N84970.1	EST_HUMAN	NUCLEOTIDE TRANSLOCATOR 3) (ANT 3)
9109	21797	34961	1.51	8.0E-27	AW855759.1	EST_HUMAN	Homo sapiens WRN (WRN) gene, complete cds
9109	21797	34962	1.51	8.0E-27	AW855759.1	EST_HUMAN	AV732214 HTF Homo sapiens cDNA clone HTFBCB06 5'
668	13444		1.23	7.0E-27	Z70684.1	NT	MR4-BT0398-260800-204-d06 BT0398 Homo sapiens cDNA
5030	17750		2.25	7.0E-27	AW629172.1	EST_HUMAN	J1751F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone J1751 5' similar to
8756	21448		1.19	7.0E-27	D86984.1	NT	REPEATITIVE ELEMENT L1
10650	23341		4.26	7.0E-27	AJ271735.1	NT	CMT-CT0315-091289-063-d07 CT0315 Homo sapiens cDNA
12484	24843		2.12	7.0E-27	AV723365.1	EST_HUMAN	Human endogenous retroviral element HC2
10627	23320	38558	2.75	6.0E-27	M26697.1	NT	h51h12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2975879 3' similar to TR:O76040
11804	24394	37728	1.57	6.0E-27	U93163.1	NT	O76040 ORF2: FUNCTION UNKNOWN ;
							Human mRNA for KIAA0231 gene, partial cds
							Homo sapiens Xq pseudautosomal region; segment 1/2
							AV723365 HTB Homo sapiens cDNA clone HTBAHE02 5'
							Human nucleolar protein (B23) mRNA, complete cds
							Homo sapiens IMAGE-B2 (IMAGE-B2), IMAGE-B3 (IMAGE-B3), IMAGE-B4 (IMAGE-B4), and IMAGE-B1 (IMAGE-B1) genes, complete cds

Table 4

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10137	22785	35988	2.82	5.0E-27	BF666814.1	EST_HUMAN	602121491F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4278627 5'
10137	22785	35987	2.82	5.0E-27	BF666814.1	EST_HUMAN	602121491F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4278627 5'
6845	19407	32421	1.65	4.0E-27	9910569	NT	Mus musculus sperm tail associated protein (Stap), mRNA
7840	20535		1.07	4.0E-27	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
7883	20578		1.54	4.0E-27	AF078779.1	NT	Rattus norvegicus putative four repeat ion channel mRNA, complete cds
9844	22288	35491	0.7	4.0E-27	AW880859.1	EST_HUMAN	QV0-OT0033-070300-152-b10 OT0033 Homo sapiens cDNA
11604	24203	37525	1.98	4.0E-27	X89211.1	NT	H. sapiens DNA for endogenous retroviral like element
2034	14769	27499	4.61	3.0E-27	X60658.1	NT	R. rattus RYA3 mRNA for a potential ligand-binding protein
4238	16979	26604	1.06	3.0E-27	BE071924.1	EST_HUMAN	PM0-BT0627-090100-001-d11 BT0627 Homo sapiens cDNA
5262	18068	30697	6.24	3.0E-27	AA077705.1	EST_HUMAN	7B44C08 Chromosome 7 Fetal Brain cDNA Library Homo sapiens cDNA clone 7B44C08
7688	20361	33475	0.63	3.0E-27	BE070351.1	EST_HUMAN	7e33102.x1 NCI CGAP Lu24 Homo sapiens cDNA clone IMAGE:3284283 3'
9205	22084	35256	2.93	3.0E-27	BF036327.1	EST_HUMAN	601458531F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:3862086 5'
40	12868	25487	14.84	2.0E-27	AF054187.1	NT	Homo sapiens alpha NAC mRNA, complete cds
1898	14625		5.12	2.0E-27	AA565345.1	EST_HUMAN	nk01b10.s1 NCI CGAP Pr11 Homo sapiens cDNA clone IMAGE:1000689 similar to gb:M17886 60S
3107	15872		10.39	2.0E-27	AW629172.1	EST_HUMAN	hi61h12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2975879 3' similar to TR:O76040
3218	15981	28632	1.96	2.0E-27	AF111167.2	NT	Homo sapiens jun dimerization protein gene, partial cds, cfos gene, complete cds, and unknown gene
3218	15981	28633	1.96	2.0E-27	AF111167.2	NT	Homo sapiens jun dimerization protein gene, partial cds, cfos gene, complete cds, and unknown gene
4009	18755	29385	1.36	2.0E-27	AF000368.1	NT	Rattus norvegicus voltage-gated sodium channel mRNA, complete cds
6577	19340	32353	0.61	2.0E-27	H02655.1	EST_HUMAN	y36e01.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:150840 5' similar to
7989	20884	33810	1.85	2.0E-27	A1866347.1	EST_HUMAN	SP:HMGC_MOUSE Q02591 HOMEBOX PROTEIN ;
							w28g07.x1 NCI CGAP U11 Homo sapiens cDNA clone IMAGE:2426268 3'
8168	21839		2.3	2.0E-27	AA551527.1	EST_HUMAN	nk08h05.s1 NCI CGAP Thy1 Homo sapiens cDNA clone IMAGE:943737 similar to contains L1.13 L1
8691	22342	35536	0.76	2.0E-27	X60658.1	NT	R. rattus RYA3 mRNA for a potential ligand-binding protein
9935	22583	35792	1.28	2.0E-27	M78590.1	EST_HUMAN	EST00738 Fetal brain, Stratagene (cat#936206) Homo sapiens cDNA clone HFBCF07
9935	22583	35793	1.28	2.0E-27	M78590.1	EST_HUMAN	EST00738 Fetal brain, Stratagene (cat#936206) Homo sapiens cDNA clone HFBCF07
10875	23555	36802	4.11	2.0E-27	AJ121685.1	EST_HUMAN	AJ121685 MAMMA1 Homo sapiens cDNA clone MAMMA100746 5'
							nk01b10.s1 NCI CGAP Pr11 Homo sapiens cDNA clone IMAGE:1000689 similar to gb:M17886 60S
11469	14625		3.31	2.0E-27	AA565345.1	EST_HUMAN	ACIDIC RIBOSOMAL PROTEIN P1 (HUMAN);
428	13212		1.51	1.0E-27	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046

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Single Exon Probes Expressed in Brain

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
976	13741	28404	1.34	1.0E-27	AB026898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
4061	16806		0.98	1.0E-27	BE350127.1	EST_HUMAN	h09g01.x1 NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3 MER29 repetitive element;
6449	19217	32215	6.28	1.0E-27	8005855	NT	Homo sapiens Retina-derived POU-domain factor-1 (RPF-1), mRNA
6771	19515	32542	1.96	1.0E-27	F30158.1	EST_HUMAN	HSPD20481 HM3 Homo sapiens cDNA clone s4000095C10
6771	19515	32543	1.96	1.0E-27	F30158.1	EST_HUMAN	HSPD20481 HM3 Homo sapiens cDNA clone s4000095C10
8508	21200	34346	0.98	1.0E-27	AB007923.1	NT	Homo sapiens mRNA for KIAA0454 protein, partial cds
8894	21575		2.28	1.0E-27	BE079780.1	EST_HUMAN	RC8-B T0627-140200-011-E06 BT0627 Homo sapiens cDNA
9822	22275	35463	2.55	1.0E-27	D87449.1	NT	Human mRNA for KIAA0260 gene, partial cds
11704	24298	37625	3.51	1.0E-27	AF111083.1	NT	Bos taurus latrophilin 3 splice variant bbah mRNA, complete cds
137	12951		2.94	9.0E-28	BE348399.1	EST_HUMAN	hw17c11.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3183188 3' similar to TR:Q07314 Q07314
303	13107	25747	3.31	9.0E-28	AU126260.1	EST_HUMAN	SECRETED NEUREXIN III-ALPHA-C PRECURSOR, [3] TR:Q07280 TR:Q07313
10289	22937	38150	0.63	9.0E-28	AA174078.1	EST_HUMAN	zpt8g12.s1 Stratagene fetal retina 937202 Homo sapiens cDNA clone NT2RP1000443.5
11951	24504		4.85	9.0E-28	BF377859.1	EST_HUMAN	CM2-TN0140-070900-372-g01 TN0140 Homo sapiens cDNA
12286	25245		2.46	8.0E-28	AW157571.1	EST_HUMAN	au83h08.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2782811 3' similar to
1158	13913	26576	7.89	7.0E-28	AU142750.1	EST_HUMAN	TR:O60302 O60302 KIAA0555 PROTEIN, contains element MER22 repetitive element;
11142	23809	37089	3.36	7.0E-28	11417868	NT	AU142750 Y79AA1 Homo sapiens cDNA clone Y79AA1000824 5'
11910	24474		2.78	7.0E-28	AV735348.1	EST_HUMAN	Homo sapiens gamma-glutamyltransferase-like activity 1 (GGTLA1), mRNA
8817	21509		0.97	6.0E-28	AF016052.1	NT	Homo sapiens zinc finger protein ZNF191 (ZNF191) gene, complete cds
12528	24873		2.35	6.0E-28	AA504562.1	EST_HUMAN	aa60e03.r1 NCI_CGAP_GC81 Homo sapiens cDNA clone IMAGE:825340 5' similar to contains Alu repetitive element; contains element PTR6 repetitive element;
310	13114		4.19	5.0E-28	AI921003.1	EST_HUMAN	wo18c07.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2455692 3' similar to contains THR.b1 THR repetitive element;
3990	16738	29372	1.44	5.0E-28	R79782.1	EST_HUMAN	y86f10.r1 Soares placenta NB2HP Homo sapiens cDNA clone IMAGE:146443 5'
2631	15343	28087	1.68	4.0E-28	AW195086.1	EST_HUMAN	xn33c09.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2695504 3' similar to SW:GG95_HUMAN
2976	15742	28389	0.78	4.0E-28	4505316	NT	Q08379 GOLGIN-95;
3108	15871	28511	2.52	4.0E-28	BE409100.1	EST_HUMAN	Homo sapiens myosin phosphatase, target subunit 1 (MYPT1), mRNA
7230	19915	32988	1.93	4.0E-28	AI198941.1	EST_HUMAN	qf66f10.x1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1755019 3' similar to gb:M19503 LINE-1 REVERSE TRANSCRIPTASE HOMOLOG (HUMAN);

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10774	23457		3.08	4.0E-28	AF029308.1	NT	Homo sapiens chromosome 9 duplication of the T cell receptor beta locus and trypsinogen gene families
10928	23608		17.24	4.0E-28	AB038241.1	NT	Felis catus GAPDH mRNA for glyceraldehyde-3-phosphate dehydrogenase, complete cds
10950	19915	32988	4.75	4.0E-28	A1198941.1	EST_HUMAN	qf66f10.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1795019 3' similar to gb:M19503 LINE-1
12312	24734		1.84	4.0E-28	AW854244.1	EST_HUMAN	REVERSE TRANSCRIPTASE HOMOLOG (HUMAN)
1260	14009						RC3-CT0254-240400-210-112 CT0254 Homo sapiens cDNA
6051	17770		2.88	3.0E-28	AF155382.1	NT	Homo sapiens metalloprotease-like, disintegrin-like, cysteine-rich protein 2 epsilon (ADAM22) mRNA, complete cds
8726	21418	34562	1.06	3.0E-28	AF009650.1	NT	Homo sapiens T cell receptor beta locus, TCRBV7S9A2 to TCRBV12S2 region
10853	23533	36778	1.89	3.0E-28	BF354030.1	EST_HUMAN	MR3-HT0713-280500-013-f09 HT0713 Homo sapiens cDNA
12344	24751		2.09	3.0E-28	U53588.1	NT	Homo sapiens MHC class 1 region
87	12913	25551	3.62	3.0E-28	A1831991.1	EST_HUMAN	wj98f07.x1 NCI CGAP_Lym12 Homo sapiens cDNA clone IMAGE:2410885 3' similar to contains Alu repetitive element; contains element HGR repetitive element ;
1023	13783	26444	10.6	2.0E-28	BE062167.1	EST_HUMAN	RC1-BT0254-220300-019-c05 BT0254 Homo sapiens cDNA
1142	13897	26558	0.86	2.0E-28	4501912	NT	Homo sapiens a disintegrin and metalloproteinase domain 23 (ADAM23) mRNA
2481	15199	27839	16.03	2.0E-28	Y11107.3	NT	Homo sapiens ITGB4 gene for integrin beta 4 subunit, exons 3-41
6215	18989	31966	2.1	2.0E-28	A1348634.1	EST_HUMAN	qo35b06.x1 NCI CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1910483 3' similar to contains L1.b2 L1 repetitive element ;
6238	19012		1.33	2.0E-28	BF224402.1	EST_HUMAN	h176c03.x1 NCI CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3134404 3' similar to contains LOR1.b1
7943	20638	33766	5.07	2.0E-28	BF212905.1	EST_HUMAN	LOR1 repetitive element ;
9484	22137		0.71	2.0E-28	AF006273.1	NT	601814196F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4048751 5'
11614	24212	37536	6.54	2.0E-28	AW972305.1	EST_HUMAN	Sus scrofa domestica submaxillary epomucin mRNA, complete cds
12322	24741		1.84	2.0E-28	AF224669.1	NT	EST384394 IMAGE resequences, MAGL Homo sapiens cDNA
1461	14208	26895	2.22	2.0E-28	H08376.1	EST_HUMAN	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
2217	14945	27685	2.84	1.0E-28	D38044.1	NT	y179c09.r1 Soares Infant brain 1N1B Homo sapiens cDNA clone IMAGE:44300 5'
7759	20455		2.37	1.0E-28	BF333236.1	EST_HUMAN	Human gene for Ah-receptor, exon 7-9
7917	20612		3.2	1.0E-28	11429885	NT	QV1-BT0821-120900-360-b03 BT0821 Homo sapiens cDNA
9178	21848	35014	3.3	1.0E-28	8922793	NT	Homo sapiens similar to ribosomal protein L12 (H. sapiens) (LOC83091), mRNA
9776	22427	35633					Homo sapiens hypopharyngeal protein FLJ10968 (FLJ10968), mRNA
9776	22427	35634	4.84	1.0E-28	AA308744.1	EST_HUMAN	EST179616 HCC cell line (metastasis to liver in mouse) II Homo sapiens cDNA 5' end similar to similar to retroviral LTR
			8.73	1.0E-28	4759431	NT	Homo sapiens gamma-glutamyltransferase-like activity1 (GGTLA1), mRNA
			8.73	1.0E-28	4759431	NT	Homo sapiens gamma-glutamyltransferase-like activity1 (GGTLA1), mRNA

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10422	23068		0.53	1.0E-28	AU149356.1	EST_HUMAN	AU149356 NT2RM4 Homo sapiens cDNA clone NT2RM4002146 3'
11915	24478		7.79	1.0E-28	AA054182.1	EST_HUMAN	zif51c01.r1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:380448 5'
12651	25143		1.88	1.0E-28	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
12749	25348	30603	3.18	9.0E-29	AW563987.1	EST_HUMAN	h176g06.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2978266 3'
12436	24806		3.32	8.0E-29	Q00130	SWISSPROT	HYPOTHETICAL GENE 50 PROTEIN
1598	14344	27034	1.37	7.0E-29	AW566447.1	EST_HUMAN	EST378521 IMAGE resequences, MAGI Homo sapiens cDNA
12794	25045		7.13	7.0E-29	AJ132352.1	NT	Rattus norvegicus mRNA for 45 kDa secretory protein, partial
581	13361	25989	16.66	6.0E-29	A1936748.1	EST_HUMAN	wp69b01.x1 NCI CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2466985 3' similar to TR:O15475
12201	24689		8.09	6.0E-29	BE940498.1	EST_HUMAN	O15475 UNNAMED HERV-H PROTEIN; contains LTR7.b1 LTR7 repetitive element;
12286	24717		1.72	6.0E-29	BF568097.1	EST_HUMAN	RC3-UT0062-210800-021-c05 UT0062 Homo sapiens cDNA
8630	21322		5.36	5.0E-29	AW887541.1	EST_HUMAN	602184092F1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:4300079 5'
3226	15989		1.84	4.0E-29	A1752367.1	EST_HUMAN	RC3-OT0091-170300-011-c12 OT0091 Homo sapiens cDNA
5919	18704		7.91	4.0E-29	BE164830.1	EST_HUMAN	cn15c02.x1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC_cn15c02 random
7979	20674	33797	0.55	4.0E-29	A1678101.1	EST_HUMAN	QV1-HT0471-280300-121-a05 HT0471 Homo sapiens cDNA
7979	20674	33798	0.55	4.0E-29	A1678101.1	EST_HUMAN	wd35g06.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2330170 3' similar to contains
8644	21336	34480	6.21	4.0E-29	J04988.1	NT	MER29.12 MER29 repetitive element;
4381	17118	29751	1.4	3.0E-29	AB042287.1	NT	Human 90 kD heat shock protein gene, complete cds
4684	17418	30054	1.07	3.0E-29	BF333236.1	EST_HUMAN	Homo sapiens PTS gene for 8-pyruvoyltransferin synthase, complete cds
5841	18829	31584	1.18	3.0E-29	BE314018.1	EST_HUMAN	QV1-BT0821-120900-360-b03 BT0821 Homo sapiens cDNA
8632	21324	34465	2.87	3.0E-29	D38044.1	NT	601152657F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3508527 5'
9200	21869	35034	1.69	3.0E-29	AW303317.1	EST_HUMAN	Human gene for Ahr-receptor, exon 7-9
9431	22109		1.87	3.0E-29	AL163246.2	NT	xv1703.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2813405 3' similar to contains Alu
9859	22509		0.61	3.0E-29	BE350127.1	EST_HUMAN	repetitive element; contains MER19.12 MER19 repetitive element;
11235	23998	37185	1.47	3.0E-29	AA403053.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C046
12102	24600		1.53	3.0E-29	D63882.1	NT	h09g01.x1 NCI CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3
12799	25376		7.53	3.0E-29	AA016177.1	EST_HUMAN	MER29 repetitive element;
480	13265	25900	1.72	2.0E-29	AF084869.1	NT	z62b01.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:726889 5' similar to TR:G1335769
							G1335769 GAG-POL_POLYPROTEIN;
							Human HsLIM15 mRNA for HsLIM15, complete cds
							z632c09.s1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:360712 3'
							Homo sapiens envelope protein RIC-6 (env) gene, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
480	13285	25501	1.72	2.0E-28	AF084869.1	NT	Homo sapiens envelope protein RIG-6 (env) gene, complete cds
1523	14270	28955	6.62	2.0E-28	A1963604.1	EST_HUMAN	W65d10.x1 NCI_CGAP_U11 Homo sapiens cDNA clone IMAGE:2492563 3' similar to TR:O15546 O15546 HERV-E ENVELOPE GLYCOPROTEIN ;
1523	14270	28956	6.62	2.0E-29	A1963604.1	EST_HUMAN	W65d10.x1 NCI_CGAP_U11 Homo sapiens cDNA clone IMAGE:2492563 3' similar to TR:O15546 O15546 HERV-E ENVELOPE GLYCOPROTEIN ;
4246	18987	28910	1.63	2.0E-28	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C068
5735	18527	31449	0.99	2.0E-29	A1082459.1	EST_HUMAN	os71e04.x1 NCI_CGAP_GC2 Homo sapiens cDNA clone IMAGE:1610814 3' similar to contains L1.12 L1 repetitive element ;
6087	18865	31830	1.48	2.0E-29	A1806418.1	EST_HUMAN	wf27g07.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2356860 3' similar to contains element MER6 repetitive element ;
7459	18865	31830	1.36	2.0E-29	A1806418.1	EST_HUMAN	wf27g07.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2356860 3' similar to contains element MER6 repetitive element ;
7876	20571	33698	1.16	2.0E-29	BE867157.1	EST_HUMAN	wf27g07.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2356860 3' similar to contains element MER6 repetitive element ;
8477	21169	34313	0.63	2.0E-28	10567821	EST_HUMAN	601442206F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3846648 5'
8477	21169	34314	0.63	2.0E-28	10567821	NT	Homo sapiens DNA-binding protein (LOC56242), mRNA
9408	22070	35241	3.61	2.0E-29	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
9408	22070	35242	3.61	2.0E-29	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
10139	22787	35999	3.61	2.0E-29	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
10139	22787	36000	3.61	2.0E-29	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
10877	23557	36804	1.31	2.0E-29	BF025647.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C048
11459	24063		2.04	2.0E-29	11425108	NT	601669934F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3952833 5'
11499	24100		1.73	2.0E-29	AW880701.1	EST_HUMAN	Homo sapiens splicing factor similar to dnaj (SPF31), mRNA
8691	21383	34527	7.37	1.0E-29	AW983880.1	EST_HUMAN	QV0-OT0032-080300-155-d01 OT0032 Homo sapiens cDNA
10518	23184	36391	0.85	1.0E-29	X60668.1	NT	RC1-HN0003-220300-021-504 HN0003 Homo sapiens cDNA R.rattus RYA3 mRNA for a potential ligand-binding protein
8487	19284	32255	2.97	9.0E-30	AA761215.1	EST_HUMAN	nz20c07.s1 NCI_CGAP_GC81 Homo sapiens cDNA clone IMAGE:1288332 3' similar to contains MER4.b1 MER4 repetitive element ;
11992	24531		1.78	9.0E-30	11422745	NT	Homo sapiens zinc/iron regulated transporter-like (ZIRT), mRNA
6227	19001		8.94	8.0E-30	F08688.1	EST_HUMAN	HSC23F051 normalized infant brain cDNA Homo sapiens cDNA clone c-23f05
8168	20862	33994	3.72	8.0E-30	AA383873.1	EST_HUMAN	EST97317 Thymus I Homo sapiens cDNA 5' and similar to EST containing O family repeat
8593	21275	34412	3.1	8.0E-30	A1567072.1	EST_HUMAN	PT2.1_13_B1.r.tumor2 Homo sapiens cDNA 3'
1505	14251		1.03	7.0E-30	BE091133.1	EST_HUMAN	PM4-BT0724-150400-004-d11 BT0724 Homo sapiens cDNA
1766	14508	27209	1.73	6.0E-30	D55303.1	NT	Human mRNA for integrin alpha subunit, complete cds
3185	15948	28598	2.3	6.0E-30	BE09026.1	EST_HUMAN	QV0-BN0147-290400-214-f12 BN0147 Homo sapiens cDNA
10437	23083	36310	0.48	6.0E-30	AF177227.1	NT	Homo sapiens CTQL tumor antigen se20-10 mRNA, partial cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12769	17897		3.38	6.0E-30	X51755.1	NT	Human lambda-immunoglobulin constant region complex (germline)
3994	16742	26376	26.19	5.0E-30	A1399992.1	EST_HUMAN	Ig92g03.x1 NCL_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2116276 3' similar to contains Alu repetitive element;
5159	25176		5.44	5.0E-30	U87631.1	NT	Human aconitase hydratase (ACO2) gene, exon 7
10802	23485		1.95	5.0E-30	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
11103	23773	37047	2.47	5.0E-30	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
2139	14869	27599	1.72	4.0E-30	AW937471.1	EST_HUMAN	QV3-DT0043-090200-080-c06 DT0043 Homo sapiens cDNA
2139	14869	27600	1.72	4.0E-30	AW937471.1	EST_HUMAN	QV3-DT0043-090200-080-c06 DT0043 Homo sapiens cDNA
6756	17925	30560	0.63	4.0E-30	P11369	SWISSPROT	RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ;
8803	21495	34641	2.82	4.0E-30	AW812488.1	EST_HUMAN	CM1-ST0181-091199-035-108 S10181 Homo sapiens cDNA
1129	13885		2.11	3.0E-30	A1338551.1	EST_HUMAN	qq93c05.x1 Soares_tal_fetus_Nb2HF9_9w Homo sapiens cDNA clone IMAGE:1938920 3' similar to contains MER29.b2 MER29 repetitive element ;
3740	16493	29128	0.93	3.0E-30	AF128893.1	NT	Homo sapiens telomerase reverse transcriptase (TER1) gene, exons 1-6
7852	20547		0.58	3.0E-30	AF078779.1	NT	Rattus norvegicus putative four repeat ion channel mRNA, complete cds
8385	21078		0.48	3.0E-30	AF078779.1	NT	Rattus norvegicus putative four repeat ion channel mRNA, complete cds
10333	22980	36200	1.7	3.0E-30	BE350127.1	EST_HUMAN	h09g01.x1 NCL_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3 MER29 repetitive element ;
10465	23111	36342	0.53	3.0E-30	AB032969.1	NT	Homo sapiens mRNA for KIAA1143 protein, partial cds
10465	23111	36343	0.53	3.0E-30	AB032969.1	NT	Homo sapiens mRNA for KIAA1143 protein, partial cds
11168	23835	37116	2.48	3.0E-30	P34056	SWISSPROT	TRANSCRIPTION FACTOR AP-2
660	13436	26077	0.92	2.0E-30	AW857315.1	EST_HUMAN	GM0-CT0307-310100-158-h03 CT0307 Homo sapiens cDNA
1062	13820		3.11	2.0E-30	F08698.1	EST_HUMAN	HSC23F051 normalized infant brain cDNA Homo sapiens cDNA clone c-23105
1462	14209	26896	5.31	2.0E-30	BE175877.1	EST_HUMAN	RC5-HT0582-110400-013-H08 HT0582 Homo sapiens cDNA
2720	15427	28165	8	2.0E-30	BE765232.1	EST_HUMAN	IL2-NT0101-280700-116-E04 NT0101 Homo sapiens cDNA
2920	15686	28331	6.39	2.0E-30	AF114159.1	NT	Homo sapiens Y-linked zinc finger protein (ZFY) gene, complete cds
3769	16521	29160	2.26	2.0E-30	AW206581.1	EST_HUMAN	UI-H-B11-af0-c-12-0-UI st NCL_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2722558 3'
4727	17459	30095	1.51	2.0E-30	BE298945.1	EST_HUMAN	601119860F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3029438 5'
4727	17459	30096	1.51	2.0E-30	BE298945.1	EST_HUMAN	601119860F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3029438 5'
8660	19420	32435	0.55	2.0E-30	BF306337.1	EST_HUMAN	601893208F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4138993 5'
8375	21068	34208	0.45	2.0E-30	AA018103.1	EST_HUMAN	z558c10.r1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:363186 5'
8435	21128	34265	4.66	2.0E-30	C18939.1	EST_HUMAN	C18939 Human placenta cDNA (TFujitara) Homo sapiens cDNA clone GEN-570C01 5'

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8533	21225	34366	3.61	2.0E-30	BE670617.1	EST_HUMAN	7e37c12.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3284662 3' similar to SW:DHSA_HUMAN P31040 SUCCINATE DEHYDROGENASE [UBIQUINONE] FLAVOPROTEIN SUBUNIT PRECURSOR ;
8533	21225	34367	3.61	2.0E-30	BE670617.1	EST_HUMAN	7e37c12.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3284662 3' similar to SW:DHSA_HUMAN P31040 SUCCINATE DEHYDROGENASE [UBIQUINONE] FLAVOPROTEIN SUBUNIT PRECURSOR ;
9897	22647	35741	3.62	2.0E-30	AW971568.1	EST_HUMAN	EST383657 IMAGE resequences, MAGL Homo sapiens cDNA
9982	22630	35839	7.37	2.0E-30	AW470791.1	EST_HUMAN	ha33d06.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2875499 3' similar to contains THR.b3 THR repetitive element ;
280	13087	25729	16.33	1.0E-30	C18939.1	EST_HUMAN	C18939 Human placenta cDNA (TFujiiwara) Homo sapiens cDNA clone IMAGE:2910991 3' similar to contains MER1.13 MER1 MER1 repetitive element ;
525	13309	25942	2.34	1.0E-30	AW468897.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C003
699	13474	26122	2.62	1.0E-30	AL163203.2	NT	ac77b08.s1 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:868599 3'
2209	14937	27675	7.16	1.0E-30	AA664377.1	EST_HUMAN	60202560F1 NCI_CGAP_Brm67 Homo sapiens cDNA clone IMAGE:4157991 5'
2464	15182	27921	2.01	1.0E-30	BF347728.1	EST_HUMAN	EST186868 HCC cell line (metastasis to liver in mouse) II Homo sapiens cDNA 5' end
3050	15816	28461	0.94	1.0E-30	AA315045.1	EST_HUMAN	601809932F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:4040694 5'
7624	20290	33399	2.46	1.0E-30	BF183230.1	EST_HUMAN	CHR220532 Chromosome 22 exon Homo sapiens cDNA clone C22_728 5'
12581	25268		6.95	1.0E-30	H55593.1	EST_HUMAN	yc65e06.r1 Stratagene liver (#937224) Homo sapiens cDNA clone IMAGE:85570 5'
3748	16501	29135	0.81	9.0E-31	T73025.1	EST_HUMAN	yc65e06.r1 Stratagene liver (#937224) Homo sapiens cDNA clone IMAGE:85570 5'
3748	16501	29136	0.81	9.0E-31	T73025.1	EST_HUMAN	yc65e06.r1 Stratagene liver (#937224) Homo sapiens cDNA clone IMAGE:85570 5'
8223	20917	34053	0.81	9.0E-31	R18214.1	EST_HUMAN	RELATED PROTEIN RAB-2 (HUMAN);
8223	20917	34054	0.81	9.0E-31	R18214.1	EST_HUMAN	y99b08.r1 Scores infant brain 1N1B Homo sapiens cDNA clone IMAGE:30566 5' similar to gb:X12953 RAS- RELATED PROTEIN RAB-2 (HUMAN);
8522	21214		1.63	9.0E-31	Z38293.1	EST_HUMAN	HSC05F032 normalized infant brain cDNA Homo sapiens cDNA clone c-05f03 3'
8524	21216	34359	0.48	9.0E-31	AF078779.1	NT	Rattus norvegicus putative four repeat ion channel mRNA, complete cds
1054	13813	26473	2.41	8.0E-31	8923389	NT	Homo sapiens hypothetical protein FLJ20420 (FLJ20420), mRNA
2414	15135		4.6	8.0E-31	AL163208.2	NT	Homo sapiens chromosome 21 segment HS21C008
4861	17590	30213	1.43	8.0E-31	P23275	SWISSPROT	OLFACTORY RECEPTOR 15 (OR3)
4861	17590	30214	1.43	8.0E-31	P23275	SWISSPROT	OLFACTORY RECEPTOR 15 (OR3)
2674	15383	28123	3.29	7.0E-31	BE326517.1	EST_HUMAN	hw05a11.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3182012 3'
2674	15383	28124	3.29	7.0E-31	BE326517.1	EST_HUMAN	hw05a11.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3182012 3'
8300	20964	34130	0.96	7.0E-31	AF208541.1	NT	Homo sapiens V1-vascular vasopressin receptor AVPR1A gene, promoter region and partial cds
8300	20964	34131	0.96	7.0E-31	AF208541.1	NT	Homo sapiens V1-vascular vasopressin receptor AVPR1A gene, promoter region and partial cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9168	21836		0.94	7.0E-31	BE408611.1	EST_HUMAN	601304125F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3638310 5'
12434	24805	31044	2.26	7.0E-31	X51755.1	NT	Human lambda-immunoglobulin constant region complex (germline)
3667	16420		2.66	6.0E-31	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
8053	20747		4.37	6.0E-31	AF055066.1	NT	Homo sapiens MHC class 1 region
8229	20923	34062	0.66	6.0E-31	BE350127.1	EST_HUMAN	h09g01.x1 NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3
12169	25195		1.96	6.0E-31	BE894488.1	EST_HUMAN	MER29 repetitive element;
187	13000	25640	3.58	5.0E-31	M60894.1	NT	601433087F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3918524 5'
187	13000	25641	3.58	5.0E-31	M60894.1	NT	Homo sapiens type I DNA topoisomerase gene, exon 8
8344	21037		0.73	5.0E-31	BF056540.1	EST_HUMAN	Homo sapiens type I DNA topoisomerase gene, exon 8
582	13362		5.18	4.0E-31	AJ271735.1	NT	7k06104.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:3443479 3' similar to TR:Q13537 Q13537
							SIMILAR TO POGO ELEMENT; contains L1 L1 repetitive element;
							Homo sapiens Xq pseudautosomal region; segment 1/2
1609	14352	27040	0.91	4.0E-31	Q10473	SWISSPROT	POLYPEPTIDE N-ACETYL GALACTOSAMINYLTRANSFERASE (PROTEIN-UDP
1810	14550		1.57	4.0E-31	AL163280.2	NT	ACETYL GALACTOSAMINYLTRANSFERASE (UDP-GALNAC:POLYPEPTIDE, N-
2792	15497		1.23	4.0E-31	5730038	NT	Homo sapiens chromosome 21 segment HS21C080
12205	24672		1.86	4.0E-31	AJ230125.1	NT	Homo sapiens SET domain and mariner transposase fusion gene (SETMAR) mRNA
12457	24826		1.86	4.0E-31	11430273	NT	Homo sapiens GGT1 gene, exon 1
							Homo sapiens KIA00569 gene product (KIA00569), mRNA
7239	19924	32999	12.23	3.0E-31			Homo sapiens NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 8 (19kD, ASH1) (NDUFB8) mRNA
7393	20072	33151	1.28	3.0E-31	11420329	NT	Homo sapiens hypothetical protein FLJ10842 (FLJ10842), mRNA
8061	20755		2	3.0E-31	AL163206.2	NT	Homo sapiens chromosome 21 segment HS21C006
9479	22132	35312	3.7	3.0E-31	D14523.1	NT	Horse mRNA for ferritin L-chain, complete cds
10498	23144	36371	0.54	3.0E-31	AA421242.1	EST_HUMAN	zu06d04.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:731047 5'
10527	23224	36459	2.04	3.0E-31	P111174	SWISSPROT	40S RIBOSOMAL PROTEIN S15 (RIG PROTEIN)
11101	23771		3.65	3.0E-31	BF033327.1	EST_HUMAN	601458531F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3862086 5'
12819	25059		1.66	3.0E-31	AB037763.1	NT	Homo sapiens mRNA for KIAA1342 protein, partial cds
1910	14647	27358	1.37	2.0E-31	AW838171.1	EST_HUMAN	QV2-LT0051-260300-111-f03 L.T0051 Homo sapiens cDNA
2211	14939	27677	1.09	2.0E-31	A1393388.1	EST_HUMAN	tg44g05.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2111672 3'
2339	15062	27800	1.89	2.0E-31	AL119245.1	EST_HUMAN	DKF4761G1513_r1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZ761G1513 5'
2442	15161	27898	4.01	2.0E-31	AA458824.1	EST_HUMAN	aa88f11.s1 Stratagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:838413 3' similar to contains THR12 THR repetitive element;

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5163	18001	30624	0.81	2.0E-31	AW444496.1	EST_HUMAN	UHH-BJ3-akb-f09-0-J1.s1 NCL_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2733833 3'
5624	18421	31334	3.57	2.0E-31	BE350127.1	EST_HUMAN	h08g01.x1 NCL_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3148256 3' similar to contains MIER29 b3 MER29 repetitive element ;
8975	21665		2.05	2.0E-31	AA877764.1	EST_HUMAN	MER37 TRANSPOSABLE ELEMENT, COMPLETE CONSENSUS SEQUENCE. ;
9107	21795	34959	3.64	2.0E-31	7661535	NT	Homo sapiens B9 protein (B9), mRNA
9806	22457	35661	0.94	2.0E-31	AV710948.1	EST_HUMAN	AV710948 Cu Homo sapiens cDNA clone CuAALB07 5'
9806	22457	35662	0.84	2.0E-31	AV710948.1	EST_HUMAN	AV710948 Cu Homo sapiens cDNA clone CuAALB07 5'
9975	22623	35829	2.35	2.0E-31	BE408611.1	EST_HUMAN	601304125F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3638310 5'
9975	22623	35830	2.35	2.0E-31	BE408611.1	EST_HUMAN	601304125F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3638310 5'
12144	24632		1.56	2.0E-31	AF148612.1	NT	Homo sapiens hexokinase II gene, promoter region
12279	25413		1.75	2.0E-31	A1114527.1	EST_HUMAN	HA1110 Human fetal liver cDNA library Homo sapiens cDNA
15	12842	25456	11.09	1.0E-31	U93163.1	NT	Homo sapiens IMAGE-B2 (IMAGE-B2), IMAGE-B3 (IMAGE-B3), IMAGE-B4 (IMAGE-B4), and IMAGE-B1 (IMAGE-B1) genes, complete cds
1658	14404	27082	1.35	1.0E-31	O95371	SWISSPROT	OLFACTORY RECEPTOR 2C1
1658	14404	27093	1.35	1.0E-31	O95371	SWISSPROT	OLFACTORY RECEPTOR 2C1
1658	14404	27094	1.35	1.0E-31	O95371	SWISSPROT	OLFACTORY RECEPTOR 2C1
4592	17327	29952	1.15	1.0E-31	AL134376.1	EST_HUMAN	DKFZp547B235_1 547 (synonym: hfar1) Homo sapiens cDNA clone DKFZp547B235 5'
4592	17327	29953	1.15	1.0E-31	AL134376.1	EST_HUMAN	DKFZp547B235_1 547 (synonym: hfar1) Homo sapiens cDNA clone DKFZp547B235 5'
5210	18018	30640	3.79	1.0E-31	AW391679.1	EST_HUMAN	MR3-ST0220-151299-028-a08_1 ST0220 Homo sapiens cDNA
8042	18922	31782	2.2	1.0E-31	AF048727.1	NT	Homo sapiens minisatellite ceb1 repeat region
7189	19875	32948	1	1.0E-31	AF126145.1	NT	Bos taurus xenobiotic/medium-chain fatty acid:CoA ligase form XL-III mRNA, nuclear mRNA encoding mitochondrial protein, complete cds
10136	22784	35995	0.51	1.0E-31	U93163.1	NT	Homo sapiens IMAGE-B2 (IMAGE-B2), IMAGE-B3 (IMAGE-B3), IMAGE-B4 (IMAGE-B4), and IMAGE-B1 (IMAGE-B1) genes, complete cds
10833	23515	38757	2.7	1.0E-31	A1080643.1	EST_HUMAN	q121h03.x1 NCL_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:1750709 3' similar to TR:Q16595 Q16595 FRAXIN. ;
11830	24414	37752	1.48	1.0E-31	U66061.1	NT	Human germline T-cell receptor beta chain TCRBV17S1A1T, TCRBV2S1, TCRBV10S1P, TCRBV28S1P, TCRBV19S1P, TCRBV15S1, TCRBV11S1A1T, HVB relic, TCRBV28S1P, TCRBV34S1, TCRBV14S1, TCRBV3S1, TCRBV4S1A1T, TRY4, TRY5, TRY6, TRY7, TRY8, TCRBD1, TCRBJ1S1, TCRBJ1S2,>
6542	19307	32312	2.38	9.0E-32	AV723976.1	EST_HUMAN	AV723976 HTB Homo sapiens cDNA clone HTBAAG01 5'
7492	20164		0.68	9.0E-32	11430822	NT	Homo sapiens hypothetical protein FLJ11294 (FLJ11294), mRNA
2070	14802	27530	2.48	8.0E-32	A1056770.1	EST_HUMAN	oz15a09.x1 Soares_fetal_liver_infls_S1 Homo sapiens cDNA clone IMAGE:1676384 3'

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Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression- Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5394	18184	30887	0.97	8.0E-32	AW997214.1	EST_HUMAN	RC2-BN0048-200300-015-e04 BN0048 Homo sapiens cDNA
4807	17538	30161	0.98	7.0E-32	P52591	SWISSPROT	NUCLEAR ENVELOPE PORE MEMBRANE PROTEIN POM 121 (PORE MEMBRANE PROTEIN OF 121 KD) (P1445)
12122	24814		8.19	7.0E-32	X17283.1	NT	Human chromosome 22 immunoglobulin V(K) gene, part with 5' breakpoint between orphon and neighbouring non-amplified region
2735	15442	28180	1.01	8.0E-32	A1478104.1	EST_HUMAN	Im34a10.x1 NCL CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2159894 3' similar to contains MER28.t3
7266	19950		1.47	6.0E-32	BE888016.1	EST_HUMAN	MER29 repetitive element;
1011	13771	28431	16.78	5.0E-32	AF116827.1	NT	601161630F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3913087 5'
910	13877		1.76	4.0E-32	AL163246.2	NT	Homo sapiens PRO1181 mRNA, complete cds
5148	17867		0.91	4.0E-32	A1885593.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C048
7503	20174	33266	2.94	4.0E-32	11432574	NT	wo08h12.x1 NCL CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2496647 3' similar to contains MER18.b3
7503	20174	33267	2.94	4.0E-32	11432574	NT	MER18 repetitive element;
8257	20951		1.2	4.0E-32	BE064410.1	EST_HUMAN	Homo sapiens AT-binding transcription factor 1 (ATBF1), mRNA
443	13229	25872	3.7	3.0E-32	Y17293.1	NT	Homo sapiens AT-binding transcription factor 1 (ATBF1), mRNA
1437	14184	28870	8.08	3.0E-32	AV731500.1	EST_HUMAN	RC4-BT0311-141199-011-h08 BT0311 Homo sapiens cDNA
9294	21961	35135	8.38	3.0E-32	AV758634.1	EST_HUMAN	Homo sapiens FLI-1 gene, partial
9294	21961	35136	8.38	3.0E-32	AV758634.1	EST_HUMAN	AV731500 HTF Homo sapiens cDNA clone HTFAK007 5'
10943	23525	36768	3.57	3.0E-32	AA777621.1	EST_HUMAN	AV758634 BM Homo sapiens cDNA clone BMFBH12 5'
12146	24634		3.51	3.0E-32	BE278086.1	EST_HUMAN	AV758634 BM Homo sapiens cDNA clone BMFBH12 5'
12507	17899	30586	2.87	3.0E-32	5174574	NT	z195a07.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:448500 3' similar to contains THR.t3 THR repetitive element;
12507	17899	30587	2.87	3.0E-32	5174574	NT	601156285F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3139701 5'
12507	17899	30587	2.87	3.0E-32	5174574	NT	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (trithorax (Drosophila) homolog), translocated to, 4 (MILLT4) mRNA
12658	24956		2.27	3.0E-32	BE278086.1	EST_HUMAN	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (trithorax (Drosophila) homolog), translocated to, 4 (MILLT4) mRNA
6158	18935	31802	0.81	2.0E-32	M35418.1	NT	601156285F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3139701 5'
6387	19156	32155	5.32	2.0E-32	Z38133.1	NT	Human cell 12-lipoxygenase mRNA, complete cds
6387	19156	32156	5.32	2.0E-32	Z38133.1	NT	H. sapiens mRNA for myosin
8176	20870	34003	2.28	2.0E-32	AA114294.1	EST_HUMAN	H. sapiens mRNA for myosin
8176	20870	34004	2.28	2.0E-32	AA114294.1	EST_HUMAN	z196c08.r1 Stratagene HeLa cell s3 937216 Homo sapiens cDNA clone IMAGE:563150 5'
11859	24443	37784	2.96	2.0E-32	T18862.1	EST_HUMAN	z196c08.r1 Stratagene HeLa cell s3 937216 Homo sapiens cDNA clone IMAGE:563150 5'
12763	25022	30961	2.42	2.0E-32	AV736449.1	EST_HUMAN	b12058 Testis 1 Homo sapiens cDNA clone b12058
							AV736449 CB Homo sapiens cDNA clone CBFIA08 5'

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12763	25022	30962	2.42	2.0E-32	AV736449.1	EST_HUMAN	AV736449 CB Homo sapiens cDNA clone CBFIA08 5'
3090	15855		1.67	1.0E-32	BE743289.1	EST_HUMAN	601573207F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3834433 5'
6955	19437	32453	7.02	1.0E-32	11439789	NT	Homo sapiens chromosome 11 open reading frame 9 (C11ORF9), mRNA
8494	21186	34329	8.08	1.0E-32	AA720574.1	EST_HUMAN	ntw21g02.s1 NCL_CGAP_GCB0 Homo sapiens cDNA clone IMAGE:1241138 3' similar to contains THR.13 THR repetitive element;
3474	16230		4.68	9.0E-33	BE327112.1	EST_HUMAN	hw07c05.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3182216 3' similar to TR:O88539 O88539 WW DOMAIN BINDING PROTEIN 11.;
6326	19096		4.05	9.0E-33	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
8687	21379	34523	1.95	9.0E-33	BF347229.1	EST_HUMAN	602021164F1 NCL_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4156670 5'
10701	23392		5.22	9.0E-33	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
58	12887	25517	3.14	7.0E-33	5031736	NT	Homo sapiens short-chain alcohol dehydrogenase family member (HEP27) mRNA
58	12887	25518	3.14	7.0E-33	5031736	NT	Homo sapiens short-chain alcohol dehydrogenase family member (HEP27) mRNA
2158	14888	27622	2.29	7.0E-33	A1590115.1	EST_HUMAN	to12b09.x1 NCL_CGAP_U12 Homo sapiens cDNA clone IMAGE:2178909 3' similar to contains OFR.t1 OFR repetitive element;
2655	15365		6.45	7.0E-33	AV730056.1	EST_HUMAN	AV730056 HTF Homo sapiens cDNA clone HTFAVE06 5'
3236	15998		9.3	7.0E-33	AW971307.1	EST_HUMAN	EST383396 MAGL Homo sapiens cDNA Homo sapiens cDNA
8845	21537		1.56	7.0E-33	X54890.1	NT	Human hLRP mRNA for leukocyte common antigen-related peptide (protein-tyrosine phosphate) (EC 3.1.3.48)
10732	23419	36660	2.41	7.0E-33	BF347229.1	EST_HUMAN	602021164F1 NCL_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4156670 5'
11213	23876	37162	1.93	7.0E-33	AW971568.1	EST_HUMAN	EST383657 MAGL Homo sapiens cDNA Homo sapiens cDNA
12127	24619	31090	4.34	7.0E-33	AA601416.1	EST_HUMAN	nt16h01.s1 NCL_CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1100881 3' similar to contains L1.H L1 repetitive element;
3720	16473		0.94	6.0E-33	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
5976	18758	31720	0.96	6.0E-33	F30631.1	EST_HUMAN	HSPD21201 HM3 Homo sapiens cDNA clone s4000107H06
5976	18758	31721	0.96	6.0E-33	F30631.1	EST_HUMAN	HSPD21201 HM3 Homo sapiens cDNA clone s4000107H06
8478	21170	34315	9.33	6.0E-33	J04038.1	NT	Human glyceraldehyde-3-phosphate dehydrogenase (GAPDH) gene, complete cds
8603	21295	34438	3.09	6.0E-33		NT	Homo sapiens similar to RAD23 (S. cerevisiae) homolog B (H. sapiens) (LOC63277), mRNA
9910	22559	35754	1.12	6.0E-33		NT	Mus musculus SRY-box containing gene 6 (Sox6), mRNA
9910	22559	35755	1.12	6.0E-33	6755609	NT	Mus musculus SRY-box containing gene 6 (Sox6), mRNA
1770	14512		1.46	5.0E-33	BF373515.1	EST_HUMAN	QV1-FT0169-100700-271-e02 F10169 Homo sapiens cDNA
1874	14612		1.19	5.0E-33	11141884	NT	Homo sapiens solute carrier family 5 (choline transporter), member 7 (SLC5A7), mRNA
1891	14628	27337	1.43	5.0E-33	4507208	NT	Homo sapiens spermidine synthase (SRM) mRNA
1891	14628	27338	1.43	5.0E-33	4507208	NT	Homo sapiens spermidine synthase (SRM) mRNA

Table 4

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2270	14986		1.29	5.0E-33	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
10148	22786	36010	0.8	5.0E-33	AW284679.1	EST_HUMAN	xq33f11.x1 NCL CGAP_Lu28 Homo sapiens cDNA clone IMAGE:2752461 3'
10148	22786	36011	0.8	5.0E-33	AW284679.1	EST_HUMAN	xq33f11.x1 NCL CGAP_Lu28 Homo sapiens cDNA clone IMAGE:2752461 3'
1106	13863		2.16	4.0E-33	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C007
2121	14852	27581	1.84	4.0E-33	4758987	NT	Homo sapiens RAB1, member RAS oncogene family (RAB1) mRNA
2419	15140		2.02	4.0E-33	AA626621.1	EST_HUMAN	ab51b11.1 Stratagene lung carcinoma 937218 Homo sapiens cDNA clone IMAGE:844317 5' similar to contains Alu repetitive element; contains MER28.b2 MER28 repetitive element ;
2547	15262	27899	4.15	4.0E-33	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
4450	17186	29811	2.15	4.0E-33	AW283349.1	EST_HUMAN	UJ-H-R12-ehc-03-0.U1.s1 NCL CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2727149 3'
5318	18122	30779	24.73	4.0E-33	AA053053.1	EST_HUMAN	z71a08.r1 Stratagene colon (#937204) Homo sapiens cDNA clone IMAGE:510038 5' similar to gb-X12671_nat1 HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1 (HUMAN);
6298	19072	32057	0.87	4.0E-33	8393984	NT	Homo sapiens polymerase (DNA directed), alpha (POLA), mRNA
6299	19072	32058	0.87	4.0E-33	8393984	NT	Homo sapiens polymerase (DNA directed), alpha (POLA), mRNA
1067	13825		5.5	3.0E-33	BE350127.1	EST_HUMAN	hi08g01.x1 NCL CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3 MER29 repetitive element ;
1068	13825		3.89	3.0E-33	BE350127.1	EST_HUMAN	hi08g01.x1 NCL CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3 MER29 repetitive element ;
2451	15595		0.92	3.0E-33	AV647851.1	EST_HUMAN	AV647851 GLC Homo sapiens cDNA clone GLCFCF09 3'
10338	22985	36203	1.04	3.0E-33	AA861510.1	EST_HUMAN	Q13579 MARINER TRANSPOSASE ;
102	12843		3.21	2.0E-33	AI160189.1	EST_HUMAN	qb67g03.x1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:1407647 3' similar to TR:Q13579 contains OFR.H OFR repetitive element ;
4385	17122		5.39	2.0E-33	BET59039.1	EST_HUMAN	MRO-HT0405-160300-202-d08 HT0405 Homo sapiens cDNA
4925	17653	30265	28.91	2.0E-33	AA626683.1	EST_HUMAN	ab51g11.1 Stratagene lung carcinoma 937218 Homo sapiens cDNA clone IMAGE:844388 5' similar to gb:X00734_cds1 TUBULIN BETA-5 CHAIN (HUMAN);
5033	17753	30365	2.75	2.0E-33	11421332	NT	Homo sapiens hypothetical protein SIRP-b2 (SIRP-b2), mRNA
5033	17753	30366	2.75	2.0E-33	11421332	NT	Homo sapiens hypothetical protein SIRP-b2 (SIRP-b2), mRNA
6329	18098	32087	1.81	2.0E-33	A127492.1	EST_HUMAN	q96d01.x1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:1880161 3'
8968	21688		2.18	2.0E-33	AI052256.1	EST_HUMAN	oz21d003.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1675973 3' similar to gb:IM28536 TRANSLATIONAL INITIATION FACTOR 2 BETA SUBUNIT (HUMAN);
10513	23159	36384	1.48	2.0E-33	11421332	NT	Homo sapiens hypothetical protein SIRP-b2 (SIRP-b2), mRNA
10513	23159	36385	1.48	2.0E-33	11421332	NT	Homo sapiens hypothetical protein SIRP-b2 (SIRP-b2), mRNA
11046	23716	36985	1.26	2.0E-33	AA463847.1	EST_HUMAN	zx48f05.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:795489 3' similar to TR:G1263081 G1263081 MARINER TRANSPOSASE ;

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descripbr
8	12835		1.16	1.0E-33	AF003528.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
5156	17873	30485	2.48	1.0E-33	4502556	NT	Homo sapiens calcium/calmodulin-dependent protein kinase IV (CAMK4) mRNA
5501	18289	31198	0.58	1.0E-33	AF199420.1	NT	Homo sapiens F-box protein FBL4 (FBL4) mRNA, complete cds
7307	19890	33087	1.04	1.0E-33	MT3975.1	NT	Homo sapiens protein kinase C beta-II type (PRKCB1) mRNA, complete cds
9920	25432		0.84	1.0E-33	U60822.1	NT	Human dystrophin (DMD) gene, exons 7, 8 and 9, and partial cds
11292	23953	37251	1.83	1.0E-33	AW998818.1	EST_HUMAN	QV3-BN0047-230200-102-103 BN0047 Homo sapiens cDNA
11663	24259	37581	3.32	1.0E-33	U60822.1	NT	Human dystrophin (DMD) gene, exons 7, 8 and 9, and partial cds
12407	24790		2.21	1.0E-33	A1927191.1	EST_HUMAN	wc88c06.x1 NCL CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2462410 3'
12570	12835		4.07	1.0E-33	AF003528.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
12602	24914	31005	1.41	1.0E-33	AV727809.1	EST_HUMAN	AV727809 HTC Homo sapiens cDNA clone HTCCNC12 5'
12780	25034		1.61	1.0E-33	A1271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
2168	14897	27631	0.96	8.0E-34	8922751	NT	Homo sapiens hypothetical protein FLJ10900 (FLJ10900), mRNA
7989	20353	33468	0.66	8.0E-34	BE069882.1	EST_HUMAN	MR4-BT0399-200100-007-H03 BT0399 Homo sapiens cDNA
1428	14173	26858	2.27	7.0E-34	T70845.1	EST_HUMAN	y415e05.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:108320 5'
9900	14173	26858	0.56	7.0E-34	T70845.1	EST_HUMAN	y415e05.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:108320 5'
12191	24662		3.05	7.0E-34	H12866.1	EST_HUMAN	y14c10.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:148722 5'
458	13243	25884	2.3	6.0E-34	U10991.1	NT	Human G2 protein mRNA, partial cds
458	13243	25885	2.3	6.0E-34	U10991.1	NT	Human G2 protein mRNA, partial cds
12011	24544	31107	2.13	6.0E-34	U03686.1	NT	Mus musculus DAB/2J hair-specific (hacl-1) gene
1873	14611		2.9	5.0E-34	7706500	NT	Homo sapiens Npw38-binding protein NpwBP (LOC51729), mRNA
5002	17725	30328	3.61	5.0E-34	U30883.1	NT	Human splicing factor SRp55-1 (SRP55) mRNA, complete cds
8765	21457	34607	1.37	5.0E-34	AF078779.1	NT	Rattus norvegicus putative four repeat ion channel mRNA, complete cds
10550	23246	36482	2.24	5.0E-34	AB037656.1	NT	Homo sapiens mRNA for KIAA1435 protein, partial cds
11219	23882		1.79	5.0E-34	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
1991	14727	27449	1.64	4.0E-34	A1804687.1	EST_HUMAN	h94c06.x1 NCL CGAP_P28 Homo sapiens cDNA clone IMAGE:2249184 3'
5770	18561	31488	0.64	4.0E-34	AA861773.1	EST_HUMAN	ak35c01.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1407936 3'
8936	21627	34769	1.28	4.0E-34	BF209778.1	EST_HUMAN	601874950F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4102213 5'
6138	18916	31886	0.78	3.0E-34	M3727.1	NT	Human Ig gamma H-chain D-region genes, partial cds
11100	23770		3.14	3.0E-34	BF035327.1	EST_HUMAN	601459531F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3862086 5'
8850	21541	34887	1.16	2.0E-34	A1678101.1	EST_HUMAN	wd35g06.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2330170 3' similar to contains MER29.12 MER29 repetitive element;

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Table 4
Single Exon Probes Expressed In Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8850	21541	34688	1.16	2.0E-34	AI878101.1	EST_HUMAN	wd35g06.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2330170 3' similar to contains
11113	23783	37057	1.34	2.0E-34	P51805	SWISSPROT	MER29.12 MER29 repetitive element ;
11113	23783	37058	1.34	2.0E-34	P51805	SWISSPROT	PLEXIN 4 PRECURSOR (TRANSMEMBRANE PROTEIN SEX)
1494	14241	26928	6.53	1.0E-34	P12236	SWISSPROT	PLEXIN 4 PRECURSOR (TRANSMEMBRANE PROTEIN SEX)
							ADP-ATP CARRIER PROTEIN, LIVER ISOFORM T2 (ADP/ATP TRANSLOCASE 3) (ADENINE NUCLEOTIDE TRANSLOCATOR 3) (ANT 3)
3663	18416	28055	1.32	1.0E-34	AF003528.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
4051	18796	29425	0.97	1.0E-34	AY008397.1	NT	Homo sapiens WNT3 precursor (WNT3) mRNA, complete cds
4051	18798	29426	0.97	1.0E-34	AY008397.1	NT	Homo sapiens WNT3 precursor (WNT3) mRNA, complete cds
4446	17182		3.44	1.0E-34	BE071414.1	EST_HUMAN	RC2-BT0506-240400-016-h08 BT0506 Homo sapiens cDNA
6047	18827	31788	2.05	1.0E-34	BE874052.1	EST_HUMAN	601484430F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3886999 5'
6047	18827	31789	2.05	1.0E-34	BE874052.1	EST_HUMAN	601484430F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3886999 5'
9225	21904	35076	0.45	1.0E-34	P23268	SWISSPROT	OLFACTORY RECEPTOR-LIKE PROTEIN F5
9596	22429	35434	7.1	1.0E-34	AL036635.1	EST_HUMAN	DKFZp564A1563_r1 564 (synonym: hfor2) Homo sapiens cDNA clone DKFZp564A1563 5'
11138	23805	37083	1.39	1.0E-34	BE781790.1	EST_HUMAN	601470592F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3873478 5'
11138	23805	37084	1.39	1.0E-34	BE781790.1	EST_HUMAN	601470592F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3873478 5'
11153	23820	37100	1.82	1.0E-34	11439599	NT	Homo sapiens nucleobindin 2 (NUCB2), mRNA
12372	25350		1.65	1.0E-34	AA807097.1	EST_HUMAN	cc31c11.s1 NCI_CGAP_GC81 Homo sapiens cDNA clone IMAGE:1351316 3' similar to gb:X68203
12593	24949		4.22	1.0E-34	AL163210.2	NT	TYROSINE-PROTEIN KINASE RECEPTOR FLT4 PRECURSOR (HUMAN);
3636	16389	28028	1.2	9.0E-35	AW66302.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C010
218	13029		7.71	8.0E-35	6031190	NT	hnt7b06.y1 NCI_CGAP_GLI1 Homo sapiens cDNA clone IMAGE:2968787 5'
1730	14472	27171	3.43	8.0E-35	BF589937.1	EST_HUMAN	Homo sapiens prohibitin (PHB) mRNA
1730	14472	27172	3.43	8.0E-35	BF589937.1	EST_HUMAN	nae33a08.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3258134 3' similar to TR:O75912
4814	17545	30170	2.69	8.0E-35	BF183195.1	EST_HUMAN	O75912 DIACYLGLYCEROL KINASE IOTA ;
10559	23283	36522	2.42	8.0E-35	BE378480.1	EST_HUMAN	nae33a08.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3258134 3' similar to TR:O75912
12119	24811		3.95	8.0E-35	BF589282.1	EST_HUMAN	O75912 DIACYLGLYCEROL KINASE IOTA ;
6393	19162	32163	2.05	7.0E-35	11425417	NT	nae33a08.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3258134 3' similar to TR:O75912
1391	14138	26815	1.83	6.0E-35	AA757115.1	EST_HUMAN	O75912 DIACYLGLYCEROL KINASE IOTA ;
1960	14996	27409	2.09	6.0E-35	6005875	NT	601809588F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:4040324 5'
4030	16775	29406	0.84	6.0E-35	AW297191.1	EST_HUMAN	601236488F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3608513 5'
							602184624T1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:4300660 3'
							Homo sapiens phosphatidylinositol glycan, class L (PIGL), mRNA
							an53h03.s1 Soares_testis_NHT Homo sapiens cDNA clone 1309397 3'
							Homo sapiens zinc finger protein 208 (ZNF208), mRNA
							UI-H-BW0-ajd-4-09-0-JI.s1 NCI_CGAP_Sub6 Homo sapiens cDNA clone IMAGE:2731433 3'

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Table 4

Single Exon Probes Expressed In Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7708	20493	33615	3.84	6.0E-35	6005921	NT	Homo sapiens triple functional domain (PTPRF Interacting) (TRIO), mRNA
8610	21302	34445	0.93	6.0E-35	X94232.1	NT	H. sapiens mRNA for novel T-cell activation protein
8610	21302	34446	0.93	6.0E-35	X94232.1	NT	H. sapiens mRNA for novel T-cell activation protein
9565	22218	35403	0.86	6.0E-35	AB002364.1	NT	Human mRNA for KIAA0366 gene, partial cds
9803	22454	35656	3.17	6.0E-35	AB037786.1	NT	Homo sapiens mRNA for KIAA1365 protein, partial cds
1704	14447	27146	1.36	5.0E-35	X83392.1	NT	H. sapiens immunoglobulin kappa light chain variable region L14
2787	15492	26232	1.07	5.0E-35	AB007866.2	NT	Homo sapiens mRNA for KIAA0406 protein, partial cds
3008	15775	28424	1.7	5.0E-35	6912639	NT	Homo sapiens Ring1 and YY1 binding protein (RYBP), mRNA
4376	17113	29746	1.7	5.0E-35	AF023268.1	NT	Homo sapiens cdk2 kinase (CLK2), prolin1, coter1, glucocerebrosidase (GBA), and melanin genes, complete cds
8084	20778		3.99	5.0E-35	BE890992.1	EST_HUMAN	601431984F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3917228 5'
8109	20803	33936	2.35	5.0E-35	A1208765.1	EST_HUMAN	q938c05.x1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1837448 3' similar to SW:Y249_HUMAN Q92539 HYPOTHETICAL PROTEIN KIAA0249 ;
8109	20803	33937	2.35	5.0E-35	A1208765.1	EST_HUMAN	q938c05.x1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1837448 3' similar to SW:Y249_HUMAN Q92539 HYPOTHETICAL PROTEIN KIAA0249 ;
11130	23798		2.46	5.0E-35	AA001786.1	EST_HUMAN	zh84f12.r1 Soares fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:428015 5'
1413	14161	26845	16.86	4.0E-35	BE257907.1	EST_HUMAN	601109719F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3350405 5'
1811	14551	27265	4.87	4.0E-35	H91193.1	EST_HUMAN	y098a07.r1 Soares fetal liver spleen_1NFLS Homo sapiens cDNA clone IMAGE:241236 5' similar to contains PTR5 repetitive element ;
4753	17485		0.72	4.0E-35	AF003528.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
7108	19796		1.81	4.0E-35	BE350127.1	EST_HUMAN	h09g01.x1 NCL_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3 MER29 repetitive element ;
8416	21109	34248	8.88	4.0E-35	AL046596.1	EST_HUMAN	DKFZp34L148_r1 434 (synonym: h1as3) Homo sapiens cDNA clone DKFZp34L148 5'
11729	24322	37646	1.38	4.0E-35	AW303317.1	EST_HUMAN	xx17f03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2813405 3' similar to contains Alu repetitive element; contains MER19.12 MER19 repetitive element ;
1573	14320	27006	7.78	3.0E-35	BE268182.1	EST_HUMAN	601125260F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3345063 5'
2330	15055		1.5	3.0E-35	AF224492.1	NT	Homo sapiens phospholipid scramblase 1 gene, complete cds
5258	18062	30690	31.47	3.0E-35	BF433100.1	EST_HUMAN	7n25a09.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3565361 3' similar to TR:Q9QZH7 Q9QZH7 F-BOX PROTEIN FBL2 ;
5258	18062	30691	31.47	3.0E-35	BF433100.1	EST_HUMAN	7n25a09.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3565361 3' similar to TR:Q9QZH7 Q9QZH7 F-BOX PROTEIN FBL2 ;

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit: Accession No.	Top Hit Database Source	Top Hit Descriptor
9388	22050		1.42	3.0E-35	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
10074	22722	35939	1.12	3.0E-35	AW003083.1	EST_HUMAN	wr03a05.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2480432 3' similar to SW:POL1_HUMAN P10266 RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE]; K6932F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone K6932 5' similar to REPETITIVE ELEMENT
106	15535	25567	1.88	2.0E-35	N88965.1	EST_HUMAN	A971F Heart Homo sapiens cDNA clone A971
1165	13919	26582	1.55	2.0E-35	T11909.1	EST_HUMAN	Homo sapiens mRNA for Gab2, complete cds
2215	14943	27683	5.73	2.0E-35	AB018413.1	NT	Homo sapiens Grb2-associated binder 2 (KIAA0571), mRNA
3306	16066	28714	1.12	2.0E-35	6912459	NT	Homo sapiens Grb2-associated binder 2 (KIAA0571), mRNA
3308	16066	28715	1.12	2.0E-35	6912459	NT	Homo sapiens mRNA for KIAA0865 protein, partial cds
3545	16300		0.94	2.0E-35	AB020702.1	NT	TCBAP2E4328 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP4328
3890	16640	29279	0.78	2.0E-35	BE247575.1	EST_HUMAN	TCBAP2E4328 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP4328
3890	16640	29280	0.78	2.0E-35	BE247575.1	EST_HUMAN	cDNA clone TCBAP4328
4621	17356		2.57	2.0E-35	H49239.1	EST_HUMAN	yq19a12.1 Scores fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:274079 5'
5495	18294	31192	2.7	2.0E-35	BF332417.1	EST_HUMAN	QV0-BT0701-210400-199-504 BT0701 Homo sapiens cDNA
7004	18696	32749	0.85	2.0E-35	BE832636.1	EST_HUMAN	CM2-MT0125-280700-297-G02 MT0125 Homo sapiens cDNA
7004	18696	32750	0.95	2.0E-35	BE832636.1	EST_HUMAN	CM2-MT0125-280700-297-G02 MT0125 Homo sapiens cDNA
7775	20471	33583	0.45	2.0E-35	AV723718.1	EST_HUMAN	AV723718 HTB Homo sapiens cDNA clone HTBAYA10 5'
7775	20471	33594	0.45	2.0E-35	AV723718.1	EST_HUMAN	AV723718 HTB Homo sapiens cDNA clone HTBAYA10 5'
10697	23388	36626	2.24	2.0E-35	X89417.1	NT	H. sapiens PROS-27 mRNA
11817	18294	31192	1.28	2.0E-35	BF332417.1	EST_HUMAN	QV0-BT0701-210400-199-504 BT0701 Homo sapiens cDNA
11889	16066	28714	1.72	2.0E-35	6912459	NT	Homo sapiens Grb2-associated binder 2 (KIAA0571), mRNA
11889	16066	28715	1.72	2.0E-35	6912459	NT	Homo sapiens Grb2-associated binder 2 (KIAA0571), mRNA
12062	24577	31120	1.36	2.0E-35	BE804878.1	EST_HUMAN	601496774F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3898699 5'
12062	24577	31121	1.36	2.0E-35	BE804878.1	EST_HUMAN	601496774F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3898699 5'
12572	24900		5.99	2.0E-35	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
12689	16535	25567	1.56	2.0E-35	N88965.1	EST_HUMAN	K6932F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone K6932 5' similar to REPETITIVE ELEMENT
45	12874	25498	6.81	1.0E-35	AA631949.1	EST_HUMAN	frnfc16 Regional genomic DNA specific cDNA library Homo sapiens cDNA clone CR12-1
45	12874	25497	6.81	1.0E-35	AA631949.1	EST_HUMAN	frnfc16 Regional genomic DNA specific cDNA library Homo sapiens cDNA clone CR12-1
735	13509	26165	19.5	1.0E-35	AW389473.1	EST_HUMAN	IL2-ST0162-131099-008-412 ST0162 Homo sapiens cDNA

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Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
735	13509	26166	19.5	1.0E-35	AW389473.1	EST_HUMAN	IL2-ST0162-131099-006-d12 ST0162 Homo sapiens cDNA
889	13658		1.3	1.0E-35	T87947.1	EST_HUMAN	yd8a01.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:115752 5' similar to SP:A44282 A44282 RETROVIRUS-RELATED POLYPROTEIN - HUMAN ;
2544	15258	27996	1.88	1.0E-35	7705994	NT	Homo sapiens hypothetical protein (LOC51233), mRNA
2770	15475	28217	1.09	1.0E-35	BE350127.1	EST_HUMAN	h09g01.x1 NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3 MER29 repetitive element ;
2770	15475	28218	1.09	1.0E-35	BE350127.1	EST_HUMAN	h09g01.x1 NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3 MER29 repetitive element ;
3140	15904	28549	1.81	1.0E-35	6006030	NT	Homo sapiens transcription elongation factor B (SII), polypeptide 1-like (TCBE1L) mRNA
3161	15924	28570	3.3	1.0E-35	AV650422.1	EST_HUMAN	AV650422 GLC Homo sapiens cDNA clone GLCCEP06 3'
3161	15924	28571	3.3	1.0E-35	AV650422.1	EST_HUMAN	AV650422 GLC Homo sapiens cDNA clone GLCCEP06 3'
4388	17125	29756	3.93	1.0E-35	7656905	NT	Mus musculus actin receptor interacting protein 1 (Arip1-pending), mRNA
4388	17125	29757	3.93	1.0E-35	7656905	NT	Mus musculus actin receptor interacting protein 1 (Arip1-pending), mRNA
5423	18222	30934	1.41	1.0E-35	11526236	NT	Homo sapiens chromatin assembly factor 1, subunit B (p60) (CHAF1B), mRNA
7383	20063	33141	0.88	1.0E-35	AB033105.1	NT	Homo sapiens mRNA for KIAA1279 protein, partial cds
7541	20211	33311	1.18	1.0E-35	11418002	NT	Homo sapiens KIAA0845 gene product (KIAA0845), mRNA
9442	25125	35297	2.16	1.0E-35	AU158595.1	EST_HUMAN	AU158595 PLACE3 Homo sapiens cDNA clone PLACE3000382 3'
9442	25125	35298	2.16	1.0E-35	AU158595.1	EST_HUMAN	AU158595 PLACE3 Homo sapiens cDNA clone PLACE3000382 3'
10477	23123	36352	0.7	1.0E-35	BF589594.1	EST_HUMAN	naa06d06.x1 NCI_CGAP_P728 Homo sapiens cDNA clone IMAGE:3254051 3' similar to TR:O31341 O31341 BETA-GALACTOSIDASE ;
10477	23123	36353	0.7	1.0E-35	BF589594.1	EST_HUMAN	naa06d06.x1 NCI_CGAP_P728 Homo sapiens cDNA clone IMAGE:3254051 3' similar to TR:O31341 O31341 BETA-GALACTOSIDASE ;
11758	24349	37680	1.46	1.0E-35	AB028980.1	NT	Homo sapiens mRNA for KIAA1057 protein, partial cds
11758	24349	37681	1.46	1.0E-35	AB028980.1	NT	Homo sapiens mRNA for KIAA1057 protein, partial cds
11768	24359		1.91	1.0E-35	AI525119.1	EST_HUMAN	prom1a-7.D01.r bvtumor Homo sapiens cDNA 5'
11917	25313		1.37	1.0E-35	11418274	NT	Homo sapiens fibulin 1 (FBLN1), mRNA
12121	24613		1.63	1.0E-35	11418110	NT	Homo sapiens casein kinase 1, epsilon (CSNK1E), mRNA
12471	24837		2.13	1.0E-35	BE792832.1	EST_HUMAN	601584833F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3538985 5'
9129	21817	34963	0.58	8.0E-36	AA349480.1	EST_HUMAN	EST54838 Hippocampus II Homo sapiens cDNA 5' end similar to similar to endogenous retrovirus 9, 5' LTR
2931	15697	28344	1.1	7.0E-36	AW857579.1	EST_HUMAN	GM1-CT0315-091295-063-407 CT0315 Homo sapiens cDNA
3116	15881		3.84	7.0E-36	4557498	NT	Homo sapiens C-terminal binding protein 2 (CTBP2) mRNA
7554	20224	33327	5.92	7.0E-36	U06672.1	NT	Human carcinoembryonic antigen gene family member 12 (CGM12) gene, exons L and L/N
7554	20224	33328	5.92	7.0E-36	U06672.1	NT	Human carcinoembryonic antigen gene family member 12 (CGM12) gene, exons L and L/N

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Single Exon Probes Expressed In Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1998	14734	27496	2	6.0E-36	7706622	NT	Homo sapiens nitrofurin 2 (NINJ2), mRNA
2418	15139		5.58	6.0E-36	AB035346.1	NT	Homo sapiens TCl6 gene, exon 12
3630	16383	29023	0.71	6.0E-36	BF515101.1	EST_HUMAN	UI-H-BW1-ant-c-12-Q-1.s1 NCI_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3083542 3'
5248	18054	30682	3.54	6.0E-36	A1435169.1	EST_HUMAN	th93b06.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2126195 3' similar to gb:M11949 PANCREATIC SECRETORY TRYPSIN INHIBITOR PRECURSOR (HUMAN);
7009	19701	32756	3.57	6.0E-36	AW780143.1	EST_HUMAN	h006h02.x1 NCI_CGAP_Cot14 Homo sapiens cDNA clone IMAGE:3036627 3' similar to SW:IMA2_HUMAN
8650	21242	34385	2.33	6.0E-36	AF208161.1	NT	P52292 IMPORTIN ALPHA-2 SUBUNIT ;
10125	22773		0.51	6.0E-36	C16927.1	EST_HUMAN	Homo sapiens syncytin precursor, mRNA, complete cds
11536	24136	37443	3.11	6.0E-36	A1380499.1	EST_HUMAN	C16927 Clontech human aorta polyA+ mRNA (#6572) Homo sapiens cDNA clone GEN-535C11 5'
134	12949	25592	10.74	5.0E-36	AJ271735.1	NT	tf95c09.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2107024 3' similar to contains MER9.b2
2755	16460	28202	6.75	5.0E-36	BE388436.1	EST_HUMAN	MER9 repetitive element ;
3599	16352	28991	1.45	5.0E-36	AL163209.2	EST_HUMAN	Homo sapiens Xq pseudautosomal region; segment 1/2
4736	17468	30104	2.15	5.0E-36	5729729	NT	Homo sapiens chromosome 21 segment HS21C009
4736	17468	30105	2.15	5.0E-36	5729729	NT	Homo sapiens APIB-like 1 (APIB1), mRNA
7886	20350	33464	0.61	5.0E-36	11079227	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
11887	12949	25592	3.53	5.0E-36	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
12168	24650	31103	3.45	5.0E-36	11417862	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
1203	13955	26619	1.69	4.0E-36	BE010038.1	EST_HUMAN	PM3-BN0176-100-001-g04 BN0176 Homo sapiens cDNA
1423	14170	26856	1.03	4.0E-36	P10266	SWISSPROT	RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ;
1640	14388	27074	1.61	4.0E-36	BE382674.1	EST_HUMAN	ENDONUCLEASE
2219	14947		2.13	4.0E-36	AW247772.1	EST_HUMAN	G01298574F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3628386 5'
3349	16108	28763	0.82	4.0E-36	BE389299.1	EST_HUMAN	2820020 5prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2820020 5'
3349	16108	28764	0.82	4.0E-36	BE389299.1	EST_HUMAN	G01282266F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3604168 5'
5629	18425		0.84	4.0E-36	R64023.1	EST_HUMAN	G01282266F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3604168 5'
5964	18746	31707	2.33	4.0E-36	11497041	NT	Y19F05.r1 Soares placenta N62HP Homo sapiens cDNA clone IMAGE:139713 5'
7553	20223	33326	1.63	4.0E-36	M33320.1	NT	Homo sapiens a disintegrin and metalloproteinase domain 22 (ADAM22), transcript variant 3, mRNA
8453	21145	34285	1.62	4.0E-36	D87875.1	NT	Human platelet Glycoprotein Iib (GPIIb) gene, exons 2-29
8453	21145	34286	1.62	4.0E-36	D87875.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
10909	23689	36835	2.84	4.0E-36	AA400370.1	EST_HUMAN	Homo sapiens DNA for amyloid precursor protein, complete cds
12183	24655		2.09	4.0E-36	11420516	EST_HUMAN	zu69c10.r1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:743250 5'
12227	25199		7.3	4.0E-36	AV753629.1	EST_HUMAN	Homo sapiens nuclear factor of activated T-cells, cytoplasmic 2 (NFA1C2), mRNA
							AV753629 TP Homo sapiens cDNA clone TFGABH01 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12798	25047		1.44	4.0E-36	D25217.2	NT	Homo sapiens mRNA for KIAA0027 protein, partial cds
680	13455	26100	2.58	3.0E-36	AF098810.1	NT	Homo sapiens neurxin III-alpha gene, partial cds
1484	14231	26917	1.32	3.0E-36	AF110239.1	NT	Homo sapiens calcium/calmodulin-stimulated cyclic nucleotide phosphodiesterase (PDE1A) gene, partial cds
1484	14231	26918	1.32	3.0E-36	AF110239.1	NT	Homo sapiens calcium/calmodulin-stimulated cyclic nucleotide phosphodiesterase (PDE1A) gene, partial cds
2297	15022	27757	1.21	3.0E-36	7662401	NT	Homo sapiens KIAA0952 protein (KIAA0952), mRNA
4467	17203	29829	5.88	3.0E-36	10181139	NT	Mus musculus junctophilin 1 (Jp1-pending), mRNA
11050	23720	36991	1.59	3.0E-36	BF035327.1	EST_HUMAN	G01458531 F1 NIH_MGC_86 Homo sapiens cDNA clone IMAGE:3862086 5'
3167	15930	28579	2.38	2.0E-36	BE259267.1	EST_HUMAN	G01108343 F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3342706 5'
4804	17631	30246	5.45	2.0E-36	AW880376.1	EST_HUMAN	QV0-OT0030-240300-174-h04 OT0030 Homo sapiens cDNA
5398	18198	30892	3.1	2.0E-36	AF267747.1	NT	Mus musculus p47-phox gene, complete cds
5758	18550	31471	3.95	2.0E-36	T08756.1	EST_HUMAN	EST T06648 Infant Brain, Bonto Soares Homo sapiens cDNA clone HIBBJ28 5' and
6481	19248	32248	12.22	2.0E-36	T08628.1	EST_HUMAN	yc44a07 r1 Stragene liver (#937224) Homo sapiens cDNA clone IMAGE:83508 5'
9288	21955	35126	1.07	2.0E-36	BF512794.1	EST_HUMAN	UJH-BW1-arnu-a-1-O-UJ.s1 NCL CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3071132 3'
9449	21999	35172	0.79	2.0E-36	4507848	NT	Homo sapiens ubiquitin specific protease 13 (isopeptidase T-3) (USP13) mRNA
9449	21999	35173	0.79	2.0E-36	4507848	NT	Homo sapiens ubiquitin specific protease 13 (isopeptidase T-3) (USP13) mRNA
865	13634	26304	1.81	1.0E-36	BE409310.1	EST_HUMAN	Homo sapiens ubiquitin specific protease 13 (isopeptidase T-3) (USP13) mRNA
2141	14871	27603	1	1.0E-36	BE146523.1	EST_HUMAN	G01300938 F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3635480 5'
2141	14871	27604	1	1.0E-36	BE146523.1	EST_HUMAN	RC1-HT0217-131199-021-h07 HT0217 Homo sapiens cDNA
2199	14928	27664	1.36	1.0E-36	BF673761.1	EST_HUMAN	G02138493 F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4272886 5'
3339	16099		1.16	1.0E-36	AF156982.1	NT	Homo sapiens human endogenous retrovirus W prov08-19 protease (pro) gene, partial cds
5810	18599	31527	1.29	1.0E-36	4827064	NT	Homo sapiens zinc finger protein 147 (estrogen-responsive finger protein) (ZNF147) mRNA
6090	18868		4.19	1.0E-36	A1887714.1	EST_HUMAN	wb37c12.x1 NCL CGAP_GG6 Homo sapiens cDNA clone IMAGE:2307862 3' similar to contains Alu repetitive element
6286	19069	32052	1.21	1.0E-36	R25012.1	EST_HUMAN	yg36g10.r1 Soares Infant brain 1N1B Homo sapiens cDNA clone IMAGE:34529 5' similar to SP:CAHP_HUMAN P35219 CARBONIC ANHYDRASE-RELATED PROTEIN ;
6296	19069	32053	1.21	1.0E-36	R25012.1	EST_HUMAN	yg36g10.r1 Soares Infant brain 1N1B Homo sapiens cDNA clone IMAGE:34529 5' similar to SP:CAHP_HUMAN P35219 CARBONIC ANHYDRASE-RELATED PROTEIN ;
6582	19345	32359	0.73	1.0E-36	AL120542.1	EST_HUMAN	DKFZ6761A229_r1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZ6761A229 5'
7326	20009	33087	0.85	1.0E-36	11426108	NT	Homo sapiens a disintegrin and metalloproteinase domain 11 (ADAM11), mRNA
7326	20009	33088	0.85	1.0E-36	11426108	NT	Homo sapiens a disintegrin and metalloproteinase domain 11 (ADAM11), mRNA
7860	20555	33679	5.13	1.0E-36	AA148034.1	EST_HUMAN	zo51a12.r1 Stragene endothelial cell 937223 Homo sapiens cDNA clone IMAGE:590398 5'
7860	20555	33680	5.13	1.0E-36	AA148034.1	EST_HUMAN	zo51a12.r1 Stragene endothelial cell 937223 Homo sapiens cDNA clone IMAGE:590398 5'

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7952	20647	33770	1.34	1.0E-36	AA420487.1	EST_HUMAN	nc60608.t1 NCL_CGAP_P1 Homo sapiens cDNA clone IMAGE:745670
7952	20647	33771	1.34	1.0E-36	AA420487.1	EST_HUMAN	nc60608.t1 NCL_CGAP_P1 Homo sapiens cDNA clone IMAGE:745670
8079	20773	33902	0.61	1.0E-36	AU141688.1	EST_HUMAN	AU141688 THYRO1 Homo sapiens cDNA clone THYRO1001033 5'
8079	20773	33903	0.61	1.0E-36	AU141688.1	EST_HUMAN	AU141688 THYRO1 Homo sapiens cDNA clone THYRO1001033 5'
8927	21618	34762	2.71	1.0E-36	AW103658.1	EST_HUMAN	xe82807.x1 NCL_CGAP_Bm35 Homo sapiens cDNA clone IMAGE:2614357 3'
10014	22862	35878	3.88	1.0E-36	BF364169.1	EST_HUMAN	QV3-NN1023-010600-199-h01 NN1023 Homo sapiens cDNA
10226	22874	36086	0.56	1.0E-36	AW855868.1	EST_HUMAN	RC3-CT0279-040500-017-a10 GT0279 Homo sapiens cDNA
10226	22874	36087	0.56	1.0E-36	AW855868.1	EST_HUMAN	RC3-CT0279-040500-017-a10 GT0279 Homo sapiens cDNA
10867	23547	36795	3.3	1.0E-36	AW897636.1	EST_HUMAN	GM3-NN0061-140400-147-h12 NN0061 Homo sapiens cDNA
11354	24044	37347	4.17	1.0E-36	AW504143.1	EST_HUMAN	UI-HF-BN0-ale-c-03-q-U1.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3079277 5'
11393	23999	37302	1.45	1.0E-36	A905536.1	EST_HUMAN	RC-BT091-210199-110 BT091 Homo sapiens cDNA
11393	23999	37303	1.45	1.0E-36	A905536.1	EST_HUMAN	RC-BT091-210199-110 BT091 Homo sapiens cDNA
12060	24575		3.81	1.0E-36	11418177	NT	Homo sapiens Ran GTPase activating protein 1 (RANGAP1), mRNA
12501	24855		3.03	1.0E-36	AL163213.2	NT	Homo sapiens chromosome 21 segment HS21C013
12747	25011		3.23	1.0E-36	AF202723.1	NT	Homo sapiens Sad1 unc-84 domain protein 2 (SUN2) mRNA, partial cds
7281	19965	33042	2.12	9.0E-37	AW009277.1	EST_HUMAN	ws80b07.x1 NCL_CGAP_Co3 Homo sapiens cDNA clone IMAGE:2504245 3'
7281	19965	33043	2.12	9.0E-37	AW009277.1	EST_HUMAN	ws80b07.x1 NCL_CGAP_Co3 Homo sapiens cDNA clone IMAGE:2504245 3'
12309	24733		1.35	9.0E-37	W22618.1	EST_HUMAN	73D4 Human retina cDNA Tsp509I-cleaved sublibrary Homo sapiens cDNA not directional
3350	16109	28765	0.99	8.0E-37	4757979	NT	Homo sapiens chimera (chimaerin) 2 (CHN2) mRNA
5168	17977		1.58	8.0E-37	BE698077.1	EST_HUMAN	GM0-UT0003-050800-503-409 UT0003 Homo sapiens cDNA
							h09g01.x1 NCL_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3
5738	18530	31451	3.75	8.0E-37	BE350127.1	EST_HUMAN	MER29 repetitive element;
							h09g01.x1 NCL_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3
5738	18530	31452	3.75	8.0E-37	BE350127.1	EST_HUMAN	MER29 repetitive element;
5787	18578	31507	8.24	8.0E-37	AW840840.1	EST_HUMAN	RC1-CN0008-210100-012-a09_1 CN0008 Homo sapiens cDNA
							H.sapiens DMA, DMB, HLA-Z1, IPP2, LMP2, TAP1, LMP7, TAP2, DOB, DOB2 and RING8, 9, 13 and 14 genes
7784	20479	33604	6.22	8.0E-37	X97344.1	NT	DKFZp434E0422_r1 434 (synonym: hles3) Homo sapiens cDNA clone DKFZp434E0422 5'
1262	14011		3.03	7.0E-37	AL042800.1	EST_HUMAN	
							Homo sapiens Jun dimerization protein gene, partial cds; complete cds; and unknown gene
1738	14480	27179	0.97	7.0E-37	AF111167.2	NT	
							Homo sapiens Jun dimerization protein gene, partial cds; complete cds; and unknown gene
1738	14480	27180	0.97	7.0E-37	AF111167.2	NT	wk25b11.x1 NCL_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2413341 3' similar to contains PTR5.12
10657	23348	36585	8.69	7.0E-37	AI817700.1	EST_HUMAN	PTR5 repetitive element;

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10811	23494	36729	2.25	7.0E-37	AI536702.1	EST_HUMAN	tm87g03.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2185140 3' similar to contains L1.b3 L1 repetitive element ;
8338	21031	34168	1.34	6.0E-37	AF169689.1	NT	Homo sapiens protocadherin alpha 10 alternate isoform (PCDH-alpha10) mRNA, complete cds
12624	24929		2.94	6.0E-37	AF202723.1	NT	Homo sapiens Sad1 unc-84 domain protein 2 (SUN2) mRNA, partial cds
6002	18783	31744	3.9	5.0E-37	AA307123.1	EST_HUMAN	EST178035 Colon carcinoma (HCC) cell line Homo sapiens cDNA 5' end
6002	18783	31745	3.9	5.0E-37	AA307123.1	EST_HUMAN	EST178035 Colon carcinoma (HCC) cell line Homo sapiens cDNA 5' end
8654	21346	34490	0.9	5.0E-37	AV750211.1	EST_HUMAN	AV750211 NPC Homo sapiens cDNA clone NPCBGH09 5'
10837	23519		4	5.0E-37	7657117	NT	Homo sapiens glycine C-acetyltransferase (2-amino-3-ketobutyrate-CoA ligase) (GCAT), mRNA
12055	24572		6.86	5.0E-37	AF149773.1	NT	Homo sapiens NOD1 protein (NOD1) gene, exons 1, 2, and 3
2423	15144	27877	2.12	4.0E-37	AA702794.1	EST_HUMAN	zib0b04.s1 Soares fetal liver spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:448015 3'
6194	18970	31945	0.81	4.0E-37	AW794502.1	EST_HUMAN	RC8-UM0014-210200-021-H05 UM0014 Homo sapiens cDNA
9256	21935	35109	0.74	4.0E-37	AA843806.1	EST_HUMAN	ek09a02.s1 Soares parathyroid tumor_NbHlPA Homo sapiens cDNA clone IMAGE:1405442 3'
2010	14745	27472	3.2	3.0E-37	AL048956.1	EST_HUMAN	DKFZp434L2418_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434L2418
2010	14745	27473	3.2	3.0E-37	AL048956.1	EST_HUMAN	DKFZp434L2418_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434L2418
2965	15731		3.15	3.0E-37	AW961150.1	EST_HUMAN	EST1373222 MAGE resequences, MAGF Homo sapiens cDNA
5774	18565	31494	0.92	3.0E-37	AL138274.1	EST_HUMAN	DKFZp547G067_r1 547 (synonym: hibr1) Homo sapiens cDNA clone DKFZp547G067 5'
7455	20129	33221	0.71	3.0E-37	AI749952.1	EST_HUMAN	at34c05.x1 Barslead colon HPLR87 Homo sapiens cDNA clone IMAGE:2373896 3' similar to TR.Q13537
372	13197	25842	0.68	2.0E-37	D89790.1	NT	Q13537 SIMILAR TO POGO ELEMENT. ;
372	13197	25843	0.68	2.0E-37	D89790.1	NT	Homo sapiens mRNA for AML1, complete cds
1058	13816	26477	2.84	2.0E-37	AU131202.1	EST_HUMAN	Homo sapiens mRNA for AML1, complete cds
1058	13816	26478	2.84	2.0E-37	AU131202.1	EST_HUMAN	AU131202 NT2RP3 Homo sapiens cDNA clone NT2RP3002166 5'
1956	14692	27405	1.87	2.0E-37	AL163247.2	NT	AU131202 NT2RP3 Homo sapiens cDNA clone NT2RP3002166 5'
3873	16623	29281	4.78	2.0E-37		NT	Homo sapiens chromosome 21 segment HS21C047
4968	17683		0.93	2.0E-37	AL163284.2	NT	Homo sapiens cytochrome P450, subfamily XXVIIA (steroid 27-hydroxylase, cerebrotendinous xanthomatosis), polypeptide 1 (CYP27A1b) mRNA
5304	18109		0.66	2.0E-37	BF035327.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C084
5561	19326	32333	3.46	2.0E-37	AA346720.1	EST_HUMAN	601458531F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3862086 5'
7895	20590	33720	0.46	2.0E-37	BE537764.1	EST_HUMAN	EST52931 Fetal heart II Homo sapiens cDNA 5' end
7895	20590	33721	0.46	2.0E-37	BE537764.1	EST_HUMAN	601067534F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3453857 5'
7937	20632	33759	2.88	2.0E-37	BF204032.1	EST_HUMAN	601067534F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3453857 5'
11549	24148	37459	11.22	2.0E-37	AF176013.1	NT	601869157F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4111406 5'
12784	25037		3.54	2.0E-37	11417972	NT	Homo sapiens J domain containing protein 1 isoform b (JDP1) mRNA, complete cds
2081	14813	27546	4.93	1.0E-37	AL163281.2	NT	Homo sapiens pascadillo (zbrabfish) homolog 1, containing BRCT domain (PES1), mRNA
			4.93	1.0E-37	AL163281.2	NT	Homo sapiens chromosome 21 segment HS21C081

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3192	16955		1.06	1.0E-37	AW862082.1	EST_HUMAN	RC3-CT0347-210400-016-h03 CT0347 Homo sapiens cDNA
3943	16993	29332	0.72	1.0E-37	AF189011.1	NT	Homo sapiens ribonuclease III (RN3) mRNA, complete cds
4888	17615	30234	2.35	1.0E-37	BF371719.1	EST_HUMAN	QV0-FN0180-280700-318-c10 FN0180 Homo sapiens cDNA
5914	18699		0.94	1.0E-37	7305360	NT	Mus musculus otogelin (Otog), mRNA
8113	20807	33940	1.25	1.0E-37	BE546032.1	EST_HUMAN	601072419F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3458308 5'
8634	21326	34468	2.57	1.0E-37	AA171406.1	EST_HUMAN	Zp21b02.11 Stratagene neuroepithelium (#937231) Homo sapiens cDNA clone IMAGE:610059 5' similar to
10597	23291	36529	2.96	1.0E-37	M22878.1	NT	contains L1.12 L1 repetitive element ;
12863	24766		2.81	1.0E-37	BE771814.1	EST_HUMAN	Human somatic cytochrome c (HC1) processed pseudogene, complete cds
5690	18483	31402	2	9.0E-38	10048482	NT	CM3-FT0096-140700-243-d07 FT0096 Homo sapiens cDNA
1200	13952	26816	2.02	8.0E-38	11436955	NT	Rattus norvegicus multidomain presynaptic cytomatrix protein Piccolo (LOC56768), mRNA
2502	15219	27962	1.8	8.0E-38	BF346221.1	EST_HUMAN	Homo sapiens Grib2-associated binder 2 (KIAA0571), mRNA
12420	13952	26616	1.6	8.0E-38	11436955	NT	602018401F1 NCI_OGAP_Bm67 Homo sapiens cDNA clone IMAGE:4153992 5'
4197	16938	29563	0.73	7.0E-38	H19092.1	EST_HUMAN	Homo sapiens Grib2-associated binder 2 (KIAA0571), mRNA
5039	17758		1.31	7.0E-38	AF267263.1	NT	yn51f07.1 Soares adult brain N255H55Y Homo sapiens cDNA clone IMAGE:171973 5'
3037	15803	28450	1.2	6.0E-38	BF033033.1	EST_HUMAN	Mus musculus ATP-binding cassette 1, sub-family A, member 1 (Abca1) gene, complete cds
5502	18300	31199	1.6	6.0E-38	11425114	NT	601455722FT NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3859348 5'
5502	18300	31200	1.6	6.0E-38	11425114	NT	Homo sapiens zinc finger protein ZNF287 (ZNF287), mRNA
7228	19913	32866	0.57	6.0E-38	8923130	NT	Homo sapiens zinc finger protein ZNF287 (ZNF287), mRNA
11918	24480		2.57	6.0E-38	11435947	NT	Homo sapiens hypothetical protein FLJ20128 (FLJ20128), mRNA
12395	24783	31038	12.79	6.0E-38	AB002059.1	NT	Homo sapiens chromosome 12 open reading frame 3 (C12ORF3), mRNA
12767	25161	30900	1.7	6.0E-38	11418164	NT	Homo sapiens DNA for Human P2XM, complete cds
710	13484	26133	1.38	5.0E-38	AW971819.1	EST_HUMAN	Homo sapiens adenylosuccinate lyase (ADSL), mRNA
2455	15173	27912	0.99	5.0E-38	AJ237740.1	NT	EST383908 MAGE resequences, MAGL Homo sapiens cDNA
3949	16446	29086	0.85	5.0E-38	7549804	NT	Homo sapiens delodinease, iodothyronine, type II (DIO2), transcript variant 2, mRNA
3917	16667	28307	0.92	5.0E-38	T83107.1	EST_HUMAN	y440h07.1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:110749 5' similar to
3917	16667	29308	0.92	5.0E-38	T83107.1	EST_HUMAN	SP:OLF3_MOUSE P23275 OLFACTORY RECEPTOR ;
6930	19666	32712	1.48	5.0E-38	BE871610.1	EST_HUMAN	y440h07.1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:110749 5' similar to
116	12938	25575	4.59	4.0E-38	Z25466.1	NT	SP:OLF3_MOUSE P23275 OLFACTORY RECEPTOR ;
116	12938	25576	4.59	4.0E-38	Z25466.1	NT	601450148FT NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3854074 5'
2093	14824		5.25	3.0E-38	AF003530.1	NT	B.taurus mitochondrial aspartate aminotransferase mRNA, complete CDS
3984	18437		2.19	3.0E-38	7549807	NT	B.taurus mitochondrial aspartate aminotransferase mRNA, complete CDS
							Homo sapiens homeobox protein CDX4 (CDX4) gene, complete cds and flanking repeat regions
							Homo sapiens HIRA interacting protein 4 (HIRIP4), mRNA

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF-SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3836	16587	29224	1.76	3.0E-38	P53538	SWISSPROT	SSU72 PROTEIN
3836	16587	29225	1.76	3.0E-38	P53538	SWISSPROT	SSU72 PROTEIN
4574	17309		1.47	3.0E-38	BE279301.1	EST_HUMAN	601157833F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3504272 5'
6655	25097	32430	8.11	3.0E-38	AL163300.2	NT	Homo sapiens chromosome 21 segment HS21C100
7144	19831	32900	0.56	3.0E-38	AW302461.1	EST_HUMAN	xx04d01.x1 NCI_CGAP_Bm53 Homo sapiens cDNA clone IMAGE:2827009 3'
7488	20160	32352	8.28	3.0E-38	BF373664.1	EST_HUMAN	CM3-FT0181-140700-241-f07 FT0181 Homo sapiens cDNA
8548	21240	34383	2.1	3.0E-38	H85494.1	EST_HUMAN	yy88b04.r1 Soares melanocyte 2NbhM Homo sapiens cDNA clone IMAGE:249775 5'
8548	21240	34384	2.1	3.0E-38	H85494.1	EST_HUMAN	yy88b04.r1 Soares melanocyte 2NbhM Homo sapiens cDNA clone IMAGE:249775 5'
9872	22522		2.24	3.0E-38	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
12630	17896	30488	1.95	3.0E-38	11435947	NT	Homo sapiens chromosome 12 open reading frame 3 (C12ORF3), mRNA
49	12878	25504	1.4	2.0E-38	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
1358	14106	26781	2.99	2.0E-38	5902097	NT	Homo sapiens SMT3 (suppressor of mit two 3, yeast) homolog 2 (SMT3H2), mRNA
1641	14387	27075	2.21	2.0E-38	AA437353.1	EST_HUMAN	zw30d01.r1 Soares ovary tumor NbhOT Homo sapiens cDNA clone IMAGE:770785 5' similar to SW:MA12_RABIT P45701 MANNOSYL-OLIGOSACCHARIDE ALPHA-1,2-MANNOSIDASE ;
1641	14387	27076	2.21	2.0E-38	AA437353.1	EST_HUMAN	zw30d01.r1 Soares ovary tumor NbhOT Homo sapiens cDNA clone IMAGE:770785 5' similar to SW:MA12_RABIT P45701 MANNOSYL-OLIGOSACCHARIDE ALPHA-1,2-MANNOSIDASE ;
2408	15129	27865	1.45	2.0E-38	W76571.1	EST_HUMAN	zw68g09.r1 Soares fetal heart NbhH19W Homo sapiens cDNA clone IMAGE:345684 5'
5632	18427	31339	0.69	2.0E-38	Z26634.2	NT	Homo sapiens mRNA for ankyrin B (440 kDa)
5632	18427	31340	0.69	2.0E-38	Z26634.2	NT	Homo sapiens mRNA for ankyrin B (440 kDa)
7619	20285	33395	1.46	2.0E-38	AV721103.1	EST_HUMAN	AV721103 HTB Homo sapiens cDNA clone HTBARH11 5'
8382	21075		4.38	2.0E-38	BE165980.1	EST_HUMAN	MR3-HT0487-150200-113-g01 HT0487 Homo sapiens cDNA
8793	21485	34631	0.56	2.0E-38	F06450.1	EST_HUMAN	HSC18F031 normalized infant brain cDNA Homo sapiens cDNA clone c-18f03
8864	21555	34700	2.04	2.0E-38	AF069755.1	NT	Homo sapiens orphan G protein-coupled receptor HG20 (HG20), complete cds
9121	21809		1.06	2.0E-38	BE222256.1	EST_HUMAN	hu08g02.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3168130 3' similar to TR:O02710 O02710
10346	22993	36212	1.71	2.0E-38	D63478.2	NT	GAG POLYPROTEIN. ;
11200	23865	37151	1.37	2.0E-38	AA595480.1	EST_HUMAN	Homo sapiens mRNA for KIAA0145 protein, partial cds
11200	23865	37152	1.37	2.0E-38	AA595480.1	EST_HUMAN	nc34g03.s1 NCI_CGAP_P23 Homo sapiens cDNA clone IMAGE:1102612 3' similar to TR:E212316
11472	24073	37382	5.79	2.0E-38	BE712790.1	EST_HUMAN	E212316 NADP DEPENDENT LEUKOTRIENE B4 12-HYDROXYDEHYDROGENASE. ;
11638	24235	37557	3.52	2.0E-38	AF190501.1	NT	nc34g03.s1 NCI_CGAP_P23 Homo sapiens cDNA clone IMAGE:1102612 3' similar to TR:E212316
							E212316 NADP DEPENDENT LEUKOTRIENE B4 12-HYDROXYDEHYDROGENASE. ;
							nc34g03.s1 NCI_CGAP_P23 Homo sapiens cDNA clone IMAGE:1102612 3' similar to TR:E212316
							E212316 NADP DEPENDENT LEUKOTRIENE B4 12-HYDROXYDEHYDROGENASE. ;
							QV2-HT0698-080800-293-a05 HT0698 Homo sapiens cDNA
							Homo sapiens leucine-rich repeat-containing G protein-coupled receptor 6 (LGR6) mRNA, partial cds

Table 4

Single Exon Probes Expressed In Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11638	24235	37558	3.52	2.0E-38	AF190501.1	NT	Homo sapiens leucine-rich repeat-containing G protein-coupled receptor 6 (LGR6) mRNA, partial cds
11971	24517		3.05	2.0E-38	AV726988.1	EST_HUMAN	AV726988 HTC Homo sapiens cDNA clone HTCAXH07 5'
11973	24518		2.06	2.0E-38	AB012723.1	NT	Homo sapiens gene for kinesin-like protein, complete cds
12260	24705	31081	6.45	2.0E-38	H55641.1	EST_HUMAN	CHR220580 Chromosome 22 exon Homo sapiens cDNA clone C22.788 5'
12323	24742		1.43	2.0E-38	S74906.1	NT	E1 beta=pyruvate dehydrogenase beta (promoter) [human, placenta, Genomic, 1280 nt]
12777	25031		3.76	2.0E-38	11418248	NT	Homo sapiens sulfoxidase-related protein (SUL-TX3), mRNA
1071	13829		2.55	1.0E-38	AA401570.1	EST_HUMAN	zu62b02.r1 Soares, tests, NHT Homo sapiens cDNA clone IMAGE:742539 5' similar to contains element
1892	14728	27450	2.53	1.0E-38	4885288	NT	MER19 repetitive element;
2012	14747	27475	1.11	1.0E-38	7661969	NT	Homo sapiens guanine nucleotide binding protein-like 1 (GNL1), mRNA
2499	15216	27960	2.34	1.0E-38	AF270831.1	NT	Homo sapiens KIAA0173 gene product (KIAA0173), mRNA
4290	17029	29655	1.23	1.0E-38	AL163203.2	NT	Homo sapiens cyclin K (CCNK) gene, exon 7
4558	17293	29921	1	1.0E-38	8922543	NT	Homo sapiens chromosome 21 segment HS21C003
5937	18719	31677	4.71	1.0E-38	7305360	NT	Homo sapiens chromosome 21 segment HS21C003
5937	18719	31678	4.71	1.0E-38	7305360	NT	Homo sapiens chromosome 21 segment HS21C003
7304	19987	33063	3.15	1.0E-38	AB014512.1	NT	Homo sapiens hypothetical protein FLJ10600 (FLJ10600), mRNA
9051	21740	34898	0.71	1.0E-38	11422250	NT	Homo sapiens hypothetical protein FLJ10600 (FLJ10600), mRNA
9310	21977	35150	5.13	1.0E-38	BE350127.1	EST_HUMAN	hi09g01.x1 NCI_CGAP_K1d13 Homo sapiens cDNA clone IMAGE:3148266 3' similar to contains MER28.b3
10301	22948	36163	0.98	1.0E-38	R18512.1	EST_HUMAN	MER29 repetitive element;
11588	24187	37503	1.28	1.0E-38	7662109	NT	yf96b08.r1 Soares Infant brain 1N1B Homo sapiens cDNA clone IMAGE:30486 5'
12118	25140		2.2	1.0E-38	AL163284.2	NT	Homo sapiens KIAA0426 gene product (KIAA0426), mRNA
53	12882	25510	15.3	8.0E-39	4502312	NT	Homo sapiens chromosome 21 segment HS21C084
1373	14121	26796	1.45	8.0E-39	47582229	NT	Homo sapiens ATPase, H+ transporting, lysosomal (vacuolar proton pump) 16kD (ATP6C) mRNA
1821	14560		1.27	8.0E-39	AI823404.1	EST_HUMAN	Homo sapiens estrogen receptor-binding fragment-associated gene 9 (EBAG9) mRNA
2087	14819	27550	5.79	7.0E-39	AL163227.2	NT	wh53f10.x1 NCI_CGAP_K1d11 Homo sapiens cDNA clone IMAGE:2384491 3' similar to TR:P87890 P87890
10711	23400	36639	2.24	6.0E-39	BF331829.1	EST_HUMAN	POL PROTEIN;
12696	24979		1.66	6.0E-39	BE670394.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C027
987	13750	26412	1.57	5.0E-39	AF003528.1	NT	QV1-BT0631-049900-357-f02 BT0631 Homo sapiens cDNA 7e34c-03.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3284356 3' similar to WP:R151.6 CE00828;
							Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions

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Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2984	15750	28397	8.82	5.0E-39	A1750154.1	EST_HUMAN	at36b04.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2374063 3' similar to TR:Q15408
12410	24783		2.04	5.0E-39	11420289	NT	Q15408 NEUTRAL PROTEASE LARGE SUBUNIT ; contains LTR7.11 LTR7 repetitive element ;
537	13320	25954	6.78	4.0E-39	AB015610.1	NT	Homo sapiens hypothetical protein FLJ10803 (FLJ10803), mRNA
3559	16314	28961	0.97	4.0E-39	AL163210.2	NT	Chlorococcus ethiops mRNA for ribosomal protein S4X, complete cds
							Homo sapiens chromosome 21 segment HS21C010
7974	20669	33791	1.27	4.0E-39	AA682949.1	EST_HUMAN	ae92g04.s1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:1020438 3' similar to contains
9228	21907	35078	0.56	4.0E-39	D84116.1	NT	OFB.b1 OFR repetitive element ;
9228	21907	35078	0.56	4.0E-39	D84116.1	NT	Homo sapiens DNA for prostacyclin synthase, exon 2
12427	24802		4.47	4.0E-39	11418177	NT	Homo sapiens Ran GTPase activating protein 1 (RANGAP1), mRNA
12534	24878		2.71	4.0E-39	BE836452.1	EST_HUMAN	QV0-FN0063-260600-278-c06 FN0063 Homo sapiens cDNA
46	12875	25498	14.86	3.0E-39	AA631949.1	EST_HUMAN	frnfc16 Regional genomic DNA specific cDNA library Homo sapiens cDNA clone CR12-1
46	12875	25498	14.86	3.0E-39	AA631949.1	EST_HUMAN	frnfc16 Regional genomic DNA specific cDNA library Homo sapiens cDNA clone CR12-1
46	12875	25500	14.86	3.0E-39	AA631949.1	EST_HUMAN	frnfc16 Regional genomic DNA specific cDNA library Homo sapiens cDNA clone CR12-1
11963	24511	37257	4.35	3.0E-39	A084557.1	EST_HUMAN	α63a10.s1 Soares_NhiHMPu_S1 Homo sapiens cDNA clone IMAGE:1660986 3' similar to SW:GTR5_RAT
11963	24511	37258	4.35	3.0E-39	A084557.1	EST_HUMAN	P43427 GLUCOSE TRANSPORTER TYPE 5, SMALL INTESTINE ;
12006	24541		5.82	3.0E-39	H37903.1	EST_HUMAN	α63a10.s1 Soares_NhiHMPu_S1 Homo sapiens cDNA clone IMAGE:1660986 3' similar to SW:GTR5_RAT
877	13646		5.8	2.0E-39	BE409203.1	EST_HUMAN	P43427 GLUCOSE TRANSPORTER TYPE 5, SMALL INTESTINE ;
892	13661		14.08	2.0E-39	A1525118.1	EST_HUMAN	yp51c06.s1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:180954 3'
1009	13789		4.2	2.0E-39	AF000573.1	NT	601301607F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3636289 5'
1520	14287		11.91	2.0E-39	AW372318.1	EST_HUMAN	promme-7.D01.r bvtumor Homo sapiens cDNA 5'
							Homo sapiens homogenisate 1,2-dioxygenase gene, complete cds
1968	14702	27419	3.28	2.0E-39	AA720574.1	EST_HUMAN	PM0-BT0340-211289-003-402 BT0340 Homo sapiens cDNA
2634	15346	28089	1.84	2.0E-39	AL163248.2	NT	nw21g02.s1 NCI_CGAP_GC80 Homo sapiens cDNA clone IMAGE:1241138 3' similar to contains THR.t3
4370	17108	28743	1.48	2.0E-39	BF370207.1	EST_HUMAN	THR repetitive element ;
5403	18203	30807	4.21	2.0E-39	AA508880.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C048
7289	18953	33028	2.36	2.0E-39	AA080867.1	EST_HUMAN	RC4-FN0037-280700-011-a10 FN0037 Homo sapiens cDNA
7431	20108	33195	0.72	2.0E-39	AL163202.2	NT	ng86603.s1 NCI_CGAP_P66 Homo sapiens cDNA clone IMAGE:941693
7431	20108	33196	0.72	2.0E-39	AL163202.2	NT	zn06102.r1 Stratagene hNT neuron (#937233) Homo sapiens cDNA clone IMAGE:546651 5'
8209	20803	34038	0.67	2.0E-39	AF078778.1	NT	Homo sapiens chromosome 21 segment HS21C002
8394	22056		0.55	2.0E-39	AA884531.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C002
							Homo sapiens chromosome 21 segment HS21C002
							Rattus norvegicus putative four repeat ion channel mRNA, complete cds
							am88c11.s1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:1630196 3'

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9526	22179		0.73	2.0E-39	AI686680.1	EST_HUMAN	tu35e03.x1 NCI_CGAP_P28 Homo sapiens cDNA clone IMAGE:2253052 3'
11409	24058	37395	2.97	2.0E-39	D86964.1	NT	Human mRNA for KIAA0209 gene, partial cds
1503	14249	26936	3.71	1.0E-39	AJ006345.1	NT	Homo sapiens KVLQT1 gene
1503	14249	26937	3.71	1.0E-39	AJ006345.1	NT	Homo sapiens KVLQT1 gene
1521	14268	26952	4.24	1.0E-39	7657020	NT	Homo sapiens DKFZp434P211 protein (DKFZP434P211), mRNA
4098	18941	29467	0.7	1.0E-39	11430303	NT	Homo sapiens catenin (cadherin-associated protein), alpha 2 (CTNNA2), mRNA
4098	18941	29468	0.7	1.0E-39	11430303	NT	Homo sapiens catenin (cadherin-associated protein), alpha 2 (CTNNA2), mRNA
4612	17347	29580	2.5	1.0E-39	AW951995.1	EST_HUMAN	EST364065 MAGe resequences, MAGB Homo sapiens cDNA
4612	17347	29581	2.5	1.0E-39	AW951995.1	EST_HUMAN	EST364065 MAGe resequences, MAGB Homo sapiens cDNA
4654	17388	30021	8.86	1.0E-39	7657020	NT	Homo sapiens DKFZp434P211 protein (DKFZP434P211), mRNA
5274	18079	30735	1.02	1.0E-39	11417342	NT	Homo sapiens sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 5A (SEMA5A), mRNA
5274	18079	30736	1.02	1.0E-39	11417342	NT	Homo sapiens sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 5A (SEMA5A), mRNA
5542	18339	31246	1.97	1.0E-39	T80876.1	EST_HUMAN	Alu repetitive element contains LTR1 repetitive element
5578	18375	31287	4.84	1.0E-39	AJ278170.1	NT	Mus musculus mRNA for neuronal interacting factor X 1 (NIX1) (Nix1 gene)
5578	18375	31288	4.84	1.0E-39	AJ278170.1	NT	Mus musculus mRNA for neuronal interacting factor X 1 (NIX1) (Nix1 gene)
6727	19581		1.97	1.0E-39	11438736	NT	Homo sapiens tubby like protein 3 (TULP3), mRNA
7264	19948	33025	1.8	1.0E-39	D78132.1	NT	Homo sapiens mRNA for ras-related GTP-binding protein, complete cds
8462	21154	34297	1.03	1.0E-39	O46530	SWISSPROT	RIBONUCLEASE K6 PRECURSOR (RNASE K6)
12557	24761		1.34	1.0E-39	U07000.1	NT	Human breakpoint cluster region (BCR) gene, complete cds
542	13325	25957	1.68	9.0E-40	5803210	NT	Homo sapiens UDP-glucose pyrophosphorylase 2 (UGP2), mRNA
1213	13963	26629	15.14	9.0E-40	4755145	NT	Homo sapiens AE-binding protein 1 (AEBP1) mRNA
1213	13963	26630	15.14	9.0E-40	4755145	NT	Homo sapiens AE-binding protein 1 (AEBP1) mRNA
1432	14179	26865	6.54	9.0E-40	4507512	NT	Homo sapiens tissue inhibitor of metalloproteinase 3 (Sorsby fundus dystrophy, pseudoinflammatory) (TIMP3) mRNA
3765	19517	29155	0.97	9.0E-40	4503764	NT	Homo sapiens fragile X mental retardation 1 (FMR1) mRNA
3956	17878	29343	3.99	9.0E-40	AB033070.1	NT	Homo sapiens mRNA for KIAA1244 protein, partial cds
3036	15802	28449	0.84	8.0E-40	AA078165.1	EST_HUMAN	7H15A04 Chromosome 7 HeLa cDNA Library Homo sapiens cDNA clone 7H15A04
3903	16653		3.35	8.0E-40	BE396541.1	EST_HUMAN	601268958F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3619166 5'
7616	20282	33390	2.03	7.0E-40	U60325.1	NT	Human DNA polymerase gamma mRNA, nuclear gene encoding mitochondrial protein, complete cds

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7616	20282	33391	2.03	7.0E-40	U60325.1	NT	Human DNA polymerase gamma mRNA, nuclear gene encoding mitochondrial protein, complete cds
10813	23496	36732	2.27	7.0E-40	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C046
2730	15437	28174	8.41	6.0E-40	AA361275.1	EST_HUMAN	EST70527 T-cell lymphoma Homo sapiens cDNA 5' end similar to zinc finger protein family
2730	15437	28175	8.41	6.0E-40	AA361275.1	EST_HUMAN	EST70527 T-cell lymphoma Homo sapiens cDNA 5' end similar to zinc finger protein family
5849	18636		2.24	6.0E-40	BE504766.1	EST_HUMAN	h240g01.x1 NCL CGAP GC8 Homo sapiens cDNA clone IMAGE:3210480 3'
6055	18835		1.11	6.0E-40	7661998	NT	Homo sapiens KIAA0211 gene product (KIAA0211), mRNA
6836	19498	32522	3.56	6.0E-40	11439783	NT	Homo sapiens fatty acid desaturase 1 (FADS1), mRNA
6836	19498	32523	3.56	6.0E-40	11439783	NT	Homo sapiens fatty acid desaturase 1 (FADS1), mRNA
9877	22627	35722	10.25	6.0E-40	AV653028.1	EST_HUMAN	AV653028 GLC Homo sapiens cDNA clone GLCDGF04 3'
9877	22627	35723	10.25	6.0E-40	AV653028.1	EST_HUMAN	AV653028 GLC Homo sapiens cDNA clone GLCDGF04 3'
1869	14607	27318	1.78	4.0E-40	AI686005.1	EST_HUMAN	tt91b01.x1 NCL CGAP_P28 Homo sapiens cDNA clone IMAGE:2248873 3' similar to TR:O73505 O73505 POL PROTEIN ;
2101	14832		2.27	4.0E-40	AF003528.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
4356	17094	29729	9.08	4.0E-40	7662117	NT	Homo sapiens KIAA0433 protein (KIAA0433), mRNA
7786	20481	33608	0.5	4.0E-40	AU127831.1	EST_HUMAN	AU127831 NT2RP2 Homo sapiens cDNA clone NT2RP2002172 5'
7890	20585	33714	6.22	4.0E-40	AA742809.1	EST_HUMAN	nt34e10.1 NCL CGAP_Br4 Homo sapiens cDNA clone IMAGE:1222122
8953	21644	34783	5.17	4.0E-40	BE009416.1	EST_HUMAN	PM0-BN0167-070500-002-h12 BN0167 Homo sapiens cDNA
8953	21644	34794	5.17	4.0E-40	BE009416.1	EST_HUMAN	PM0-BN0167-070500-002-h12 BN0167 Homo sapiens cDNA
10616	23309	36548	3.03	4.0E-40	AW841585.1	EST_HUMAN	RC1-CN0017-120200-012-e04 CN0017 Homo sapiens cDNA
4111	16854	29481	1.02	3.0E-40	AI925949.1	EST_HUMAN	wh1207.x1 NCL CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2380549 3'
6543	19308	32313	7.02	3.0E-40	11417342	NT	Homo sapiens sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 5A (SEMA5A), mRNA
8280	20974	34115	3.62	3.0E-40	5454167	NT	Homo sapiens HBV associated factor (XAP4) mRNA
8668	21559	34704	1.25	3.0E-40	AF078779.1	NT	Rattus norvegicus putative four repeat ion channel mRNA, complete cds
9111	21799	34963	1.42	3.0E-40	AF078779.1	NT	Rattus norvegicus putative four repeat ion channel mRNA, complete cds
11232	23895	37182	8.36	3.0E-40	6005813	NT	Homo sapiens serine threonine protein kinase (NDR), mRNA
11563	24162	37473	2.23	3.0E-40	AW118799.1	EST_HUMAN	xd96h02.x1 Soares_NFL_I_GBC_S1 Homo sapiens cDNA clone IMAGE:2605491 3' similar to TR:Q15804 Q15804 SIMILAR TO ENV OF TYPE A AND TYPE B RETROVIRUSES AND TO CLASS II HERVS ;
317	13120		8.63	2.0E-40	AI223036.1	EST_HUMAN	gg52h08.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1838847 3'

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
777	13549		1.61	2.0E-40	AW303888.1	EST_HUMAN	x24e10.x1 NCI_CGAP_U14 Homo sapiens cDNA clone IMAGE:2761098 3' similar to SW.RS5_MOUSE
1818	14557		0.92	2.0E-40	AV731601.1	EST_HUMAN	P97461.40S RIBOSOMAL PROTEIN S6 ;
1927	14663	27375	1.58	2.0E-40	4506188	NT	AV731601.HTF Homo sapiens cDNA clone HTFAZE05 5'
1927	14663	27376	1.58	2.0E-40	4506188	NT	Homo sapiens proteasome (prosome, macropain) subunit, alpha type, 7 (PSMA7) mRNA, and translated products
2064	14796	27522	1.21	2.0E-40	AI988562.1	EST_HUMAN	Homo sapiens proteasome (prosome, macropain) subunit, alpha type, 7 (PSMA7) mRNA, and translated products
2166	14895	27630	2.48	2.0E-40	5453592	NT	w60a11.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2514716 3' similar to TR:Q91929 Q91929
2695	15404		1.44	2.0E-40	BE275932.1	EST_HUMAN	ZINC FINGER PROTEIN ;
3123	15888	28529	4.28	2.0E-40	5453592	NT	Homo sapiens adenyl cyclase-associated protein 2 (CAP2) mRNA
4843	17573	30197	1.88	2.0E-40	AL163280.2	NT	601121667F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3345784 5'
4843	17573	30198	1.68	2.0E-40	AL163280.2	NT	Homo sapiens adenyl cyclase-associated protein 2 (CAP2) mRNA
863	13632		1.78	1.0E-40	AA225989.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C080
2627	15339	28083	0.93	1.0E-40	BF036881.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C080
2692	15401		1.34	1.0E-40	BE018348.1	EST_HUMAN	nc09a09.s1 NCI_CGAP_P11 Homo sapiens cDNA clone IMAGE:1007608
2741	15447	28185	1.18	1.0E-40	BF541030.1	EST_HUMAN	601480375F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3863803 5'
2741	15447	28186	1.18	1.0E-40	BF541030.1	EST_HUMAN	bb79a10.y1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3048570 5' similar to TR:Q92158 Q92158
3292	16053		1.27	1.0E-40	4507142	NT	SYNTAXIN 17 ;
4571	17308	29634	4.52	1.0E-40	4508012	NT	Homo sapiens sorting nexin 3 (SNX3) mRNA
6161	18338	31907	0.75	1.0E-40	W92708.1	EST_HUMAN	Homo sapiens zinc finger protein 200 (ZNF200) mRNA, and translated products
6161	18338	31908	0.75	1.0E-40	W92708.1	EST_HUMAN	zh79f11.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:418317 3'
6987	19680	32727	1.77	1.0E-40	AA573201.1	EST_HUMAN	zh79f11.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:418317 3'
6987	19680	32728	1.77	1.0E-40	AA573201.1	EST_HUMAN	h42f04.s1 NCI_CGAP_AA1 Homo sapiens cDNA clone IMAGE:995167 3'
7133	19820	32886	0.69	1.0E-40	P26808	SWISSPROT	h42f04.s1 NCI_CGAP_AA1 Homo sapiens cDNA clone IMAGE:995167 3'
10834	23516	38758	8.34	1.0E-40	AU149345.1	EST_HUMAN	POL POLYPROTEIN [CONTAINS: PROTEASE ; REVERSE TRANSCRIPTASE ; RIBONUCLEASE H]
11694	24289	37612	1.89	1.0E-40	AA614255.1	EST_HUMAN	AU149345.NT2RM4 Homo sapiens cDNA clone NT2RM4002122 3'
11694	24289	37613	1.89	1.0E-40	AA614255.1	EST_HUMAN	np09h03.s1 NCI_CGAP_P13 Homo sapiens cDNA clone IMAGE:1115861 similar to TR:G1136406
12376	25274		10.09	1.0E-40	BF334112.1	EST_HUMAN	G1136406 KIAA0173 PROTEIN ;
7822	20517	33943	1.62	8.0E-41	AL163203.2	NT	G1136406 KIAA0173 PROTEIN ;
							MR2-CT0222-21099-002-e10 CT0222 Homo sapiens cDNA
							Homo sapiens chromosome 21 segment HS21C003

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit: Accession No.	Top Hit Database Source	Top Hit Descriptor
809	15553	26246	1.24	7.0E-41	A1934364.1	EST_HUMAN	wp04h04.x1 NCL CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2463895 3'
809	15553	26247	1.24	7.0E-41	A1934364.1	EST_HUMAN	wp04h04.x1 NCL CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2463895 3'
4609	17344	29976	0.92	7.0E-41	BE389592.1	EST_HUMAN	601282077F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3603955 5'
4609	17344	29977	0.92	7.0E-41	BE389592.1	EST_HUMAN	601282077F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3603955 5'
5183	17991	30507	1.2	7.0E-41	11545770	NT	Homo sapiens hypothetical protein FLJ13188 (FLJ13188), mRNA
5918	18703	31656	3.49	7.0E-41	11419208	NT	Homo sapiens a disintegrin and metalloproteinase domain 22 (ADAM22), mRNA
6260	18034	32009	0.61	7.0E-41	11433010	NT	Homo sapiens IQ motif containing GTPase activating protein 1 (IQGAP1), mRNA
6895	17971	30528	0.68	7.0E-41	U72335.1	NT	Human platelet activating factor acetylhydrolase, brain isoform, 45 kDa subunit (LIS1) gene, exons 3 and 4
11411	24060	37366	2.23	7.0E-41	4758445	NT	Homo sapiens guanine nucleotide binding protein 10 (GNG10) mRNA
11631	24228	37552	1.73	7.0E-41	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
12782	25271	25724	4.35	7.0E-41	AB037163.1	NT	Homo sapiens pscadillo (zehrafish) homolog 1, containing BRCT domain (PES1), mRNA
274	13081	27569	1.19	6.0E-41	7657042	NT	Homo sapiens DSCR5b mRNA, complete cds
2104	14835	27569	2.04	6.0E-41	7657042	NT	Homo sapiens Down syndrome candidate region 1 (DSCR1), mRNA
4433	17189	29797	0.91	6.0E-41	BE67816.1	EST_HUMAN	601340485F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3682677 5'
7871	20566	33692	1.44	6.0E-41	BF513783.1	EST_HUMAN	UIH-BW1-amp-b-03-Q-UI.s1 NCL CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3070421 3'
1795	14535	27244	1.11	5.0E-41	T62628.1	EST_HUMAN	yc03e10.s1 Stragene lung (#937210) Homo sapiens cDNA clone IMAGE:79628 3'
4087	16830		1.07	5.0E-41	4885636	NT	Homo sapiens target of myb1 (chicken) homolog (TOM1), mRNA
6452	19220		2.29	5.0E-41	BE067042.1	EST_HUMAN	PM4-BT0341-251199-002-F11 BT0341 Homo sapiens cDNA
382	13189		2.42	4.0E-41	BE156318.1	EST_HUMAN	QV0-HT0367-160200-114-g09 HT0367 Homo sapiens cDNA
1076	13834	26492	1.26	4.0E-41	AU119344.1	EST_HUMAN	AU119344 HEMBA1 Homo sapiens cDNA clone HEMBA1005583 5'
1388	14135	26810	15.51	4.0E-41	A1027117.1	EST_HUMAN	ow45a06.s1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:1649794 3' similar to TR:O00597 O00597 CYTOCHROME C-LIKE POLYPEPTIDE.; contains LTR5.b1 LTR5 repetitive element;
1388	14135	26811	15.51	4.0E-41	A1027117.1	EST_HUMAN	ow45a06.s1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:1649794 3' similar to TR:O00597 O00597 CYTOCHROME C-LIKE POLYPEPTIDE.; contains LTR5.b1 LTR5 repetitive element;
1403	14150	26830	1.88	4.0E-41	AB008681.1	NT	Homo sapiens gene for activin receptor type IIB, complete cds
1632	14378	27085	6.08	4.0E-41	A1500406.1	EST_HUMAN	Im98c04.x1 NCL CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2165958 3' similar to contains OFR.b1 OFR repetitive element;
2891	15658	28302	3.55	4.0E-41	A1229041.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3
2891	15658	28303	3.55	4.0E-41	A1229041.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3
4124	16866	29493	2.24	4.0E-41	X62685.1	NT	H.sapiens DNase I hypersensitive site (HSS-3) enhancer element

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Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6418	19184		1.41	4.0E-41	AV758295.1	EST_HUMAN	AV758295 BM Homo sapiens cDNA clone BMFBHC08 5'
9593	22246	35430	7.24	4.0E-41	BF304683.1	EST_HUMAN	60188099F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4122119 5'
11671	24266		11.07	4.0E-41	AV710480.1	EST_HUMAN	AV710480 Cu Homo sapiens cDNA clone CUAACC07 5'
12546	25164		1.63	4.0E-41	AV708431.1	EST_HUMAN	AV708431 ADC Homo sapiens cDNA clone ADCARE02 5'
12727	24998	30971	1.69	4.0E-41	BE897118.1	EST_HUMAN	601508315F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3910059 5'
927	13694	26358	2.88	3.0E-41	AB030176.1	NT	Homo sapiens PAD-H19 mRNA for peptidylarginine deiminase type II, complete cds
4301	17040	29687	2.45	3.0E-41	AB026998.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
6404	18204	30908	7.78	3.0E-41	X87689.1	NT	H. sapiens mRNA for putative p64 CLCP protein
6288	19061	32043	1.59	3.0E-41	AB037808.1	NT	Homo sapiens mRNA for KIAA1387 protein, partial cds
7159	19846	32616	0.71	3.0E-41	AA365168.1	EST_HUMAN	EST64683 Jurkat T-cells VI Homo sapiens cDNA 5' end
11730	24323	37647	1.28	3.0E-41	AI229041.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3
11924	24485		1.52	3.0E-41	AA609768.1	EST_HUMAN	af17710.s1 Soares, testis, NIH Homo sapiens cDNA clone IMAGE:1031947 3'
12456	24825		1.48	3.0E-41	BF125922.1	EST_HUMAN	601762940F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:4026081 5'
1817	14299	26987	5.17	2.0E-41	U43701.1	NT	Human ribosomal protein L23a mRNA, complete cds
1951	14686	27393	1.84	2.0E-41	AA331940.1	EST_HUMAN	EST35818 Embryo, 8 week I Homo sapiens cDNA 5' end
2216	14944	27684	1.54	2.0E-41	D86962.1	NT	Human mRNA for KIAA0207 gene, complete cds
2284	14990	27730	3.34	2.0E-41	X89631.1	NT	G. gorilla DNA for ZNF80 gene homolog
2831	14299	26987	4.65	2.0E-41	U43701.1	NT	Human ribosomal protein L23a mRNA, complete cds
3321	18081	28731	1.41	2.0E-41	AA449549.1	EST_HUMAN	zx08504.r1 Soares, fetal, fetus Nb2HF8, 9w Homo sapiens cDNA clone IMAGE:765839 5'
4579	17314	29942	1.17	2.0E-41	AL163267.2	NT	Homo sapiens chromosome 21 segment HS21C067
4579	17314	29943	1.17	2.0E-41	AL163267.2	NT	Homo sapiens chromosome 21 segment HS21C067
5141	17859	30475	0.9	2.0E-41	AW236547.1	EST_HUMAN	xm4706.x1 NCI_CGAP_GCB Homo sapiens cDNA clone IMAGE:2687363 3' similar to TR:O70343 O70343 PPAR GAMMA COACTIVATOR 1;
6530	19296	32300	0.76	2.0E-41	4504778	NT	Homo sapiens integrin, beta 8 (ITGB8) mRNA
7572	20241	33346	8.08	2.0E-41	AF038404.1	NT	Homo sapiens homolog of Nedd5 (hNedd5) mRNA, complete cds
7867	20662	33786	1.45	2.0E-41	M96944.1	NT	Human B-cell specific transcription factor (BSAP) mRNA, complete cds
7967	20662	33787	1.45	2.0E-41	M96944.1	NT	Human B-cell specific transcription factor (BSAP) mRNA, complete cds
7966	20660	33818	1.12	2.0E-41	AA328265.1	EST_HUMAN	EST31723 Embryo, 12 week I Homo sapiens cDNA 5' end
8874	21595	34710	1.61	2.0E-41	P82742	SWISSPROT	ZINC FINGER PROTEIN 135
9317	21984	35155	0.52	2.0E-41	11417118	NT	Homo sapiens KIAA0433 protein (KIAA0433), mRNA
9317	21984	35156	0.52	2.0E-41	11417118	NT	Homo sapiens KIAA0433 protein (KIAA0433), mRNA
11468	24071	37379	2.76	2.0E-41	AA372637.1	EST_HUMAN	EST184555 Colon adenocarcinoma IV Homo sapiens cDNA 5' end
3201	15984	28616	1.05	1.0E-41	BE869735.1	EST_HUMAN	601445847F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3849803 5'

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Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3201	15964	28617	1.05	1.0E-41	BE869735.1	EST_HUMAN	801445047F1 NIH_MGC_85 Homo sapiens cDNA clone IMAGE:3849803 5'
4529	17264	28897	14.08	1.0E-41	6878468	NT	Mus musculus tubulin alpha 6 (Tuba6), mRNA
6749	17918	30582	0.66	1.0E-41	H99079.1	EST_HUMAN	Y18b03.s1 Soares melanocyte 2N8HM Homo sapiens cDNA clone IMAGE:262061 3'
9318	21985	35157	1.69	1.0E-41	A1217868.1	EST_HUMAN	q75c10.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1755968 3'
11111	23781	37056	1.66	1.0E-41	AW847612.1	EST_HUMAN	IL3-C10213-190200-040-F09 CT0213 Homo sapiens cDNA
12054	24571		2.81	1.0E-41	11526281	NT	Homo sapiens hypothetical protein FLJ20454 (FLJ20454), mRNA
8418	21111		1.14	9.0E-42	BE179191.1	EST_HUMAN	RC0-HT0813-210300-032-g01 HT0813 Homo sapiens cDNA
9072	21761	34922	3.49	9.0E-42	11560151	NT	Homo sapiens hypothetical C2H2 zinc finger protein FLJ22504 (FLJ22504), mRNA
9072	21761	34923	3.49	9.0E-42	11560151	NT	Homo sapiens hypothetical C2H2 zinc finger protein FLJ22504 (FLJ22504), mRNA
450	13236	25876	7.71	8.0E-42	AF003630.1	NT	Homo sapiens hornetbox protein CDX4 (CDX4) gene, complete cds and flanking repeat regions
2102	14833	27567	0.92	8.0E-42	AB026898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
12093	26277		4.4	8.0E-42	AA493896.1	EST_HUMAN	rh07c02.s1 NCI_CGAP_Thy1 Homo sapiens cDNA clone IMAGE:943586 similar to TR:G434304 G434304 367BP EXPRESSED SEQUENCE TAG MRNA ;
12111	25154		1.56	8.0E-42	AW088062.1	EST_HUMAN	xc97a04.x1 NCI_CGAP_Bm35 Homo sapiens cDNA clone IMAGE:2592174 3' similar to contains OFR.12
911	13678		2.58	7.0E-42	AL163285.2	NT	OFR repetitive element ;
9143	21874	35039	1.57	7.0E-42	A1204358.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C085
11126	23795	37071	1.3	7.0E-42	AA568592.1	EST_HUMAN	q58g12.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1754278 3'
11126	23795	37072	1.3	7.0E-42	AA568592.1	EST_HUMAN	nf23g07.s1 NCI_CGAP_Pr1 Homo sapiens cDNA clone IMAGE:914652
1848	14586	27299	3.21	6.0E-42	AF012872.1	NT	nf23g07.s1 NCI_CGAP_Pr1 Homo sapiens cDNA clone IMAGE:914652
1848	14586	27300	3.21	6.0E-42	AF012872.1	NT	Homo sapiens phosphatidylinositol 4-kinase 230 (p4K230) mRNA, complete cds
2287	15012		3.55	6.0E-42	AW238656.1	EST_HUMAN	Homo sapiens phosphatidylinositol 4-kinase 230 (p4K230) mRNA, complete cds
5381	18181	30871	1.63	6.0E-42	AB028990.1	NT	xp29f08.x1 NCI_CGAP_HN10 Homo sapiens cDNA clone IMAGE:2741769 3' similar to contains L1.11 L1 repetitive element ;
5630	18181	30871	1.45	6.0E-42	AB028990.1	NT	Homo sapiens mRNA for KIAA1067 protein, partial cds
132	12947		7.53	5.0E-42	AJ271735.1	NT	Homo sapiens mRNA for KIAA1067 protein, partial cds
428	13214	25859	1.41	5.0E-42	BE217913.1	EST_HUMAN	Homo sapiens Xq pseudautosomal region; segment 1/2
474	13260		2.57	5.0E-42	5730038	NT	h31e11.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3175052 3'
475	13261		2.74	5.0E-42	5730038	NT	Homo sapiens SET domain and mafin transposase fusion gene (SETMAR) mRNA
6587	19350	32363	1.04	5.0E-42	11433063	NT	Homo sapiens SET domain and mafin transposase fusion gene (SETMAR) mRNA
6587	19350	32364	1.04	5.0E-42	11433063	NT	Homo sapiens ubiquitin protein ligase E3A (human papilloma virus E6-associated protein, Angelman syndrome) (UBE3A), mRNA

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Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6704	18619	32662	3.12	5.0E-42	11417957	NT	Homo sapiens myotubularin related protein 3 (MTMR3), mRNA
7101	19789	32854	1.59	5.0E-42	AF071689.1	NT	Homo sapiens multifunctional calcium/calmodulin-dependent protein kinase II delta2 isoform mRNA, complete cds
7711	20375	33489	0.57	5.0E-42	4826877	NT	Homo sapiens reelin (RELN), mRNA
8677	21369	34515	3.55	5.0E-42	AB037715.1	NT	Homo sapiens mRNA for KIAA1294 protein, partial cds
10920	23600	36949	2.44	5.0E-42	8823162	NT	Homo sapiens hypothetical protein FLJ20163 (FLJ20163), mRNA
736	13510	26167	5.09	4.0E-42	AF050566.1	NT	Homo sapiens MHC class 1 region
736	13510	26168	5.09	4.0E-42	AF050568.1	NT	Homo sapiens MHC class 1 region
1044	13803	28462	3.46	4.0E-42	AF189011.1	NT	Homo sapiens ribonuclease III (RN3), mRNA, complete cds
4171	18911	29541	1.22	4.0E-42	X59417.1	NT	H. sapiens PROS-27 mRNA
4202	18943	29570	1.07	4.0E-42	AF246219.1	NT	Homo sapiens SNARE protein kinase SNAX mRNA, complete cds
4223	18964	29589	4.15	4.0E-42	4508496	NT	Homo sapiens regulatory factor X, 4 (influences HLA class II expression) (RFY4), mRNA
4543	17278	29809	15.12	4.0E-42	4508008	NT	Homo sapiens zinc finger protein 177 (ZNF177), mRNA
10545	23241	36475	1.56	4.0E-42	AW818630.1	EST_HUMAN	RC1-ST0278-040400-018-h11 ST0278 Homo sapiens cDNA
10545	23241	36476	1.56	4.0E-42	AW818630.1	EST_HUMAN	RC1-ST0278-040400-018-h11 ST0278 Homo sapiens cDNA
11389	23995	37297	1.5	4.0E-42	BF035327.1	EST_HUMAN	607456531F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3862086 5'
1466	14213	26902	2.81	2.0E-42	BF378834.1	EST_HUMAN	RC0-TN0079-110900-024-g07 TN0079 Homo sapiens cDNA
2413	15134		2.92	2.0E-42	AW898344.1	EST_HUMAN	RC3-NN0070-270400-011-h10 NN0070 Homo sapiens cDNA
2425	15146	27879	2.22	2.0E-42	AW250059.1	EST_HUMAN	2819283 3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2818293 3'
5670	18465	31379	7.8	2.0E-42	AW955368.1	EST_HUMAN	EST367433 IMAGE ressequences, MAGC Homo sapiens cDNA
5670	18465	31380	7.8	2.0E-42	AW955368.1	EST_HUMAN	EST367433 IMAGE ressequences, MAGC Homo sapiens cDNA
6654	19416	32429	1.46	2.0E-42	AJ052586.1	EST_HUMAN	ow83d05.x1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:2721871 3'
9741	22392	35596	1.32	2.0E-42	BE538919.1	EST_HUMAN	607061294F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3447620 5'
9955	22603	35807	0.68	2.0E-42	P81649	SWISSPROT	RIBONUCLEASE K3 (RNASE K3)
9955	22603	35808	0.68	2.0E-42	P81649	SWISSPROT	RIBONUCLEASE K3 (RNASE K3)
11742	24334	37660	1.37	2.0E-42	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
717	13490	26143	1.21	1.0E-42	X57147.1	NT	Human endogenous retrovirus pHE.1 (ERV9)
1019	13779	26441	1.1	1.0E-42	AW295809.1	EST_HUMAN	UI-H-B1-aff-e-04-UJ-s1 NCJ_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2721871 3'
1079	13837	26495	1.18	1.0E-42	AJ251818.1	NT	Homo sapiens partial C9 gene for complement component C9, exon 1
1079	13837	26496	1.18	1.0E-42	AJ251818.1	NT	Homo sapiens partial C9 gene for complement component C9, exon 1
1220	15563	26641	16.49	1.0E-42	AF067166.1	NT	Homo sapiens NADH-ubiquinone oxidoreductase AGGG subunit precursor homolog mRNA, nuclear gene encoding mitochondrial protein, complete cds
1220	15563	26642	16.49	1.0E-42	AF067166.1	NT	Homo sapiens NADH-ubiquinone oxidoreductase AGGG subunit precursor homolog mRNA, nuclear gene encoding mitochondrial protein, complete cds

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Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1696	14439	27137	1.13	1.0E-42	11423219	NT	Homo sapiens rec (LOC51201), mRNA
2546	15261	27998	1.63	1.0E-42	5174458	NT	Homo sapiens major histocompatibility complex, class II, DM alpha (HLA-DMA) mRNA
2964	15730	28380	10.26	1.0E-42	4505524	NT	Homo sapiens origin recognition complex, subunit 5 (yeast homolog-like (ORC5L) mRNA, and translated products
3695	16449	28088	2.6	1.0E-42	7662027	NT	Homo sapiens KIAA0255 gene product (KIAA0255), mRNA
3905	16655	29298	1.17	1.0E-42	AL163287.2	NT	Homo sapiens chromosome 21 segment HS21C067
4221	16982	29587	1.92	1.0E-42	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
4554	17289	29918	0.75	1.0E-42	AW813617.1	EST_HUMAN	RC3-STO197-161099-012-a03 ST0197 Homo sapiens cDNA
4697	17431	30062	1.88	1.0E-42	5803122	NT	Homo sapiens proteasome inhibitor (PI31), mRNA
4728	17460	30063	1.88	1.0E-42	5803122	NT	Homo sapiens proteasome inhibitor (PI31), mRNA
5044	17763	30378	1.08	1.0E-42	4506758	NT	Homo sapiens ryanodine receptor 3 (RYR3) mRNA
5044	17763	30379	1.08	1.0E-42	4501912	NT	Homo sapiens a disintegrin and metalloproteinase domain 23 (ADAM23) mRNA
9886	22634	35844	4.03	9.0E-43	4757969	NT	Homo sapiens chromodomain protein, Y chromosome-like (CDYL) mRNA
637	13416	26052	19.69	8.0E-43	AV736824.1	EST_HUMAN	Homo sapiens OB Homo sapiens cDNA clone CBLAKH08 5'
637	13416	26053	19.69	8.0E-43	AV736824.1	EST_HUMAN	AV736824 OB Homo sapiens cDNA clone CBLAKH08 5'
684	13459	26104	6.03	8.0E-43	8923278	NT	Homo sapiens hypothetical protein FLJ20297 (FLJ20297), mRNA
684	13459	26105	6.03	8.0E-43	8923278	NT	Homo sapiens hypothetical protein FLJ20297 (FLJ20297), mRNA
684	13459	26106	6.03	8.0E-43	8923278	NT	Homo sapiens hypothetical protein FLJ20297 (FLJ20297), mRNA
5612	18408	31321	0.76	8.0E-43	H13952.1	EST_HUMAN	y08e11.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:148172 5'
3632	16385	29025	6.42	7.0E-43	AW246442.1	EST_HUMAN	2822251.5prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2822251 5'
8667	21359		4.09	7.0E-43	AB36748.1	EST_HUMAN	wp9b01.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2466985 3' similar to TR:O15475
1321	14070		10.45	6.0E-43	AA491890.1	EST_HUMAN	O15475 UNNAMED HERV-H PROTEIN ; contains LTR7.b1 LTR7 repetitive element ;
2600	15314		2.25	6.0E-43	AV708201.1	EST_HUMAN	RIBOSOMAL PROTEIN L30 (HUMAN);
6219	18993	31969	2.24	6.0E-43		NT	AV708201 ADC Homo sapiens cDNA clone ADCACC10 5'
6808	19469	32492	2.09	6.0E-43	AW468897.1	EST_HUMAN	Homo sapiens ATP-binding cassette, sub-family C (CFTR/MRP), member 3 (ABCC3), transcript variant MRP3B, mRNA
9751	22402	35607	2.16	6.0E-43	AA195154.1	EST_HUMAN	hd30b04.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2910991 3' similar to contains MER1.13 MER1 MER1 repetitive element ;
11044	23714		2.55	6.0E-43	AL119158.1	EST_HUMAN	z35e06.r1 Soares_NhlMPu_S1 Homo sapiens cDNA clone IMAGE:665410 5' similar to TR:G529641
138	12953		2.64	5.0E-43	AL163213.2	NT	G529641 DB1, COMPLETE CDS ; contains element PTR7 repetitive element ;
							DKFZ761L1712_r1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761L1712 5'
							Homo sapiens chromosome 21 segment HS21C013

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Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
490	13275	25909	4.55	5.0E-43	AA382780.1	EST_HUMAN	EST96033 Testis 1 Homo sapiens cDNA 5' end
2850	15618	28284	1.52	5.0E-43	AV732578.1	EST_HUMAN	AV732578 HTF Homo sapiens cDNA clone HTF-ANC08 5'
6213	19463	32484	1.17	5.0E-43	AI613509.1	EST_HUMAN	tw22607.x1 NCL_CGAP_Bm52 Homo sapiens cDNA clone IMAGE:2260452 3'
6802	19463	32484	0.72	5.0E-43	AI613509.1	EST_HUMAN	tw22607.x1 NCL_CGAP_Bm52 Homo sapiens cDNA clone IMAGE:2260452 3'
8778	21470		0.46	5.0E-43	H74277.1	EST_HUMAN	y449g12.r1 Soares fetal liver spleen 1N1FLS Homo sapiens cDNA clone IMAGE:229510 5'
9248	21927	35098	0.47	5.0E-43	AA044450.1	EST_HUMAN	zk55a02.r1 Soares pregnant uterus NBHPU Homo sapiens cDNA clone IMAGE:486698 5' similar to gb:D29805 N-ACETYL LACTOSAMINE SYNTHASE (HUMAN);
9248	21927	35099	0.47	5.0E-43	AA044450.1	EST_HUMAN	gb:D29805 N-ACETYL LACTOSAMINE SYNTHASE (HUMAN);
9264	22018	35188	4.44	5.0E-43	AA465288.1	EST_HUMAN	aa33308.r1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:815055 5'
10297	22944	36158	2.31	5.0E-43	AI733244.1	EST_HUMAN	oo52c10.x5 NCL_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1569810 3' similar to TR:P90591 P90591 PV14 GENE;
10335	22982	36201	1.21	5.0E-43	AL049110.1	EST_HUMAN	DKFZp434D0119.1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434D0119
10663	23354	36593	5.29	5.0E-43	AW863007.1	EST_HUMAN	MR2-SN0007-290400-004-c02 SN0007 Homo sapiens cDNA
10891	23571	36822	1.84	5.0E-43	W29011.1	EST_HUMAN	55e4 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA
952	15519	26383	5.9	4.0E-43	AF003528.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
6178	17987	30502	1.02	4.0E-43	AI056338.1	EST_HUMAN	gy47h03.x1 NCL_CGAP_Bm23 Homo sapiens cDNA clone IMAGE:1669013 3'
6278	19049	32028	0.7	4.0E-43	6996009	NT	Homo sapiens glycyl-tRNA synthetase (GARS), mRNA
7030	19722		2.32	4.0E-43	11416793	NT	Homo sapiens protocadherin beta 8 (PCDH8), mRNA
8077	20771	33900	5.21	4.0E-43	AI244341.1	EST_HUMAN	q176a02.x1 NCL_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1865354 3' similar to contains MER10.13 MER10 repetitive element;
8077	20771	33901	5.21	4.0E-43	AI244341.1	EST_HUMAN	q176a02.x1 NCL_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1865354 3' similar to contains MER10.13 MER10 repetitive element;
10213	22861	36074	1.23	4.0E-43	6005967	NT	Homo sapiens zinc finger protein 161 (ZNF161), mRNA
11275	23936	37228	1.68	4.0E-43	T77380.1	EST_HUMAN	y472h10.r1 Soares fetal liver spleen 1N1FLS Homo sapiens cDNA clone IMAGE:113827 5'
12030	24558		3.05	4.0E-43	R20950.1	EST_HUMAN	yg08b05.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:31363 5' similar to contains MER10 repetitive element;
1191	13943		4.59	3.0E-43	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
1690	14434	27130	2.07	3.0E-43	X97869.1	NT	H. sapiens gene encoding La autoantigen
3558	16313	28960	1.31	3.0E-43	S69002.1	NT	AML1-EVI-1-FAM11-1 fusion protein [rearranged translocation] (human, leukemic cell line SKH1, mRNA Mutant, 5938 nt)
4258	16999	29629	1.04	3.0E-43	AA548154.1	EST_HUMAN	nk55d06.s1 NCL_CGAP_P17 Homo sapiens cDNA clone IMAGE:1017419

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Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5803	18593	31518	0.72	3.0E-43	D34613.1	NT	Human TBXAS1 gene for thromboxane synthase, promoter region and exon 1
6264	19038	32013	2.24	3.0E-43	7305360	NT	Mus musculus obogelin (Obog), mRNA
6264	19038	32014	2.24	3.0E-43	7305360	NT	Mus musculus obogelin (Obog), mRNA
6628	19390	32404	4.29	3.0E-43	U65487.1	NT	Human ribosomal RNA upstream binding transcription factor (UBTF) gene, partial cds
8063	20757		8.38	3.0E-43	AA458824.1	EST_HUMAN	aa88f1.1 st Stralagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:838413 3' similar to contains
8719	21411	34654	1.87	3.0E-43	7661721	NT	THR12 THR repetitive element
9764	22415	35622	0.58	3.0E-43	11420217	NT	Homo sapiens hypothetical protein (HSA011916), mRNA
							Homo sapiens similar to ornithine carbamoyltransferase (H. sapiens) (LOC63848), mRNA
179	12991		7.67	2.0E-43	AI190784.1	EST_HUMAN	qd61 c09.x1 Soares_testis_NHT: Homo sapiens cDNA clone IMAGE:1733968 3' similar to contains P TR7.13
6383	19152	32151	1.13	2.0E-43	BE222778.1	EST_HUMAN	hu53a08.x1 NCI_CGAP_Brn41 Homo sapiens cDNA clone IMAGE:3173760 3' similar to contains element
6383	19152	32152	1.13	2.0E-43	BE222778.1	EST_HUMAN	hu53a08.x1 NCI_CGAP_Brn41 Homo sapiens cDNA clone IMAGE:3173760 3' similar to contains element
7176	19892	32933	1.32	2.0E-43	AW207390.1	EST_HUMAN	UI-H-B11-af1-a-09-0-U1.st NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2721712 3'
8207	20801		5.59	2.0E-43	U43701.1	NT	Human ribosomal protein L23a mRNA, complete cds
11156	23823		4.94	2.0E-43	T03007.1	EST_HUMAN	FB1G5 Fetal brain, Stralagene Homo sapiens cDNA clone FB1G5 3'end similar to LINE-1
1845	14391	27080	2.94	1.0E-43	AF154836.1	NT	Homo sapiens Ras-like GTP-binding protein (RAB27A) gene, exons 1b and 2
1845	14391	27081	2.94	1.0E-43	AF154836.1	NT	Homo sapiens Ras-like GTP-binding protein (RAB27A) gene, exons 1b and 2
1700	14443	27142	1.57	1.0E-43	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
2727	15434	28170	3.85	1.0E-43	BF348283.1	EST_HUMAN	602022313F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4157668 5'
5325	18128	30788	0.74	1.0E-43	4885544	NT	Homo sapiens pyruvate dehydrogenase kinase, isoenzyme 3 (PDK3) mRNA
6514	19279	32280	8.45	1.0E-43	4507168	NT	Homo sapiens Sp4 transcription factor (SP4) mRNA
6514	19279	32281	8.45	1.0E-43	4507168	NT	Homo sapiens Sp4 transcription factor (SP4) mRNA
6870	17947	30542	1.36	1.0E-43	R19751.1	EST_HUMAN	Y940e01.r1 Soares infant brain 1N18 Homo sapiens cDNA clone IMAGE:34732 5' similar to
7833	20528	33655	1.13	1.0E-43	AF175265.1	NT	SPBD38_MOUSE P28656 BRAIN PROTEIN DN38 ;
7865	20660		4.03	1.0E-43	AF198490.1	NT	Homo sapiens vacuolar sorting protein 35 (VPS35) mRNA, complete cds
8736	21428	34574	25.49	1.0E-43	AW963676.1	EST_HUMAN	Homo sapiens 8q22.1 region and MTG8 (CBFA2T1) gene, partial cds
10189	22937	36052	0.86	1.0E-43	AW953229.1	EST_HUMAN	EST1375749 MAGE resequences, MAGE Homo sapiens cDNA
10884	23564	36812	8.11	1.0E-43	AI984961.1	EST_HUMAN	EST365296 MAGE resequences, MAGE Homo sapiens cDNA
11338	24028	37332	4.78	1.0E-43	11424378	NT	wr87h01.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2494705 3'
11975	24520		3.04	1.0E-43	AL137964.1	EST_HUMAN	Homo sapiens calcium channel, voltage-dependent, alpha 1E subunit (CACNA1E), mRNA
12253	24999	31079	1.89	1.0E-43	AI675416.1	EST_HUMAN	DKFZp781D1015_r1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp781D1015 5'
							wb68b04.x1 NCI_CGAP_P128 Homo sapiens cDNA clone IMAGE:2313776 3'

Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12469	24835	31032	3.41	9.0E-44	11418322	NT	Homo sapiens cadherin EGF LAG seven-pass G-type receptor 1 (CELSR1), mRNA
870	13639	26309	6.23	8.0E-44	A1222985.1	EST_HUMAN	qh23g01.x1 Scores_NFL_T_GBC S1 Homo sapiens cDNA clone IMAGE:1845552 3'
870	13639	26310	6.23	8.0E-44	A1222985.1	EST_HUMAN	qh23g01.x1 Scores_NFL_T_GBC S1 Homo sapiens cDNA clone IMAGE:1845552 3'
8437	21129	34268	2.67	8.0E-44	X94354.1	NT	Hi.sapiens DNA for Cone cGMP-PDE gene
10236	22884	36097	0.47	8.0E-44	11423497	NT	Homo sapiens small proline-rich protein 2C (SPRR2C), mRNA
10236	22884	36098	0.47	8.0E-44	11423497	NT	Homo sapiens small proline-rich protein 2C (SPRR2C), mRNA
11117	23787	37084	3.78	8.0E-44	Y10498.2	NT	Homo sapiens myosin mRNA, partial cds
11688	24283	37606	1.38	8.0E-44	Z91396.1	NT	Homo sapiens myosin mRNA, partial cds
12207	24673	31073	4.09	8.0E-44	11527389	NT	Homo sapiens putative nuclear protein (HRIHFB2122), mRNA
12248	25009	30978	1.38	8.0E-44	11418086	NT	Homo sapiens putative nuclear protein (PRKCABP), mRNA
12589	25186	30808	2.55	8.0E-44	11418099	NT	ye89a0.1.1 Scores fetal liver spleen 1NFS Homo sapiens cDNA clone IMAGE:124920 5'
844	13423		0.69	7.0E-44	R03035.1	EST_HUMAN	Homo sapiens LIM domain-containing preferred translocation partner in lipoma (LPP) mRNA
2228	14956	27696	1.08	7.0E-44	5031886	NT	Homo sapiens minisatellite ms32 repeat region
2666	15732	28381	2.58	7.0E-44	AF048729.1	NT	Homo sapiens minisatellite ms32 repeat region
2866	15732	28382	2.58	7.0E-44	AF048729.1	NT	Homo sapiens minisatellite ms32 repeat region
3843	16594	29231	2.54	7.0E-44	AL183284.2	NT	Homo sapiens chromosome 21 segment HS21C084
4217	16958	29581	1.12	7.0E-44	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
4217	16958	29582	1.12	7.0E-44	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
5142	17850	30476	1.01	7.0E-44	4505646	NT	Homo sapiens propionin convertase subtilisin/kexin type 2 (PCSK2) mRNA
8085	20779	33908	2.28	7.0E-44	AU159839.1	EST_HUMAN	AU159839 Y79AA1 Homo sapiens cDNA clone Y79AA1000496 3'
6012	18783	31756	0.94	6.0E-44	Z20946.1	EST_HUMAN	HSAAADEYU P, Human fetal Brain Whole tissue Homo sapiens cDNA
11781	24372	37702	1.76	6.0E-44	AW954050.1	EST_HUMAN	EST366120 MAGC resequences, MAGC Homo sapiens cDNA
296	13102		3.3	5.0E-44	AJ289880.1	NT	Homo sapiens KIAA0851 gene (partial), X13 gene and LZTFL1 gene
323	13124		2.72	5.0E-44	AJ289880.1	NT	Homo sapiens KIAA0851 gene (partial), X13 gene and LZTFL1 gene
7788	20483	33607	4.98	5.0E-44	A1568523.1	EST_HUMAN	In40d02.x1 NCL_CGAP_Brm25 Homo sapiens cDNA clone IMAGE:2170083 3' similar to contains OFR.11
9284	22038		2.34	5.0E-44	AU124571.1	EST_HUMAN	OFR OFR repetitive element;
3409	16167	28816	3.75	4.0E-44	AL163303.2	NT	AU124571 NT2RM4 Homo sapiens cDNA clone NT2RM4000218 5'
7370	20050	33131	0.88	4.0E-44	BE883178.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C103
8169	20863	33995	0.76	4.0E-44	BE17948.1	NT	601508601F1 NIH_MGC 71 Homo sapiens cDNA clone IMAGE:3910152 5'
8777	21469		0.51	4.0E-44	BE17948.1	EST_HUMAN	Human fibrillin (FBN1) locus polymorphism
11202	23868	37153	5.38	4.0E-44	U90878.1	NT	RC3-PT0585-010400-023-d08 HT0585 Homo sapiens cDNA
3094	15659	28500	5.77	3.0E-44	AA169851.1	EST_HUMAN	Homo sapiens carboxyl terminal LIM domain protein (CLIM1) mRNA, complete cds zp18b05.r1 Stratiogene fetal retina g37202 Homo sapiens cDNA clone IMAGE:609777 5'

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3870	18020	28260	1.37	3.0E-44	AA337234.1	EST_HUMAN	EST42289 Endometrial tumor Homo sapiens cDNA 5' end similar to similar to alpha-1-antitrypsinase F
9419	22097	35269	0.55	3.0E-44	AF005273.1	NT	Sus scrofa domestica submaxillary apomucin mRNA, complete cds
1027	13787	28446	2.84	2.0E-44	4826685	NT	Homo sapiens DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 1 (DDX1) mRNA
1027	13787	28447	2.84	2.0E-44	4826685	NT	Homo sapiens DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 1 (DDX1) mRNA
1185	13937	26602	3.36	2.0E-44	5803200	NT	Homo sapiens transmembrane trafficking protein (TMP21), mRNA
1185	13937	26603	3.36	2.0E-44	5803200	NT	Homo sapiens transmembrane trafficking protein (TMP21), mRNA
1289	14038	26711	4.08	2.0E-44	AF133588.1	NT	Homo sapiens RAB38 (RAB38) mRNA, complete cds
1347	14095	26770	1.3	2.0E-44	BE465325.1	EST_HUMAN	hw14g06.x1 NCL_GGAP_Lu24 Homo sapiens cDNA clone IMAGE:3182938 3' similar to SW:OXYB_HUMAN
2147	14877	27612	2.22	2.0E-44	AF070651.1	NT	P22059 OXYSTEROL-BINDING PROTEIN ;
2616	15327	28873	1.31	2.0E-44	5901933	NT	Homo sapiens tissue-type bone marrow zinc finger protein 4 mRNA, complete cds
3463	16219	28873	1.13	2.0E-44	D87675.1	NT	Homo sapiens adaptor-related protein complex 4, sigma 1 subunit (CLAPS4), mRNA
4531	17288	28899	1.54	2.0E-44	AW864379.1	EST_HUMAN	Homo sapiens DNA for amyloid precursor protein, complete cds
6004	18785	31747	1.87	2.0E-44	11449901	NT	PM4-SN0016-120500-003-a04 SN0016 Homo sapiens cDNA
6758	17927	30582	3.31	2.0E-44	AF038988.1	NT	Homo sapiens chemokine (C-C motif) receptor 9 (CCR9), mRNA
7313	19986	33074	4.57	2.0E-44	11419228	NT	Homo sapiens general transcription factor 2-J (GTF2J) mRNA, alternatively spliced product, complete cds
7313	19986	33075	4.57	2.0E-44	11419228	NT	Homo sapiens glutamate receptor, metabotropic 3 (GRM3), mRNA
8327	21020	34155	0.87	2.0E-44	7706370	NT	Homo sapiens glutamate receptor, metabotropic 3 (GRM3), mRNA
8327	21020	34156	0.87	2.0E-44	7706370	NT	Homo sapiens vesicle transport-related protein (KIAA0817), mRNA
8517	21209	34352	1.58	2.0E-44	BE388058.1	EST_HUMAN	Homo sapiens vesicle transport-related protein (KIAA0817), mRNA
11883	24456		1.82	2.0E-44	BE244902.1	EST_HUMAN	601286914F1 NIH_MGC 44 Homo sapiens cDNA clone IMAGE:3613688 5'
12760	25020		1.4	2.0E-44	11526283	NT	TCBAP1E2795 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP2795
51	12880	25507	2.43	1.0E-44	7657334	NT	Homo sapiens cat eye syndrome chromosome region, candidate 1 (CECR1), mRNA
51	12880	25508	2.43	1.0E-44	7657334	NT	Homo sapiens Misschappen/NIK-related kinase (MINK), mRNA
596	13347	25975	2.44	1.0E-44	AW853132.1	EST_HUMAN	Homo sapiens Misschappen/NIK-related kinase (MINK), mRNA
1175	13928		1.9	1.0E-44	AW984803.1	EST_HUMAN	RC1-CT0249-030300-026-h12 CT0249 Homo sapiens cDNA
1567	14314		5.78	1.0E-44	AL163303.2	NT	RC1-BN0039-110300-012-b01 BN0039 Homo sapiens cDNA
2221	14949	27887	3.74	1.0E-44	AA434554.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C103
2221	14949	27888	3.74	1.0E-44	AA434554.1	EST_HUMAN	zw53d02.r1 Scores total_fetus_Nb2Hf8_9w Homo sapiens cDNA clone IMAGE:773763 5' similar to contains THR.13 THR repetitive element;
2221	14949	27888	3.74	1.0E-44	AA434554.1	EST_HUMAN	zw53d02.r1 Scores total_fetus_Nb2Hf8_9w Homo sapiens cDNA clone IMAGE:773763 5' similar to contains THR.13 THR repetitive element;

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2280	15590	27746	0.96	1.0E-44	AA398099.1	EST_HUMAN	z188g11.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:729476 5'
2763	15468	28211	1.44	1.0E-44	AF196779.1	NT	Homo sapiens transcription factor IGEM enhancer 3, JM11 protein, JM4 protein, JM5 protein, T54 protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synaptophysin genes, complete cds; and L-type calcium channel a2
3712	16465		3.73	1.0E-44	AA455869.1	EST_HUMAN	aa01c09.s1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:811984 3'
5048	17767	30385	1.04	1.0E-44	AJ130755.1	NT	Homo sapiens alpha satellite DNA, M1 monomer type
5048	17767	30386	1.04	1.0E-44	AJ130755.1	NT	Homo sapiens alpha satellite DNA, M1 monomer type
8163	20857	33988	0.98	1.0E-44	AJ130755.1	EST_HUMAN	ES1379147 MAGE sequences, MAGJ Homo sapiens cDNA
8163	20857	33989	0.98	1.0E-44	AW967073.1	EST_HUMAN	ES1379147 MAGE sequences, MAGJ Homo sapiens cDNA
8544	21236	34380	0.98	1.0E-44	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
8924	21815	34759	0.89	1.0E-44	AJ337183.1	EST_HUMAN	g488g07.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2009828 3'
10936	23616		4.04	1.0E-44	AV714608.1	EST_HUMAN	AV714608 DCB Homo sapiens cDNA clone DCBBYE03 5'
11516	24116	37427	3.92	1.0E-44	10092864	NT	Homo sapiens Sush1 domain (SCR repeat) containing (BK65A6.2), mRNA
11583	24182	37496	3.17	1.0E-44	AW848967.1	EST_HUMAN	RC1-CT0198-150999-071-C08 CT0198 Homo sapiens cDNA
11583	24182	37497	3.17	1.0E-44	AW848967.1	EST_HUMAN	RC1-CT0198-150999-071-C08 CT0198 Homo sapiens cDNA
4539	17274	29906	1.38	9.0E-45	8922391	NT	Homo sapiens hypothetical protein FLJ10379 (FLJ10379), mRNA
4539	17274	29907	1.38	9.0E-45	8922391	NT	Homo sapiens hypothetical protein FLJ10379 (FLJ10379), mRNA
6552	19317	32323	1.31	9.0E-45	AB023212.1	NT	Homo sapiens mRNA for KIAA0995 protein, partial cds
2527	15243	27982	3.12	8.0E-45	5174718	NT	Homo sapiens TRK-fused gene (NOTE: non-standard symbol and name) (TFG) mRNA
5023	17744	30355	6.41	8.0E-45	5174718	NT	Homo sapiens TRK-fused gene (NOTE: non-standard symbol and name) (TFG) mRNA
6414	19182	32181	0.66	8.0E-45	AW892763.1	EST_HUMAN	CM0-NN0005-130300-283-609 NN0005 Homo sapiens cDNA
8006	20701	33630	0.91	8.0E-45	AA377985.1	EST_HUMAN	EST190893 Synovial sarcoma Homo sapiens cDNA 5' end
1545	14291		1.01	6.0E-45	AI675425.1	EST_HUMAN	wb99c06.x1 NCI_CGAP_P728 Homo sapiens cDNA clone IMAGE:2313802 3' similar to contains L1.11 L1 repetitive element
3960	16709		4.09	6.0E-45	AW157570.1	EST_HUMAN	au83h07.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2782909 3' similar to SW.F13A_HUMAN P40429 60S RIBOSOMAL PROTEIN L13A
12555	25378		1.65	6.0E-45	11418213	NT	Homo sapiens ADP-ribosylation factor GTPase activating protein 1 (ARFGAP1), mRNA
872	13641		1.03	5.0E-45	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
1965	14731	27453	3.65	5.0E-45	BF333627.1	EST_HUMAN	CM4-CN0044-180200-516-701 CN0044 Homo sapiens cDNA
3204	15967	28621	1.79	5.0E-45	AI523796.1	EST_HUMAN	tg94f07.x1 NCI_CGAP_OLL1 Homo sapiens cDNA clone IMAGE:2116453 3' similar to SW:PAX1_MOUSE P09084 PAIRED BOX PROTEIN PAX-1
5425	18224	30935	8.76	5.0E-45	AA397781.1	EST_HUMAN	z172d03.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:727877 3' similar to contains element TAR1 repetitive element
5929	18713	31669	1.31	5.0E-45	Y18933.1	NT	Homo sapiens MCP-1 gene and enhancer region

Table 4

Single Exon Probes Expressed In Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5929	18713	31670	1.31	5.0E-45	Y18933.1	NT	Homo sapiens MCP-1 gene and enhancer region
5974	18756	31717	0.79	5.0E-45	AB022318.1	NT	Homo sapiens mRNA for inducible nitric oxide synthase, complete cds
5974	18756	31718	0.79	5.0E-45	AB022318.1	NT	Homo sapiens mRNA for inducible nitric oxide synthase, complete cds
6096	18874	31842	1.02	5.0E-45	11496268	NT	Homo sapiens zinc finger protein 277 (ZNF277), mRNA
6096	18874	31843	1.02	5.0E-45	11496268	NT	Homo sapiens zinc finger protein 277 (ZNF277), mRNA
8174	20868	34000	0.73	5.0E-45	11418704	NT	Homo sapiens bone morphogenetic protein 5 (BMP5), mRNA
8939	21630	34773	1.95	5.0E-45	4759223	NT	Homo sapiens programmed cell death 5 (PDCD5), mRNA
11697	24292	37617	2.59	5.0E-45	8923698	NT	Homo sapiens golgin-like protein (GLP), mRNA
1121	13877	26536	9.58	4.0E-45	X95826.1	NT	H. sapiens ART4 gene
2289	15014	27750	2.42	4.0E-45	BE265622.1	EST_HUMAN	601194440F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3538425 5'
8855	21546		0.82	4.0E-45	AA226220.1	EST_HUMAN	nc26a07 s1 NCI_CGAP_P1 Homo sapiens cDNA clone IMAGE:1009284 similar to contains element L1 repetitive element 1;
4068	16085		1.35	3.0E-45	Y71480.1	EST_HUMAN	yc3507.r1 Soares fetal liver spleen 1NFSL Homo sapiens cDNA clone IMAGE:110245 5'
6142	18920	31890	1.36	3.0E-45	6753651	NT	Mus musculus dynein, axon, heavy chain 11 (Dnahc11), mRNA
6142	18920	31891	1.36	3.0E-45	6753651	NT	Mus musculus dynein, axon, heavy chain 11 (Dnahc11), mRNA
8350	21043		1.4	3.0E-45	AV723976.1	EST_HUMAN	AV723976 HTB Homo sapiens cDNA clone HTBAAG01 5'
8690	21382	34526	3.74	3.0E-45	4759461	NT	Homo sapiens golgi autoantigen, golgin subfamily a, 2 (GOLGA2) mRNA
10208	22854	36068	13.43	3.0E-45	AL163227.2	NT	Homo sapiens chromosome 21 segment HS21C027
10208	22854	36069	13.43	3.0E-45	AL163227.2	NT	Homo sapiens chromosome 21 segment HS21C027
12670	26314		2.35	3.0E-45	X89211.1	NT	H. sapiens DNA for endogenous retroviral like element
2508	18223		2.21	2.0E-45	AL163218.2	NT	Homo sapiens chromosome 21 segment HS21C018
3029	16795	28441	1.22	2.0E-45	AJ243213.1	NT	Homo sapiens partial 5-HT4 receptor gene, exons 2 to 5
6429	19197	32194					
7510	20181	33274	5.15	2.0E-45	L01865.1	NT	Human eosinophil Charcot-Leyden crystal (CLC) protein (lysophospholipase) gene, promoter and exon 1
8314	21007	34145	1.22	2.0E-45	BE782184.1	EST_HUMAN	601467793F1 NIH_MGC_87 Homo sapiens cDNA clone IMAGE:3870838 5'
9485	22138	35318	0.78	2.0E-45	AW834834.1	EST_HUMAN	RCO-LT0001-150200-032-d11 L T0001 Homo sapiens cDNA
10705	25130	36633	0.48	2.0E-45	AJ636786.1	EST_HUMAN	ts56a01.x1 NCI_CGAP_Kid8 Homo sapiens cDNA clone IMAGE:2232552 3'
			18.28	2.0E-45	BE934350.1	EST_HUMAN	MRO-HT0923-190800-201-a02 HT0923 Homo sapiens cDNA
11129	23797	37073					aa87H12.r1 Strabegene fetal retina 937202 Homo sapiens cDNA clone IMAGE:836319 5' similar to
11488	24089	37400	4.16	2.0E-45	AA458770.1	EST_HUMAN	TR.G1144569 G1144569 R-SLY1.;
11488	24089	37401	1.75	2.0E-45	AW270280.1	EST_HUMAN	xp72a03.x1 NCI_CGAP_Ov40 Homo sapiens cDNA clone IMAGE:2745868 3'
12711	24987		1.78	2.0E-45	AW270280.1	EST_HUMAN	xp72a03.x1 NCI_CGAP_Ov40 Homo sapiens cDNA clone IMAGE:2745868 3'
			3.93	2.0E-45	11418157	NT	Homo sapiens calcium channel, voltage-dependent, alpha 11 subunit (CACNA11), mRNA
120	13185		-1.6	1.0E-45	BE389855.1	EST_HUMAN	601284360F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3606183 5'

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
400	13185		2.17	1.0E-45	BE389855.1	EST_HUMAN	601284360F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3806183 5'
460	13245	25887	1.38	1.0E-45	4506412	NT	Homo sapiens RAP1A, member of RAS oncogene family (RAP1A), mRNA
1151	13906	26569	1.79	1.0E-45	7657280	NT	Homo sapiens Langerhans cell specific c-type lectin (LANGERIN), mRNA
3101	15868	28507	7.42	1.0E-45	U32169.1	NT	Human pro- $\alpha 2$ chain of collagen type XI (COL11A2) gene, complete cds
3483	16240	28897	1.38	1.0E-45	8659553	NT	Homo sapiens chromosome 21 open reading frame 1 (C21orf4), mRNA
3560	16315	28962	1.19	1.0E-45	AB046811.1	NT	Homo sapiens mRNA for KIAA1591 protein, partial cds
4442	17178	29804	5.01	1.0E-45	BE396633.1	EST_HUMAN	601289116F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3619803 5'
4677	17411		1.04	1.0E-45	H57443.1	EST_HUMAN	Y05002.1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:204363 5'
7930	20625	33752	0.77	1.0E-45	11422236	NT	Homo sapiens peroxisomal biogenesis factor 14 (PEX14), mRNA
7930	20625	33753	0.77	1.0E-45	11422236	NT	Homo sapiens peroxisomal biogenesis factor 14 (PEX14), mRNA
8505	21197	34341	0.86	1.0E-45	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
9019	21709	34861	5.08	1.0E-45	BE887843.1	EST_HUMAN	601511226F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3912535 5'
9422	22100	35272	1.22	1.0E-45	AB002297.1	NT	Human mRNA for KIAA0269 gene, partial cds
11734	24327	37651	1.33	1.0E-45	7019570	NT	Homo sapiens alpha-catenin-like protein (VR22), mRNA
12087	24592	31125	6.93	1.0E-45	11418099	NT	Homo sapiens protein kinase C, alpha binding protein (PRKCABP), mRNA
12263	24708		11.18	1.0E-45	11526291	NT	Homo sapiens hypothetical protein FLJ20454 (FLJ20454), mRNA
12269	24711		5.28	1.0E-45	11418177	NT	Homo sapiens Ran GTPase activating protein 1 (RANGAP1), mRNA
12680	24969	30991	2.6	1.0E-45	11418157	NT	Homo sapiens calcium channel, voltage-dependent, alpha 11 subunit (CACNA11), mRNA
8127	20821	33958	1.7	9.0E-46	9910293	NT	Mus musculus keratin complex 2, gene 6g (Krt2-6g), mRNA
8532	21224		5.86	9.0E-46	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
10378	23024	36239	11.23	9.0E-46	AW246964.1	EST_HUMAN	2822449 Sprime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2822449 5'
2443	15162	27899	13.53	8.0E-46	AI433261.1	EST_HUMAN	932708.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2132199 3' similar to gb:J00314_rna2
2443	15162	27900	13.53	8.0E-46	AI433261.1	EST_HUMAN	TUBULIN BETA-1 CHAIN (HUMAN);
7953	20648		5.69	8.0E-46	BE187244.1	EST_HUMAN	TUBULIN BETA-1 CHAIN (HUMAN);
2232	14960	27700	1.03	7.0E-46	U46007.1	NT	RC5-HT0506:280200-012-C12 HT0506 Homo sapiens cDNA
4541	17276		3.38	7.0E-46	BE386165.1	EST_HUMAN	Rattus norvegicus espin mRNA, complete cds
4756	17487		1.33	7.0E-46	BE006436.1	EST_HUMAN	601277292F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3618119 5'
5951	18733	31892	4.01	7.0E-46	8922708	NT	RC4-BT0310-110300-015-f10 BT0310 Homo sapiens cDNA
6402	19171	32170	1.14	7.0E-46	BF105845.1	EST_HUMAN	Homo sapiens hypothetical protein FLJ10847 (FLJ10847), mRNA
2759	15464	28207	3.99	6.0E-46	AI884381.1	EST_HUMAN	601822835F1 NIH_MGC_77 Homo sapiens cDNA clone IMAGE:4042736 5'
							wn3108.x1 NCI_CGAP_U14 Homo sapiens cDNA clone IMAGE:2437575 3' similar to contains MER19.12
							MER19 repetitive element;

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Table 4

Single Exon Probes Expressed In Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2759	15484	28208	3.89	6.0E-46	A1894381.1	EST_HUMAN	wm31f08.x1 NCI_CGAP_U14 Homo sapiens cDNA clone IMAGE:2437575 3' similar to contains MER19.12
6038	18818	31779	10.94	6.0E-46	A1635448.1	EST_HUMAN	MER19 repetitive element ; ts58h10.x1 NCI_CGAP_Kid8 Homo sapiens cDNA clone IMAGE:2232835 3' similar to TR:O60363 O60363 SA GENE ;
7116	19804	32868	0.72	6.0E-46	AW513244.1	EST_HUMAN	x042a04.x1 NCI_CGAP_U11 Homo sapiens cDNA clone IMAGE:2706654 3' similar to gb:108069 DNAJ
11384	23175		2.04	6.0E-46	BE784971.1	EST_HUMAN	PROTEIN HOMOLOG 2 (HUMAN);
199	13012		8.9	5.0E-46	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
3519	16275	28929	1.07	6.0E-46	BE677194.1	EST_HUMAN	7d81g01.x1 Lupski_dorsal_root_ganglion Homo sapiens cDNA clone IMAGE:3279408 3'
3519	16275	28930	1.07	6.0E-46	BE677194.1	EST_HUMAN	7d81g01.x1 Lupski_dorsal_root_ganglion Homo sapiens cDNA clone IMAGE:3279408 3'
6836	19398	32413	1.86	5.0E-46	BF590442.1	EST_HUMAN	naa3807.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:4156670 5'
6842	18542	32570	4.29	5.0E-46	BF347229.1	EST_HUMAN	O75202 HOMOLOG OF RAT KIDNEY-SPECIFIC ;
6995	19687	32736	0.62	5.0E-46	AW592253.1	EST_HUMAN	60202184F1 NCI_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4156670 5'
9515	22168	35350	0.47	5.0E-46	AA398381.1	EST_HUMAN	QV4-ST0212-120100-075-f09 ST0212 Homo sapiens cDNA
							z62c08.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:726926 3'
626	13405		1.4	4.0E-46	AA601143.1	EST_HUMAN	nc54a09.s1 NCI_CGAP_SS1 Homo sapiens cDNA clone IMAGE:1104520 3' similar to gb:X63741_rna1 FIBULIN-1, ISOFORM A PRECURSOR (HUMAN);
1699	14442	27140	6.86	4.0E-46	AW770544.1	EST_HUMAN	h186c03.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3008836 3' similar to gb:X14008_rna1 LYSOZYME C PRECURSOR (HUMAN);contains element MER37 repetitive element ;
1699	14442	27141	6.86	4.0E-46	AW770544.1	EST_HUMAN	h186c03.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3008836 3' similar to gb:X14008_rna1 LYSOZYME C PRECURSOR (HUMAN);contains element MER37 repetitive element ;
2743	15449	28188	2.82	4.0E-46	M18048.1	NT	Human endogenous retrovirus RTVL-H2
4384	17121	28753	1.04	4.0E-46	AB014522.1	NT	Homo sapiens mRNA for KIAA0622 protein, partial cds
4384	17121	28754	1.04	4.0E-46	AB014522.1	NT	Homo sapiens mRNA for KIAA0622 protein, partial cds
5350	18153	30834	2.43	4.0E-46	M36852.1	NT	Human Ig germline gamma-3 heavy-chain gene V region, partial cds
5350	18153	30835	2.43	4.0E-46	M36852.1	NT	Human Ig germline gamma-3 heavy-chain gene V region, partial cds
12513	24863	31014	2.71	4.0E-46	AB02059.1	NT	Homo sapiens DNA for Human P2XV, complete cds
2155	14885	27818	0.9	3.0E-46	5453620	NT	Homo sapiens solute carrier family 35 (CMP-sialic acid transporter), member 1 (SLC35A1), mRNA
2429	15150	27884	0.95	3.0E-46	AF160212.1	NT	Homo sapiens VAMP-associated 33 kDa protein mRNA, complete cds
4362	17100	29735	0.79	3.0E-46	4506376	NT	Homo sapiens mitogen-activated protein kinase kinase 3 (MAP4K3), mRNA
4724	17456	30091	1.2	3.0E-46	Z73660.1	NT	H.sapiens Ig lambda light chain variable region gene (7c.11.2) germline; Ig-Lambda; VLambda

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4724	17456	30092	1.2	3.0E-46	Z73660.1	NT	H.sapiens Ig lambda light chain variable region gene (7c.11.2) germline; Ig-Light-Lambda; VLambda
8647	21339	34483	7.59	3.0E-46	A1831462.1	EST_HUMAN	wj49c04.x1 NCI_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2406150 3' similar to contains THR.b2
11564	24163	37474	2.19	3.0E-46	D31765.1	NT	THR repetitive element.
817	13588	26255	7.64	2.0E-46	AA468646.1	EST_HUMAN	Human mRNA for KIAA0081 gene, partial cds
1554	14301		1.55	2.0E-46	AA678246.1	EST_HUMAN	ne06a09.s1 NCI_CGAP_C03 Homo sapiens cDNA clone IMAGE:860408 3' similar to contains THR.b2 THR
1637	14363	27070	3.43	2.0E-46	U78027.1	NT	repetitive element.
4917	17645	30258	1.2	2.0E-46	AA399286.1	EST_HUMAN	z127a11.s1 Soares fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:431986 3'
7384	20664	33142	7.67	2.0E-46	9910569	NT	Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein
7968	20663		1.46	2.0E-46	BE869151.1	EST_HUMAN	(L44L) and FTP3 (FTP3) genes, complete cds
12257	25179		1.5	2.0E-46	H48391.1	EST_HUMAN	z159a02.r1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:726650 5' similar to SW/RSP1_MOUSE
12575	25170	30902	3.38	2.0E-46	AW277214.1	EST_HUMAN	mus musculus sperm tail associated protein (Stap), mRNA
1211	13961	26628	7.67	1.0E-46		EST_HUMAN	601445137F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3849297 5'
1568	14313	26999	1.23	1.0E-46	4502694	NT	y332d01.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:206977 5'
1566	14313	27000	1.23	1.0E-46	7662177	NT	xq78h03.x1 NCI_CGAP_Lu34 Homo sapiens cDNA clone IMAGE:2756789 3'
2279	15005	27745	3.44	1.0E-46	AW978516.1	EST_HUMAN	Homo sapiens cell division cycle 10 (homologous to CDC10 of S. cerevisiae) (CDC10) mRNA
2399	15120	27657	3.06	1.0E-46	H97530.1	EST_HUMAN	Homo sapiens KIAA0555 gene product (KIAA0555), mRNA
3243	16005	28654	4.55	1.0E-46	AA631912.1	EST_HUMAN	Homo sapiens KIAA0555 gene product (KIAA0555), mRNA
4818	17549		3.17	1.0E-46	AB023197.1	NT	EST390625 MAGE resequences, MAGP Homo sapiens cDNA
5613	18409	31322	6.88	1.0E-46	BF194707.1	EST_HUMAN	EST48b095 WATM1 Homo sapiens cDNA clone 48b095
5888	25080	31617	6.14	1.0E-46	8923762	NT	np78b02.s1 NCI_CGAP_Pt2 Homo sapiens cDNA clone IMAGE:1132395 similar to gb:X76717 H.sapiens
5888	25080	31618	6.14	1.0E-46	8923762	NT	MT-11 mRNA. (HUMAN);
10770	18409	31322	5.27	1.0E-46	BF194707.1	EST_HUMAN	Homo sapiens mRNA for KIAA0980 protein, partial cds
11747	24338	37665	1.53	1.0E-46	AW023178.1	EST_HUMAN	Homo sapiens mRNA for KIAA0980 protein, partial cds
11747	24338	37666	1.53	1.0E-46	AW023178.1	EST_HUMAN	7c02b01.x1 NCI_CGAP_Ov18 Homo sapiens cDNA clone IMAGE:3643705 3'
12044	24564	31115	2.28	1.0E-46	BF531102.1	EST_HUMAN	Homo sapiens centaurin-alpha 2 protein (HSA272195), mRNA
12044	24564	31116	2.28	1.0E-46	BF531102.1	EST_HUMAN	Homo sapiens centaurin-alpha 2 protein (HSA272195), mRNA
12778	25032		2.37	1.0E-46	AV715377.1	EST_HUMAN	7c02b01.x1 NCI_CGAP_Ov18 Homo sapiens cDNA clone IMAGE:3643705 3'
750	13522		6.18	9.0E-47	AJ271735.1	NT	df50e03.y1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:2486861 5'

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4879	17606	30229	3.02	9.0E-47	AW770928.1	EST_HUMAN	h93404.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3008534 3' similar to TR:075703 O75703
6284	19057	32037	0.6	9.0E-47	11425439	NT	HYPOTHETICAL 12.4 KD PROTEIN.
12531	25270	30725	2	9.0E-47	11417966	NT	Homo sapiens zinc finger protein ZNF286 (ZNF286), mRNA
1801	14541	27252	6.88	8.0E-47	Y18536.1	NT	Homo sapiens SEC14 (S. cerevisiae)-like 2 (SEC14L2), mRNA
1801	14541	27253	6.88	8.0E-47	Y18536.1	NT	Homo sapiens HLA-C gene, exon 5, individual 19323
2722	15429	28167	1.04	8.0E-47	5453955	NT	Homo sapiens HLA-C gene, exon 5, individual 19323
3024	15790	28438	1.99	8.0E-47	AJ229043.1	NT	Homo sapiens protein phosphatase 2, regulatory subunit B (B56), epsilon isoform (PPP2R5E) mRNA
3613	16366	29009	0.68	8.0E-47	AB041926.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22, segment 3/3
3613	16366	29010	0.68	8.0E-47	AB041926.1	NT	Homo sapiens mRNA for GCK family kinase MINK-2, complete cds
12604	25169		1.38	7.0E-47	AV683284.1	EST_HUMAN	Homo sapiens mRNA for GCK family kinase MINK-2, complete cds
2550	15265	28000	1.66	6.0E-47	AL163246.2	NT	AV683284 GKC Homo sapiens cDNA clone GKCASH11 5'
8592	21284	34423	0.49	6.0E-47	U77054.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C046
9178	21846	35012	6.76	6.0E-47	AI695189.1	EST_HUMAN	HSU77054 Human Homo sapiens cDNA clone NT
9612	22265	35450	0.68	6.0E-47	AB042824.1	NT	ts88h02.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2296659 3'
9612	22265	35451	0.68	6.0E-47	AB042824.1	NT	Homo sapiens RECQL5 beta mRNA for DNA helicase recQ5 beta, complete cds
6482	19249	32249	6.67	5.0E-47	11423972	NT	Homo sapiens RECQL5 beta mRNA for DNA helicase recQ5 beta, complete cds
10696	23387		5.27	5.0E-47	M78590.1	EST_HUMAN	Homo sapiens CDC37 (cell division cycle 37, S. cerevisiae, homolog) (CDC37), mRNA
1379	14126	26801	3.29	4.0E-47	4557656	NT	EST00738 Fetal brain, Stragelene (cat#363206) Homo sapiens cDNA clone HFBCF07
6733	19567	32599	1.9	4.0E-47	BE938896.1	EST_HUMAN	Homo sapiens E1A binding protein p300 (EP300) mRNA
8379	21072	34210	2.42	4.0E-47	BE616483.1	EST_HUMAN	MR4-TN0108-280800-201-404 TN0108 Homo sapiens cDNA
8379	21072	34211	2.42	4.0E-47	BE616483.1	EST_HUMAN	601280486F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3622437 5'
8516	21208	34351	0.61	4.0E-47	AW96377.1	EST_HUMAN	601280486F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3622437 5'
11635	24232		2.83	4.0E-47	AW515509.1	EST_HUMAN	RC3-BN0034-220300-015-105 BN0034 Homo sapiens cDNA
631	13315	25950	2.05	3.0E-47	BE907634.1	EST_HUMAN	xx68b07.x1 NCL_CGAP_Lym12 Homo sapiens cDNA clone IMAGE:2848597 3' similar to SW:INT6_MOUSE
631	13315	25951	2.05	3.0E-47	BE907634.1	EST_HUMAN	O64252 VIRAL INTEGRATION SITE PROTEIN INT-6, [1];
799	13671	26232	6.45	3.0E-47	N57483.1	EST_HUMAN	601497639F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3899721 5'
924	13691	26355	10.25	3.0E-47	AL163284.2	NT	601497639F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3899721 5'
3298	16058	28707	0.79	3.0E-47	4504116	NT	y54b04.s1 Scores_multiple_sclerosis_2NblMSP Homo sapiens cDNA clone IMAGE:277327 3'
3948	16098		5.77	3.0E-47	U93181.1	NT	Homo sapiens chromosome 21 segment HS21C084
4329	17088	28696	1.32	3.0E-47	M12959.1	NT	Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1) mRNA
5922	18707	31659	5.41	3.0E-47	AW408800.1	EST_HUMAN	Homo sapiens nuclear dual-specificity phosphatase (SBF1) mRNA, partial cds
							Human T-cell receptor active alpha-chain mRNA from JM cell line, complete cds
							UI-HF-BM0-adv-d-07-q-UJ.r1 NIH_MGC_38 Homo sapiens cDNA clone IMAGE:3063205 5'

Table 4

Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5822	18707	31660	5.41	3.0E-47	AW408800.1	EST_HUMAN	UI-HF-BMO-adv-d-07-0-JL1 NIH_MGC_38 Homo sapiens cDNA clone IMAGE:3083205 5'
6469	18236		1.76	3.0E-47	A1224213.1	EST_HUMAN	qh04e07.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1843716 3'
8732	21424	34569		3.0E-47	AW963796.1	EST_HUMAN	EST375869 IMAGE resequences, MAGH Homo sapiens cDNA
8732	21424	34570	0.71	3.0E-47	AW963796.1	EST_HUMAN	EST375869 IMAGE resequences, MAGH Homo sapiens cDNA
143	12958	25600	1.61	2.0E-47	4505318	NT	Homo sapiens myosin phosphatase, target subunit 2 (MYPT2), mRNA
947	13713	26377	2.69	2.0E-47	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
947	13713	26378	2.69	2.0E-47	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
1560	14307		0.98	2.0E-47	A163209.2	EST_HUMAN	wq96b02.x1 NCL_CGAP_GC8 Homo sapiens cDNA clone IMAGE:2478851 3'
1588	14334	27022	1.75	2.0E-47	A1969279.1	EST_HUMAN	Homo sapiens KIAA0426 gene product (KIAA0426), mRNA
1873	14418	27111	3.41	2.0E-47	AA524514.1	EST_HUMAN	ng43h12.s1 NCL_CGAP_Cc3 Homo sapiens cDNA clone IMAGE:937607 3'
4313	17052	29677	2	2.0E-47	4504868	NT	Homo sapiens ring finger protein (C3HC4 type) 8 (RNF8), mRNA
4351	17090	29722	1.5	2.0E-47	AA569592.1	EST_HUMAN	nt23g07.s1 NCL_CGAP_P1 Homo sapiens cDNA clone IMAGE:914652
4351	17090	29723	1.5	2.0E-47	AA569592.1	EST_HUMAN	nt23g07.s1 NCL_CGAP_P1 Homo sapiens cDNA clone IMAGE:914652
4471	17206	29832	1.66	2.0E-47	5174648	NT	Homo sapiens Rev/Rex activation domain binding protein-related (RAB-R) mRNA
4761	17493	30121	1.3	2.0E-47	AW965166.1	EST_HUMAN	EST377239 IMAGE resequences, MAGI Homo sapiens cDNA
5699	18490	31411	1.12	2.0E-47	AF073921.1	NT	Homo sapiens regulator of G-protein signaling 6 variant form (RGS6) mRNA, complete cds
5887	18673	31615	1.23	2.0E-47	BE778475.1	EST_HUMAN	601463932F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3867487 5'
5887	18673	31616	1.23	2.0E-47	BE778475.1	EST_HUMAN	601463932F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3867487 5'
7598	25116		1.43	2.0E-47	L09731.1	NT	Homo sapiens 5-hydroxytryptamine 1D receptor pseudogene with an Alu repeat insertion
7864	20559	33685	1.92	2.0E-47	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
7864	20559	33686	1.92	2.0E-47	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
8618	21310	34452	1.67	2.0E-47	AF071771.1	NT	Homo sapiens BTG family, member 3 (BTG3), mRNA
9389	22051	35222	0.77	2.0E-47	11526136	NT	Human tyrosine kinase receptor (axl) mRNA, complete cds
11451	23218	36451	1.27	2.0E-47	M76125.1	NT	Human tyrosine kinase receptor (axl) mRNA, complete cds
12077	25312	30709	1.75	2.0E-47	R42423.1	EST_HUMAN	y92e08.s1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:29966 3' similar to contains OFR repetitive element
1384	14131	26804	7.35	1.0E-47	A1333429.1	EST_HUMAN	qp99h03.x1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:1931189 3'
5017	17738	30347	1.96	1.0E-47	AW813906.1	EST_HUMAN	RC3-ST0197-130400-017-402 ST0197 Homo sapiens cDNA
6944	19426	32441	6.79	1.0E-47	A1880886.1	EST_HUMAN	at19e06.x1 Barslead aorta HPLRB6 Homo sapiens cDNA clone IMAGE:2355588 3' similar to gb:M22985
8767	21459		0.56	1.0E-47	AW684648.1	EST_HUMAN	RAS-RELATED PROTEIN RAP-1A (HUMAN);
10254	22902	36112	2.28	1.0E-47	L30115.1	NT	h184a11.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2978972 3' similar to gb:M26326 KERATIN, TYPE I CYTOSKELETAL 18 (HUMAN);
							Papio hemadys alcohol dehydrogenase class I (ADH) gene, 5' region